

170160

STIC-Biotech/ChemLib

From: Myers, Carla
Sent: Tuesday, November 01, 2005 8:38 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 10788,779

Please search SEQ ID NO: 1-10 (these sequences are primers of 24 to 30 nucleotides) and limit the length of the search hits to 50 nucleotides.

Please provide a printout of the first 40 results.

The CRF has been entered http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10788779

Thank you-

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 11/15/05
Date completed: 11/21/05
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# 10 AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 104
WWW/Internet: _____
Other (Specify): _____

This Page Blank (uspto)



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



This Page Blank (uspto)

**(ORIGINAL COPY
OF THE ORIGINAL
DOCUMENT)**

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 665.886 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGCTACGGCTCCTGGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_to.*

11: gb_sts.*

12: gb_by.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	6	I12894
2	16.2	67.5	26	6	BD271387
3	16.2	67.5	26	6	AX049220
4	16.2	67.5	26	6	AX049825
5	16.2	67.5	26	6	AX050823
6	16.2	67.5	26	6	AX511114
7	16	66.7	38	11	BV142795
8	16	66.7	38	11	BV142796
9	16	66.7	38	11	BV142797
10	16	66.7	38	11	BV142798
11	16	66.7	38	11	BV142799
12	16	66.7	38	11	BV142800
13	16	66.7	38	11	BV142801
14	15	62.5	33	6	AR079445
15	15	62.5	33	6	AR168767
16	15	62.5	33	6	AR217267
17	15	62.5	33	6	AR264164
18	15	62.5	33	6	AR404008
19	15	62.5	33	6	AR406110

20	14.6	60.8	24	6	AX444885
21	14.6	60.8	32	6	A98580
22	14.6	60.8	32	6	E38129
23	14.6	60.8	32	6	AR437122
24	14.4	60.0	32	6	AR143248
25	14.4	60.0	32	6	AR448674
26	14.4	60.0	32	6	BD085791
27	14	58.3	30	6	AX004095
28	13.8	57.5	36	6	AR123280
29	13.6	56.7	21	6	AR393694
30	13.6	56.7	21	6	AX092759
31	13.6	56.7	31	6	AX962045
32	13.6	56.7	40	6	AR095496
33	13.6	56.7	49	6	AR031823
34	13.4	55.8	24	6	AR177808
35	13.4	55.8	24	6	CQ875256
36	13.4	55.8	30	6	AR065612
37	13.4	55.8	30	6	AR448962
38	13.4	55.8	34	6	BD062912
39	13.4	55.8	44	6	AX457963
40	13.4	55.8	50	4	CST438207
41	13.4	55.8	50	6	CQ009087
42	13.2	55.0	19	6	AX129908
43	13.2	55.0	25	6	CQ864330
44	13.2	55.0	25	6	AX476206
45	13.2	55.0	25	6	AX476207

ALIGNMENTS

RESULT 1
LOCUS I12894 24 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 1 from patent US 5429923.
ACCESSION I12894
VERSION I12894.1 GI:910871
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 1 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 1 CAAGGATCGCTACGGCTCCTGGAT 24

RESULT 2
LOCUS BD271387 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Molecular interactions in hematopoietic cells.
ACCESSION BD271387
VERSION BD271387.1 GI:33081155
KEYWORDS JP 2002543825-A/41.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Lu,P.S.

TITLE Molecular interactions in hematopoietic cells
JOURNAL Patent: JP 2002543825-A 41 24-DEC-2002;
COMMENT ARBOR VITA CORP
 OS Artificial Sequence
 PN JP 2002543825-A/41
 PD 24-DEC-2002
 PF 12-MAY-2000 JP 2000618312
 PR 14-MAY-1999 US 60/134114, 14-MAY-1999 US 60/134117 PR
 14-MAY-1999 US 60/134118, 21-OCT-1999 US 60/160860 PR
 29-OCT-1999 US 60/162498, 13-DEC-1999 US 60/170453 PR
 14-JAN-2000 US 60/176195, 14-FEB-2000 US 60/182296 PR
 11-APR-2000 US 09/547276, 11-APR-2000 US 60/196460 PR
 11-APR-2000 US 60/196528, 11-APR-2000 US 60/196 527 PR
 11-APR-2000 US 60/196287
 PI PETER S LU
 PC C12N5/06, A61K45/00, A61P7/00, A61P29/00, A61P37/06, A61P43/00, PC
 C12N5/00
 CC Description of Artificial Sequence: primer
 FH Key Location/Qualifiers
 FT source 1. .26
FEATURES Location/Qualifiers
 source 1. .26
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
ORIGIN
 Query Match 67.5%; Score 16.2; DB 6; Length 26;
 Best Local Similarity 85.7%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGGCTCCTCG 22
 Db 2 AAGGATCCCTCCGGCTCCTCG 22
RESULT 3
 AX049220
 LOCUS AX049220 26 bp DNA linear PAT 12-JAN-2001
 DEFINITION Sequence 329 from Patent WO0069896.
 ACCESSION AX049220
 VERSION AX049220.1 GI:12226040
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Lu, P.S.
 TITLE Molecular interactions in hematopoietic cells
 JOURNAL Patent: WO 0069896-A 329 23-NOV-2000;
 ARBOR VITA CORPORATION (US)
FEATURES Location/Qualifiers
 source 1. .26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"
ORIGIN
 Query Match 67.5%; Score 16.2; DB 6; Length 26;
 Best Local Similarity 85.7%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGGCTCCTCG 22
 Db 2 AAGGATCCCTCCGGCTCCTCG 22
RESULT 4
 AX049825
 LOCUS AX049825 26 bp DNA linear PAT 12-JAN-2001
 DEFINITION Sequence 329 from Patent WO0069898.
 ACCESSION AX049825
 VERSION AX049825.1 GI:12226255
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Rabinowitz, J.D., Lu, P.S. and Schweizer, J.
 TITLE Molecular interactions in hematopoietic cells

ACCESSION AX049825
VERSION AX049825.1 GI:12226255
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lu, P.S.
TITLE Molecular interactions in allergy cells
JOURNAL Patent: WO 0069898-A 329 23-NOV-2000;
 Arbor Vita Corporation (US)
FEATURES Location/Qualifiers
 source 1. .26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"
ORIGIN
 Query Match 67.5%; Score 16.2; DB 6; Length 26;
 Best Local Similarity 85.7%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGGCTCCTCG 22
 Db 2 AAGGATCCCTCCGGCTCCTCG 22
RESULT 5
 AX050823
 LOCUS AX050823 26 bp DNA linear PAT 12-JAN-2001
 DEFINITION Sequence 329 from Patent WO0069897.
 ACCESSION AX050823
 VERSION AX050823.1 GI:12226738
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Lu, P.S.
 TITLE Molecular interactions in t cells
 JOURNAL Patent: WO 0069897-A 329 23-NOV-2000;
 Arbor Vita Corporation (US)
FEATURES Location/Qualifiers
 source 1. .26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"
ORIGIN
 Query Match 67.5%; Score 16.2; DB 6; Length 26;
 Best Local Similarity 85.7%; Pred. No. 9.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 AAGGATCGCTACGGCTCCTCG 22
 Db 2 AAGGATCCCTCCGGCTCCTCG 22
RESULT 6
 AX511114
 LOCUS AX511114 26 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 362 from Patent WO0231512.
 ACCESSION AX511114
 VERSION AX511114.1 GI:23392022
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Rabinowitz, J.D., Lu, P.S. and Schweizer, J.
 TITLE Molecular interactions in hematopoietic cells

```

JOURNAL Patent: WO 0231512-A 362 18-APR-2002;
FEATURES   Arbor Vita Corporation (US)
source     Location/Qualifiers
1. .26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="158KIF forward primer"

ORIGIN
Query Match 67.5%; Score 16.2; DB 6; Length 26;
Best Local Similarity 85.7%; Pred. No. 9.8e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

Qy 2 AAGGATCGCTACGGCTCCTGG 22
||||| ||| |||||
Db 2 AAGGATCCCTCCGGCTCCTCG 22

RESULT 7
BV142795 38 bp DNA linear STS 05-MAY-2004
LOCUS PZ02991 Zea mays ssp. mays Oh43 Zea mays Oh43 Zea mays STS genomic,
DEFINITION sequence tagged site.
ACCESSION BV142795
VERSION BV142795.1 GI:47024996
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 38)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Contact: Brandon S. Gaut
TITLE Dept. Ecology and Evolutionary Biology
JOURNAL U.C. Irvine
COMMENT 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttctctcaagcag
Primer B: gtacgtttatttcgacaagcagcc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 47 56 62 62 50 50 52 59 67 55 59 52 53
51 46 55 52 35 23 35 35 38 42 35 35 26 26 26 48 44 44
57 52 52.
Location/Qualifiers
1. .38
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="OH43"

FEATURES
source
/db_xref="taxon:4577"
/clone_lib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .38

ORIGIN
Query Match 66.7%; Score 16; DB 11; Length 38;
Best Local Similarity 79.2%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
||||| ||| |||||
Db 10 CAAGAACCCTGCGGCGCGGAT 33

RESULT 8
BV142796 38 bp DNA linear STS 05-MAY-2004
LOCUS PZ02991 Zea mays ssp. mays Mol7(1) Zea mays Mol7(1) Zea mays STS
DEFINITION genomic, sequence tagged site.
ACCESSION BV142796
VERSION BV142796.1 GI:47024997
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 38)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Contact: Brandon S. Gaut
TITLE Dept. Ecology and Evolutionary Biology
JOURNAL U.C. Irvine
COMMENT 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttctctcaagcag
Primer B: gtacgtttatttcgacaagcagcc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 59 69 66 64 52 52 41 51 49 61 60 68 69
69 60 54 57 57 52 55 61 58 57 51 47 58 63 70 77 77 72 72 67
64 68 66.
Location/Qualifiers
1. .38
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Mol7(1)"
/db_xref="taxon:4577"
/clone_lib="Zea mays Mol7(1)"
/dev_stage="seedling"

FEATURES
source

```

```
/note="Organ: leaf; genomic DNA from inbred line"  
<1. .>38
```

SIS	acc=0.98; pos=1.00; genomic DNA from induced line					
ORIGIN	<1..>38					
Query Match	66.7%	Score 16;	DB 11;	Length 38;		
Best Local Similarity	79.2%;	Pred. No.	1.2e+04;			
Matches	19;	Conservative	0;	Mismatches	5;	Indels
					0;	Gaps
						0;
Qy	1	CAAGGATCGCTACGGCTCCTGGAT	24			
Db	10	CAAGAACCCTTCGGCGCCGGGAT	33			

[illegible]

Contact: Brandon S. Gaut.
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Tel: (949) 824-2181
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatggagaagttcctccaagcag
Primer B: gtacgtttatttcacaaagcgc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequencing ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 50 61 61 55 55 63 60 51 50 50 50
50 51 39 51 43 23 19 29 29 35 32 28 28 23 23 35 35 42 33 56
53 55 48.

```

33 33 40. Location/Qualifiers
source
1. .38
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Mol7(2)"
/db_xref="taxon:4577"
/clone_lib="Zea mays Mol7(2)"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>38
STS

```

```

Query Match      66.7%; Score 16; DB 11; Length 38;
Best Local Similarity 79.2%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTTGAT 24
    ||||| ||||| ||||| |||||
Db 10 CAAGAACCCTGTCGGCGCCGGGAT 33
    ||||| ||||| ||||| |||||

```

RESULT	10
LOCUS	BV142798
DEFINITION	P202991 Zea mays ssp. mays CML69 Zea mays STS genomic, sequence tagged site.
ACCESSION	BV142798
VERSION	BV142798.1
KEYWORDS	GI:47024999
SOURCE	Zea mays
ORGANISM	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 38) McMullen,M.D., Vroeh Bi,I., Schroeder,S.S. and Gaut,B.S. MPZ-UCI Joint SNP Discovery Unpublished (2003)
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Contact: Brandon S. Gaut.
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Tel: (949) 824-2181
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: gagatgagagaagttcctccaagcag
Primer B: gtacgtttttattcacagcagcc
STS size: 38
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase
Sequence ran on ABI 3700 sequencer.

[illegible]

```

43 44 45 46.
FEATURES
  source
    Location/Qualifiers
      1..38
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /cultivar="CML69"
        /db_xref="taxon:4577"
        /clone_lib="Zea mays CML69"
        /dev_stage="seedling"
        /note="Organ: leaf; genomic DNA from inbred line"
      <1..>38
    STS
    ORIGIN
      Query Match          66.7%;   Score 16;   DB 11;   Length 38;
      Best Local Similarity 79.2%;   Pred. No. 1.2e+04;

```

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
 ||||| ||||| ||||| ||||| |||||
 Db 10 CAAGAACCGCTCGCGCGCGGAT 33

RESULT 11
 BV142799
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays subsp. parviglumis
 Zea mays subsp. parviglumis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 38)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)
 CONTACT: Brandon S. Gaut
 Dept.: Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: gagatgagaagtctcctcaagcag
 Primer B: gtacgtttattgacacagcgc
 STS size: 38
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)
 PHRED/PHRAP Quality Scores 84 77 75 80 73 65 61 68 85 79 77 77 72
 70 74 69 72 71 66 69 81 77 77 77 72 75 79 77 82 82 90 82 82 82
 85 85 85.

FEATURES
 source
 1..38
 Location/Qualifiers
 /organism="Zea mays subsp. parviglumis"
 /mol_type="genomic DNA"
 /cultivar="teol"
 /db_xref="taxon:76912"
 /clone_lib="Zea mays JSGyLOS 130"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA"
 <1..>38

STS
 ORIGIN
 Query Match 66.7%; Score 16; DB 11; Length 38;
 Best Local Similarity 79.2%; Pred. No. 1.2e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24

Db 10 CAAGAACCGCTCGCGCGCGGAT 33
 ||||| ||||| ||||| ||||| |||||

RESULT 12
 BV142800
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Zea mays subsp. parviglumis
 Zea mays subsp. parviglumis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 38)
 McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
 MPZ-UCI Joint SNP Discovery
 Unpublished (2003)
 CONTACT: Brandon S. Gaut
 Dept.: Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: gagatgagaagtctcctcaagcag
 Primer B: gtacgtttattgacacagcgc
 STS size: 38
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 67 56 55 55 55 60 55 64 37 40 40 40
 24 24 24 29 25 33 28 35 35 35 23 23 23 35 38 37 37 37 56 57
 57 58 57.

FEATURES
 source
 1..38
 Location/Qualifiers
 /organism="Zea mays subsp. parviglumis"
 /mol_type="genomic DNA"
 /cultivar="teol"
 /db_xref="taxon:76912"
 /clone_lib="Zea mays USDA PI566686"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA"
 <1..>38

STS
 ORIGIN
 Query Match 66.7%; Score 16; DB 11; Length 38;
 Best Local Similarity 79.2%; Pred. No. 1.2e+04;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
 ||||| ||||| ||||| ||||| |||||
 Db 10 CAAGAACCGCTCGCGCGCGGAT 33

```

RESULT 13
BV142801
LOCUS
DEFINITION
  BV142801
  38 bp
  DNA
  linear
  STS 05-MAY-2004
  Zea mays subsp. parviglumis Wilkes Site 6 Zea mays Wilkes
  Site 6 Zea mays subsp. parviglumis STS genomic, sequence tagged
  site.
ACCESSION
  BV142801
  GI:47025002
VERSION
  BV142801.1
  GI:47025002
KEYWORDS
  STS.
SOURCE
  Zea mays subsp. parviglumis
  Zea mays subsp. parviglumis
  Zea mays subsp. parviglumis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 38)
REFERENCE
  McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
  MP2-UCI Joint SNP Discovery
  Unpublished (2003)
COMMENT
  Contact: Brandon S. Gaut
  Dept. Ecology and Evolutionary Biology
  U.C. Irvine
  321 Steinhaus Hall, Irvine, CA 92697-2525, USA
  Tel: (949) 824-2564
  Fax: (949) 824-2181
  Email: bgaut@uci.edu
  Primer A: gagatggagaagtctctcaagcag
  Primer B: gtacgttttatttcgacaagcagcc
  STS size: 38
Protocol:
  PCR amplification of genomic DNA
  Template: 50 ng
  Primer: each 0.5 uM
  dNTPs: each 200 uM
  Taq Polymerase: RedTaq (Sigma)
  Total Vol: 10 ul
  Amplicon sequencing
  ABI protocol - using d-Rhodamine terminator cycle
  sequencing ready reaction with ampliTaq DNA polymerase FS
  Sequence ran on ABI 3700 sequencer.
Buffer:
  Genomic DNA amplification
  RedTaq (Sigma)
  Sequencing buffer
  d-Rhodamine kit (ABI)
PHRED/PHRAP Quality Scores 44 46 40 46 56 56 40 40 40 30 30 30
33 19 19 27 34 42 43 38 42 36 44 44 44 44 44 44 44 48 48 43 36
42 38 29.
FEATURES
  source
  1. 38
  /organism="Zea mays subsp. parviglumis"
  /mol_type="genomic DNA"
  /cultiivar="teol7"
  /db xref="taxon:76912"
  /clone lib="Zea mays Wilkes Site 6"
  /dev stage="seedling"
  /note="Organ: leaf; genomic DNA"
  <1. .>38
STS
ORIGIN
  Query Match 66.7%; Score 16; DB 11; Length 38;
  Best Local Similarity 79.2%; Pred. No. 1.2e+04;
  Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 10 CAAGAACCGCTGCGCGCGCGGAT 33
  ||||| ||||| ||||| |||||

```

```

RESULT 14
AR079445
LOCUS
DEFINITION
  AR079445
  33 bp
  DNA
  linear
  PAT 31-AUG-2000
  Sequence 12 from patent US 5965528.
ACCESSION
  AR079445
  GI:10006190
VERSION
  AR079445.1
  GI:10006190
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unknown.
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita,R.A.
  TITLE
  Recombinant human alpha-fetoprotein as an immunosuppressive agent
  JOURNAL
  Patent: US 5965528-A 12 12-OCT-1999;
  FEATURES
  Location/Qualifiers
  source
  1. 33
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN
  Query Match 62.5%; Score 15; DB 6; Length 33;
  Best Local Similarity 78.3%; Pred. No. 3.7e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 2 AAGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 5 AAGATCCTTAGCTCTCCTGGAT 27
  ||||| ||||| ||||| |||||
RESULT 15
AR168767
LOCUS
DEFINITION
  AR168767
  33 bp
  DNA
  linear
  PAT 17-DEC-2001
  Sequence 12 from patent US 6288034.
ACCESSION
  AR168767
  GI:17904858
VERSION
  AR168767.1
  GI:17904858
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unknown.
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita,R.A.
  TITLE
  Recombinant human alpha-fetoprotein as an immunosuppressive agent
  JOURNAL
  Patent: US 6288034-A 12 11-SEP-2001;
  FEATURES
  Location/Qualifiers
  source
  1. 33
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN
  Query Match 62.5%; Score 15; DB 6; Length 33;
  Best Local Similarity 78.3%; Pred. No. 3.7e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 2 AAGATCGCTACGGCTCCTGGAT 24
  ||||| ||||| ||||| |||||
  Db 5 AAGATCCTTAGCTCTCCTGGAT 27
  ||||| ||||| ||||| |||||
RESULT 16
AR217267
LOCUS
DEFINITION
  AR217267
  33 bp
  DNA
  linear
  PAT 25-SEP-2002
  Sequence 13 from patent US 6416734.
ACCESSION
  AR217267
  GI:23316737
VERSION
  AR217267.1
  GI:23316737
KEYWORDS
  .
SOURCE
  Unknown.
  ORGANISM
  Unknown.
  Unclassified.
  1 (bases 1 to 33)
REFERENCE
  Murgita,R.A.
  TITLE
  Recombinant alpha-fetoprotein for treating and diagnosing cancers
  JOURNAL
  Patent: US 6416734-A 13 09-JUL-2002;
  FEATURES
  Location/Qualifiers

```


1 (pages 1 to 32)	Wurst, W.D. and Prochiantz, A.D.	Method for the identification of target genes for transcription
REFERENCES	AUTHORS	TITLE

factors		REFERENCE		1 (bases 1 to 32)				
JOURNAL	Patent: EP 0902092-A 5 17-MAR-1999;	AUTHORS	Wurst,W. and Prochiantz,A.					
FEATURES	GSF FORSCHUNGSZENTRUM UMWELT (DE); CENTRE NAT RECH SCIENT (FR)	TITLE	Method for identification of target genes of transcription factors					
source	Location/Qualifiers	JOURNAL	Patent: US 6656735-A 5 02-DEC-2003;					
	1. .32	FEATURES	Location/Qualifiers					
	/organism="unidentified"	source	1. .32					
	/mol_type="unassigned DNA"		/organism="unknown"					
	/db_xref="taxon:32644"		/mol_type="genomic DNA"					
ORIGIN								
Query Match		60.8%;		Score 14.6; DB 6; Length 32;				
Best Local Similarity		81.0%;		Pred. No. 5.9e+04;				
Matches	17; Conservative		0; Mismatches	4; Indels	0; Gaps 0;			
QY	4 GGATCGCTACGGCTCCTGGAT 24							
Db	4 GGATCCCTACGCCTTCTTGAT 24							
RESULT 22								
LOCUS	E38129	AR143248/c	32 bp	DNA	linear PAT 18-JUN-2001			
DEFINITION	Method for identifying target gene of transcription factor.							
ACCESSION	E38129	Sequence	44	from patent	US 6204232.			
VERSION	E38129.1	AR143248						
KEYWORDS	JP 1999187876-A/5.	AR143248.1	GI:15104534					
SOURCE	unidentified							
ORGANISM	unclassified.							
REFERENCE	1 (bases 1 to 32)							
AUTHORS	Borufugangu,B. and Alan,P.							
TITLE	Method for identifying target gene of transcription factor							
JOURNAL	Patent: JP 1999187876-A 5 13-JUL-1999;							
COMMENT								
OS	Unidentified							
PN	JP 1999187876-A/5							
PD	13-JUL-1999							
PF	14-SEP-1998 JP 1998260205							
PR	15-SEP-1997 DE 19740578.9							
PI	BORUFUGANGU BURUSUTO,ALAN PLOSIANZ							
PC	C12N15/09,C12N15/00							
CC	Strandedness: Double;							
CC	Topology: Linear;							
FH	Key							
FT	Location/Qualifiers							
FT	1. .32							
source	Location/Qualifiers							
1. .32	/organism="Unidentified".							
/organism="unidentified"								
/mol_type="genomic DNA"								
/db_xref="taxon:32644"								
ORIGIN								
Query Match		60.8%;		Score 14.6; DB 6; Length 32;				
Best Local Similarity		81.0%;		Pred. No. 5.9e+04;				
Matches	17; Conservative		0; Mismatches	4; Indels	0; Gaps 0;			
QY	4 GGATCGCTACGGCTCCTGGAT 24							
Db	4 GGATCCCTACGCCTTCTTGAT 24							
RESULT 23								
LOCUS	AR437122	AR437122	32 bp	DNA	linear PAT 18-DEC-2003			
DEFINITION	Sequence 5 from patent US 6656735.							
ACCESSION	AR437122							
VERSION	AR437122.1	GI:40200206						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
Query Match		60.0%;		Score 14.4; DB 6; Length 32;				
Best Local Similarity		75.0%;		Pred. No. 7.4e+04;				
Matches	18; Conservative		0; Mismatches	6; Indels	0; Gaps 0;			

factors		REFERENCE		1 (bases 1 to 32)				
JOURNAL	Patent: EP 0902092-A 5 17-MAR-1999;	AUTHORS	Wurst,W. and Prochiantz,A.					
FEATURES	GSF FORSCHUNGSZENTRUM UMWELT (DE); CENTRE NAT RECH SCIENT (FR)	TITLE	Method for identification of target genes of transcription factors					
source	Location/Qualifiers	JOURNAL	Patent: US 6656735-A 5 02-DEC-2003;					
	1. .32	FEATURES	Location/Qualifiers					
	/organism="unidentified"	source	1. .32					
	/mol_type="unassigned DNA"		/organism="unknown"					
	/db_xref="taxon:32644"		/mol_type="genomic DNA"					
ORIGIN								
Query Match		60.8%;		Score 14.6; DB 6; Length 32;				
Best Local Similarity		81.0%;		Pred. No. 5.9e+04;				
Matches	17; Conservative		0; Mismatches	4; Indels	0; Gaps 0;			
QY	4 GGATCGCTACGGCTCCTGGAT 24							
Db	4 GGATCCCTACGCCTTCTTGAT 24							
RESULT 22								
LOCUS	E38129	AR143248/c	32 bp	DNA	linear PAT 18-JUN-2001			
DEFINITION	Method for identifying target gene of transcription factor.							
ACCESSION	E38129	Sequence	44	from patent	US 6204232.			
VERSION	E38129.1	AR143248						
KEYWORDS	JP 1999187876-A/5.	AR143248.1	GI:15104534					
SOURCE	unidentified							
ORGANISM	unclassified.							
REFERENCE	1 (bases 1 to 32)							
AUTHORS	Borufugangu,B. and Alan,P.							
TITLE	Method for identifying target gene of transcription factor							
JOURNAL	Patent: JP 1999187876-A 5 13-JUL-1999;							
COMMENT								
OS	Unidentified							
PN	JP 1999187876-A/5							
PD	13-JUL-1999							
PF	14-SEP-1998 JP 1998260205							
PR	15-SEP-1997 DE 19740578.9							
PI	BORUFUGANGU BURUSUTO,ALAN PLOSIANZ							
PC	C12N15/09,C12N15/00							
CC	Strandedness: Double;							
CC	Topology: Linear;							
FH	Key							
FT	Location/Qualifiers							
FT	1. .32							
source	Location/Qualifiers							
1. .32	/organism="Unidentified".							
/organism="unidentified"								
/mol_type="genomic DNA"								
/db_xref="taxon:32644"								
ORIGIN								
Query Match		60.8%;		Score 14.6; DB 6; Length 32;				
Best Local Similarity		81.0%;		Pred. No. 5.9e+04;				
Matches	17; Conservative		0; Mismatches	4; Indels	0; Gaps 0;			
QY	4 GGATCGCTACGGCTCCTGGAT 24							
Db	4 GGATCCCTACGCCTTCTTGAT 24							
RESULT 23								
LOCUS	AR437122	AR437122	32 bp	DNA	linear PAT 18-DEC-2003			
DEFINITION	Sequence 5 from patent US 6656735.							
ACCESSION	AR437122							
VERSION	AR437122.1	GI:40200206						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
Query Match		60.0%;		Score 14.4; DB 6; Length 32;				
Best Local Similarity		75.0%;		Pred. No. 7.4e+04;				
Matches	18; Conservative		0; Mismatches	6; Indels	0; Gaps 0;			

[illegible]

Query Match 55.8%; Score 13.4; DB 6; Length 24;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTGGAT 24
||||| ||||| ||||| ||||| |||||
Db 2 AAGGATCGCTACCAACCCCTTGGT 24

RESULT 35
CQ875256/c
LOCUS CQ875256 24 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 162 from Patent WO2004075733.
ACCESSION CQ875256
VERSION CQ875256.1 GI:52748344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Greinwald,J.H., Wenstrup,R.J., Aronow,B.J. and Peetian,J.P.
TITLE Construction of a deafness gene chip
JOURNAL Patent: WO 2004075733-A 162 10-SEP-2004;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer sequence"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 24;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGGA 23
||||| ||||| ||||| ||||| |||||
Db 24 CAAGTAICTGTATGGCTCTAGGA 2

RESULT 36
AR065612
LOCUS AR065612 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849534.
ACCESSION AR065612
VERSION AR065612.1 GI:5995828
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
AUTHORS Grotendorst,G.R. and Iida,N.
TITLE DNA encoding leukocyte derived growth factor-2 (LDGF-2)
JOURNAL Patent: US 5849534-A 11 15-DEC-1998;
FEATURES
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 30;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGGA 23
||||| ||||| ||||| ||||| |||||
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 37
AR448962
LOCUS AR448962 30 bp mRNA linear PAT 20-FEB-2004

DEFINITION Sequence 11 from patent US 6673893.
ACCESSION AR448962
VERSION AR448962.1 GI:42677748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Grotendorst,G.R. and Iida,N.
TITLE Leukocyte derived growth factor 2
JOURNAL Patent: US 6673893-A 11 06-JAN-2004;
FEATURES
source
1..30
/organism="unknown"
/mol_type="mRNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 30;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGGA 23
||||| ||||| ||||| ||||| |||||
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 38
BD062912
LOCUS BD062912 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Thermostable phosphatases.
ACCESSION BD062912
VERSION BD062912.1 GI:22608515
KEYWORDS JP 2001510983-A/12.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Mathur,E.J., Lee,E. and Bylina,E.
TITLE Thermostable phosphatases
JOURNAL Patent: JP 2001510983-A 12 07-AUG-2001;
COMMENT DIVERSA CORP
PN JP 2001510983-A/12
PD 07-AUG-2001
PF 19-JUN-1997 JP 1998503409
PR 19-JUN-1996 US 60/033752
PI ERIC J MATHUR,EDD LEE,EDWARD BYLINA
PC A61K38/46.C07H19/00.C07H21/02.C07H21/04.C12N9/14.C12N1/20, PC
C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1..34
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 34;
Best Local Similarity 73.9%; Pred. No. 2.3e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTCGGA 23
||||| ||||| ||||| ||||| |||||
Db 2 CGAGGATCCTTAAGGCTTCTCGA 24

RESULT 39
AX457963
LOCUS AX457963 44 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 5 from Patent WO0246456.
ACCESSION AX457963
VERSION AX457963.1 GI:21724858

Search completed: November 18, 2005, 17:42:46
Job time : 667.986 secs

```
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Mayer, P.
TITLE       Isothermal amplification of nucleic acids on a solid support
JOURNAL     Patent: WO 0246456-A 5 13-JUN-2002;
            Applied Research Systems' ARS Holding N.V. (AN)
FEATURES
  source
    1..44
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="synthetic construct"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 44;
Best Local Similarity 73.9%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 AAGATCGTACGGCTCTGGAT 24
      ||||| | | | | | | | |
Db      17 AAGGAGGATCCGCTCTGGGT 39

RESULT 40
CST438207
LOCUS      Chrysochloris stuhlmanni partial prmp gene for prion protein.
DEFINITION
ACCESSION  AJ438207
VERSION    AJ438207.1 GI:22798965
KEYWORDS   prion protein; prmp gene.
SOURCE     Chrysochloris stuhlmanni
            Chrysochloris stuhlmanni
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Insectivora; Chrysochloridae; Chrysochloris.
REFERENCE   1
AUTHORS     Poux, C., Van Rheede, T., Madsen, O. and De Jong, W.W.
TITLE       Sequence gaps join mice and men: phylogenetic evidence from
            deletions in two proteins
JOURNAL     Mol. Biol. Evol. 19 (11), 2035-2037 (2002)
MEDLINE    22300338
PUBMED     12411613
REFERENCE   2 (bases 1 to 50)
AUTHORS     Poux, C.
TITLE       Direct Submission
JOURNAL     Submitted (06-MAR-2002) Poux C., Biochemistry (161), University of
            Nijmegen, NCMLS, PO Box 9101, 6500 HB Nijmegen, NETHERLANDS
FEATURES
  source
    1..50
    /organism="Chrysochloris stuhlmanni"
    /mol_type="genomic DNA"
    /db_xref="taxon:185454"
  gene
    1..50
    /gene="prmp"
  CDS
    1..>50
    /gene="prmp"
    /codon_start=1
    /product="prion protein"
    /protein_id="CAD27292.1"
    /db_xref="GI:22798966"
    /db_xref="UniProt/TREMBL:Q8MIG7"
    /translation="MWKSGIGCWILLFMAT"

ORIGIN
Query Match      55.8%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 AAGATCGTACGGCTCTGGAT 24
      ||||| | | | | | | | |
Db      7 AAGAGTGGCTTGGGCTCTGGAT 29
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGATGCTACGGCTCTCTGGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	2	AAQ91121
2	24	100.0	24	9	ACA63111
3	24	100.0	24	13	ADR05297
4	16.4	68.3	33	11	ADM68395
5	16.2	67.5	26	4	AAF16851
6	16.2	67.5	26	4	AAF17495
7	16.2	67.5	26	4	AAAC99432
8	16.2	67.5	26	6	ABT06636
9	16.2	67.5	26	6	ABQ96682
10	15.2	63.3	24	10	ADJ80120
11	15.2	63.3	25	9	ACK06221
12	15.2	63.3	25	9	ACK05595
13	15	62.5	33	2	AAT35182
14	15	62.5	33	6	ABZ70298
15	15	62.5	36	2	ABQ04591
16	14.6	60.8	24	6	ABQ01333
17	14.6	60.8	24	6	ABQ06613
18	14.6	60.8	24	6	ABQ06654
19	14.6	60.8	25	9	ACK06282
20	14.6	60.8	32	2	AAX22971

21	14.6	60.8	36	3	AAA76301
22	14.4	60.0	31	8	ACD54952
23	14.4	60.0	31	12	ADM63061
24	14.4	60.0	32	2	AAX59667
25	14.4	60.0	33	6	ABQ83921
26	14.4	60.0	33	6	ABQ50283
27	14.4	60.0	33	8	ABX12001
28	14.2	59.2	25	9	ACI28366
29	14	58.3	26	10	AAD59416
30	14	58.3	30	2	AAX57219
31	14	58.3	32	12	ADO43696
32	14	58.3	33	6	ABX14381
33	13.8	57.5	22	3	AAZ35063
34	13.8	57.5	36	2	AAT34298
35	13.6	56.7	21	3	AAC69334
36	13.6	56.7	21	4	AAF93000
37	13.6	56.7	25	9	ACK06220
38	13.6	56.7	25	9	ACI04808
39	13.6	56.7	25	9	ACK05594
40	13.6	56.7	28	2	AAZ35681
41	13.6	56.7	31	6	ABS79090
42	13.6	56.7	31	6	ADE71167
43	13.6	56.7	31	10	ACD27669
44	13.6	56.7	31	12	ADI00667
45	13.6	56.7	33	6	ABZ21018

ALIGNMENTS

RESULT 1

AAQ91121
ID AAQ91121 standard; cdna; 24 BP.

XX
AC AAQ91121;

XX
DT 19-FEB-1996 (first entry)

XX
DE Beta-cardiac myosin heavy chain PCR primer A.

XX
KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.

XX
OS Synthetic.

XX
PN US5429923-A.

XX
PD 04-JUL-1995.

XX
PF 11-DEC-1992; 92US-00989160.

XX
PR 11-DEC-1992; 92US-00989160.

XX
PA (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GHEO-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX
PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX
WP1; 1995-245715/32.

XX
PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

XX
PS Example 1; Col 10; 22pp; English.

XX
CC AAQ91121-091130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 CC
 CC Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
 |||||
 Db 1 CAAGGATCGCTACGGCTCCTGGAT 24

RESULT 2

ACA63111
 ID ACA63111 standard; DNA; 24 BP.

AC ACA63111;

DT 28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer A.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

XX US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 FT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain cDNA containing an FHC-associated mutation

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 9; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
 |||||

Db 1 CAAGGATCGCTACGGCTCCTGGAT 24

RESULT 3

ADR05297
 ID ADR05297 standard; DNA; 24 BP.

XX ADR05297;

XX 21-OCT-2004 (first entry)

DE Human beta cardiac myosin heavy chain mutation detection primer A.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
 PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 PT myosin heavy-chain DNA and detecting the mutation in the amplified
 FT product.

XX Claim 18; SEQ ID NO 1; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridizable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 13; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGGATCGCTACGGCTCCTGGAT 24
 Db 1 CAAGGATCGCTACGGCTCCTGGAT 24

RESULT 4
 ADM68395/c
 ID ADM68395 standard; DNA; 33 BP.
 XX
 AC ADM68395;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE PCR primer Seq ID6 related to human zinc finger protein 57_21.
 XX
 KW human; zinc finger protein 57_21; diabetes; cancer; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CNI376698-A.
 XX
 PD 30-OCT-2002.
 XX
 PF 22-MAR-2001; 2001CN-00105751.
 XX
 PR 22-MAR-2001; 2001CN-00105751.
 XX
 PA (BTOW-) BTOWINDOW GENE DEV INC SHANGHAI.
 XX
 XX Mao Y, Xie Y;
 XX
 XX WPI; 2003-184955/19.
 XX
 XX Polypeptide-human zinc finger protein -57.21.
 XX
 PS Example 5; SEQ ID NO 6; 34pp; Chinese.
 XX

CC This invention relates to a novel protein, human zinc finger protein
 CC 57_21, and the DNA sequence encoding it. The protein of the invention may
 CC be useful for the treatment of diseases such as diabetes and cancer. The
 CC present sequence is that of a PCR primer which was used in the

CC exemplification of the invention.

XX Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 68.3%; Score 16.4; DB 11; Length 33;
 Best Local Similarity 94.4%; Pred. No. 6.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AGGATCGCTACGGCTCCT 20
 Db 32 AGGATCGCTACGGTTCCT 15

RESULT 5
 AAF16851
 ID AAF16851 standard; DNA; 26 BP.
 XX
 AC AAF16851;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE KIAA0316 PDZ domain PCR primer #1.

KW Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer;
 KW PL domain protein; leukocyte activation; synapse formation;
 KW transmembrane neurotransmitter receptor; autoimmune disease;
 KW transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease; ss.

XX Homo sapiens.
 XX
 PN WO200069897-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US013166.
 XX
 PR 14-MAY-1999; 99US-0134114P.
 PR 14-MAY-1999; 99US-0134117P.
 PR 14-MAY-1999; 99US-0134118P.
 PR 21-OCT-1999; 99US-0160860P.
 PR 29-OCT-1999; 99US-0162498P.
 PR 13-DEC-1999; 99US-0170453P.
 PR 14-JAN-2000; 2000US-0176195P.
 PR 14-FEB-2000; 2000US-0182296P.
 PR 11-APR-2000; 2000US-00547276.
 PR 11-APR-2000; 2000US-0196460P.
 PR 11-APR-2000; 2000US-0196527P.
 PR 11-APR-2000; 2000US-0196528P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for inhibiting
 XX T cell-mediated response by hematopoietic cells, or for treating diseases
 XX characterized by inflammatory and humoral immune responses, e.g.
 XX inflammation, cancer.

XX Disclosure; Page 37; 139pp; English.

XX The present invention relates to a method for modulating a biological
 XX function of an endothelial cell or haematopoietic cell, comprises
 XX introducing into a cell an antagonist that inhibits binding between a PDZ
 XX domain protein and a PL domain protein to result in inhibition of
 XX leukocyte activation. The present sequence is a PCR primer for a PDZ
 XX domain. PDZ domains of proteins are named after three prototypical
 XX proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1
 XX protein. PDZ domain proteins are involved in synapse formation by

CC organising transmembrane neurotransmitter receptors through intracellular
CC interactions. The inhibitors identified by the present invention can be
CC used to treat a disease mediated by haematopoietic cells, e.g. autoimmune
CC disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel
CC diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic
CC diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes,
CC Hashimoto thyroiditis, osteoarthritis), atherosclerosis, cancers,
CC infectious diseases (e.g. viral infection), ischaemia, vasculitis and
CC Crohn's disease. The inhibitors can also be used to prevent
CC transplanted rejection of a solid organ transplant
XX
SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

Db 2 AAGGATCCCTCCGGCTCTCTGG 22

RESULT 6

AAFI7495

ID AAFI7495 standard; DNA; 26 BP.

XX AC

XX AAFI7495;

XX DT 12-MAR-2001 (first entry)

XX DE KIAA0316 PDZ domain PCR primer #1.

XX Endothelial cell; haematopoietic cell; PDZ domain protein; PCR primer;

XX PL domain protein; leukocyte activation; synapse formation;

XX transmembrane neurotransmitter receptor; autoimmune disease;

XX transplanted rejection; inflammation; allergy;

XX inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

XX asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

XX ischaemia; vasculitis; Crohn's disease; ss.

XX Homo sapiens.

XX WO200069898-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US013205.

XX 14-MAY-1999; 99US-01341114P.

XX 14-MAY-1999; 99US-01341117P.

XX 14-MAY-1999; 99US-01341118P.

XX 29-OCT-1999; 99US-0160860P.

XX 29-OCT-1999; 99US-0162498P.

XX 13-DEC-1999; 99US-0170453P.

XX 14-JAN-2000; 2000US-0176195P.

XX 14-FEB-2000; 2000US-0182296P.

XX 11-APR-2000; 2000US-00547276.

XX 11-APR-2000; 2000US-0196460P.

XX 11-APR-2000; 2000US-0196527P.

XX 11-APR-2000; 2000US-0196528P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-061214/07.

XX Modulating a biological function of a hematopoietic cell for treating an

XX allergic response, or diseases mediated by immune system cells, comprises

XX introducing into the cell a PDZ-PL interaction enhancer or inhibitor.

XX Disclosure; Page 39; 143pp; English.

XX

CC The present invention relates to a method for modulating a biological

CC function of an endothelial cell or haematopoietic cell, comprises

CC introducing into a cell an antagonist that inhibits binding between a PDZ

CC domain protein and a PL domain protein to result in inhibition of

CC leukocyte activation. The present sequence is a PCR primer for a PDZ

CC domain. PDZ domains of proteins are named after three prototypical

CC proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1

CC protein. PDZ domain proteins are involved in synapse formation by

CC organising transmembrane neurotransmitter receptors through intracellular

CC interactions. The inhibitors identified by the present invention can be

CC used to treat a disease mediated by haematopoietic cells, e.g. autoimmune

CC disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel

CC diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic

CC diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g.

CC Hashimoto thyroiditis, osteoarthritis), atherosclerosis, cancers,

CC infectious diseases (e.g. viral infection), ischaemia, vasculitis and

CC Crohn's disease. The inhibitors can also be used to prevent

CC transplanted rejection of a solid organ transplant

XX

SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

Db 2 AAGGATCCCTCCGGCTCTCTGG 22

RESULT 7

AAC99432

ID AAC99432 standard; DNA; 26 BP.

XX AC

XX AAC99432;

XX DT 07-MAR-2001 (first entry)

XX DE Primer #41 used to amplify PDZ encoded domain.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation; allergy;

XX asthma; multiple sclerosis; cancer; infection; primer; ss.

XX Synthetic.

XX WO200069896-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US013161.

XX 14-MAY-1999; 99US-01341114P.

XX 14-MAY-1999; 99US-01341117P.

XX 14-MAY-1999; 99US-01341118P.

XX 21-OCT-1999; 99US-0160860P.

XX 29-OCT-1999; 99US-0162498P.

XX 13-DEC-1999; 99US-0170453P.

XX 14-JAN-2000; 2000US-0176195P.

XX 14-FEB-2000; 2000US-0182296P.

XX 11-APR-2000; 2000US-00547276.

XX 11-APR-2000; 2000US-0196460P.

XX 11-APR-2000; 2000US-0196527P.

XX 11-APR-2000; 2000US-0196528P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or hematopoietic

XX cell, comprises

XX introducing into the cell a PDZ-PL interaction enhancer or inhibitor.

XX Disclosure; Page 39; 143pp; English.

PT cell, useful for treating autoimmune diseases and infectious diseases, by
PT administering an antagonist that inhibits binding between a PDZ protein
PT and a PL protein.

PS Disclosure, Page 28-43; 141pp; English.

XX The present invention relates to a new method for modulating a biological
CC function of an endothelial cell or hematopoietic cell. The method
CC involves introducing into a cell, an antagonist that inhibits binding
CC between a PDZ protein and a PL protein. The inhibitor is used to treat a
CC disease mediated by hematopoietic cells, e.g. autoimmune disease. It may
CC also be used to prevent transplantation rejection of a solid organ
CC transplant. The method may also be used in the treatment of inflammation,
CC allergy, inflammatory bowel diseases, ulcerative colitis, ileitis,
CC psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes,
CC Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation
CC rejection), atherosclerosis, cancers, infectious diseases, ischemia,
CC vasculitis and Crohn's disease

SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

DB 2 AAGGATCCTCCGGCTCTCTCG 22

RESULT 8

ABT06636

ID ABT06636 standard; DNA; 26 BP.

XX ABT06636;

XX 07-NOV-2002 (first entry)

DE PDZ domain PCR primer SEQ ID No 362.

XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;
KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;
KW inflammatory; humoral immune response; inflammation; PCR; primer; ss.

XX Unidentified.

XX WO200231512-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US032150.

XX 13-OCT-2000; 2000US-00688017.

XX (ARBO-) ARBOR VITA CORP.

XX Rabinowitz JD, Lu PS, Schweizer J;

XX WPI; 2002-416878/44.

XX Assays for determining the affinity of binding between a PDZ domain and a
PT ligand, and determining the Ki of an inhibitor of the binding, comprises
PT using a polypeptide comprising a PDZ domain and a non-PDZ domain.

PS Disclosure, Page 43; 164pp; English.

XX The invention relates to methods and reagents for determining the
CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The
CC invention also relates to methods and reagents for determining the Ki of
CC an inhibitor of binding between a PDZ domain and a ligand, identifying an
CC agent that enhances binding of a PDZ domain and a ligand, and determining
CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by

CC determining the ligand bound with an immobilised polypeptide comprising a
CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,
CC an inhibitor) of interaction between PDZ and PL is useful for treating a
CC disease characterised by leukocyte activation, e.g., an autoimmune
CC disease that is characterised by inflammatory or humoral immune response,
CC and for reducing inflammation in a subject. This sequence represents a
CC PDZ domain protein related PCR primer of the invention

SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 26;

Best Local Similarity 85.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGATCGCTACGGCTCTCTGG 22

DB 2 AAGGATCCTCCGGCTCTCTCG 22

RESULT 9

ABQ96682

ID ABQ96682 standard; DNA; 26 BP.

XX ABQ96682;

XX 28-OCT-2002 (first entry)

XX KIAA 0316 PDZ domain forward PCR primer 159KIP.

XX Molecular interaction; hematopoietic cell; immune response; T cell;
KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;
KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;
KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cyostatic;
KW antimicrobial; vasotropic; inflammatory immune response; inflammation;
KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;
KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
KW angiogenesis-dependent disorder; infectious disease; PCR primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242422-A2.

XX 30-MAY-2002.

XX 09-NOV-2001; 2001WO-US044138.

XX 11-NOV-2000; 2000US-00710059.

XX 24-NOV-2000; 2000US-00721915.

XX 24-NOV-2000; 2000US-00722069.

XX 28-NOV-2000; 2000US-00724553.

XX (ARBO-) ARBOR VITA CORP.

XX Lu P, Rabinowitz JD, Schweizer J;

XX WPI; 2002-608221/65.

XX Modulating the biological function of an endothelial cell or

PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ
PT ligand protein in the cell.

PS Disclosure, Page 48-49; 207pp; English.

XX The present invention describes a method (M1) for modulating a biological
CC function of an endothelial cell or hematopoietic cell. M1 comprises
CC introducing into the cell, an agent that inhibits binding of a PDZ
CC (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)
CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the

biological function. Also described is a method (M2) for determining whether a test compound is an inhibitor of binding between a PDZ protein and a PL protein. M1 is used for modulating a biological function of an endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an inflammatory or humoral immune response, or an autoimmune disease. An inhibitor (I) is useful for treating a disease characterised by leukocyte activation, where the disease is characterised by an inflammatory or humoral immune response, e.g., an autoimmune disease. The compounds e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating symptoms of) a variety of diseases and conditions characterised by inflammatory and humoral immune responses e.g., inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis, diseases such as asthma, allergic rhinitis, scleroderma, respiratory allergic (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver, autologous, bone marrow, xenotransplantation), atherosclerosis, cancers, angiogenesis-dependent disorders, infectious diseases and ischaemia. ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used in the exemplification of the present invention

XX SQ Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 26;
Best Local Similarity 85.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGG 22
||||| |||||
Db 2 AAGGATCGCTCGGCTCTCTGG 22

RESULT 10

ADJ80120
ID ADJ80120 standard; DNA; 24 BP.

XX AC ADJ80120;

XX DT 06-MAY-2004 (first entry)

XX DE RE-DSB cassette internal primer, SEQ ID NO 79.

XX KW in vivo; site-directed mutagenesis; mutation;
KW integrative recombinant oligonucleotide; IRO; CORE-cassette; primer; ss;
KW counterselectable reporter.

XX OS Unidentified.

XX PN WO2003012036-A2.

XX PD 13-FEB-2003.

XX PF 26-JUL-2002; 2002WO-US023634.

XX PR 27-JUL-2001; 2001US-0308426P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Storici F, Resnick MA, Lewis LX;

XX DR WPI; 2003-289875/28.

XX PT In vivo mutagenesis enabling site-specific mutations, deletions and
PT insertions with integrative oligonucleotides, useful as diagnostic tools
PT where biological consequences are assessed in the creation of strains or
PT cell lines.

XX PS Disclosure; SEQ ID NO 79; 96pp; English.

XX CC The invention relates to a novel method for in vivo site-directed
CC mutagenesis which involves introducing a mutation into a target double-
CC stranded nucleic acid sequence having a first and second strand in a
CC cell. The method comprises introducing a double-stranded nucleic acid
CC cassette into a target nucleic acid sequence at an insertion point,

transforming the cell with a first oligonucleotide, and selecting for loss of the nucleic acid sequence encoding the reporter gene. The method employs using integrative recombinant oligonucleotides (IROs). The cassette is an Reporter (RE)-cassette and contains a first portion homologous to a nucleic acid sequence on a first side of the insertion point, a second portion homologous to a second nucleic acid sequence on a second side of the insertion point, and a nucleic acid sequence encoding a reporter located between the first portion and the second portion. The first oligonucleotide comprises a nucleic acid sequence homologous to one strand (the chosen strand) of the target nucleic acid sequence at a position on the first side of the insertion point, and a nucleic acid sequence homologous to the same strand of the target nucleic acid sequence at a position on the second side of the insertion point, and comprising at least one nucleotide that differs from the chosen strand of the target nucleic acid sequence. The loss of the nucleic acid sequence encoding the reporter gene indicates integration of the oligonucleotide sequence comprising at least one nucleotide that differs from the target nucleic acid sequence. The methods and compositions are useful as diagnostic tools where a series of strains or cell lines are created, each with the cassette at a different position within a gene, such that mutations can be introduced anywhere within the gene and the biological consequences assessed. They can also be used in targeted changes in the genome of various organisms, modification of large human genes and larger windows of site-directed mutagenesis. This polynucleotide represents a primer used in the method of the invention.

XX SQ Sequence 24 BP; 2 A; 9 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 63.3%; Score 15.2; DB 10; Length 24;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTCTGG 22
||||| |||||
Db 3 AGGATCGCGGCTCTCTGG 22

RESULT 11

ACK06221/c
ID ACK06221 standard; DNA; 25 BP.

XX AC ACK06221;

XX DT 14-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 106202.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 106202; 9pp; English.

XX

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 63.3%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCGGAT 24
 |||||
 Db 25 GGTCCCTACGGTCTCTGGAT 6

RESULT 12
 ACK05595/c
 ID ACK05595 standard; DNA; 25 BP.
 XX
 AC ACK05595;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 105576.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (APFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 105576; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its

CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 63.3%; Score 15.2; DB 9; Length 25;
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCGGAT 24
 |||||
 Db 25 GGTCCCTACGGTCTCTGGAT 6

RESULT 13
 AAT35182
 ID AAT35182 standard; DNA; 33 BP.
 XX
 AC AAT35182;
 XX
 DT 27-NOV-1996 (first entry)
 XX
 DE Human alpha-foetoprotein DNA primer DomiI3.
 XX
 KW Alpha-foetoprotein; AFP; cell proliferation; bone marrow;
 KW autoimmune disease; breast cancer; prostate cancer; neoplasm; tumour;
 KW myelotoxicity; therapy; cell culture medium; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN W09622787-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 24-JAN-1996; 96WO-US0000996.
 XX
 PR 24-JAN-1995; 95US-00377309.
 PR 24-JAN-1995; 95US-00377311.
 PR 24-JAN-1995; 95US-00377316.
 PR 24-JAN-1995; 95US-00377317.
 PR 21-JUL-1995; 95US-00505012.
 XX
 PA (MURG/) MURGITA R A.
 XX
 PI Murgita RA;
 XX
 DR WPI; 1996-362459/36.
 XX
 PT New isolated recombinant human alpha-fetoprotein - used for treating
 PT autoimmune diseases or neoplasms, for inhibiting myelotoxicity or
 PT promoting bone marrow cell proliferation.
 XX
 PS Example; Page 40; 133pp; English.

```
XX PCR primers (AAT35179-85) were used to amplify cDNA coding for fragments
CC of human mature recombinant alpha-fetoprotein (AFP). Plasmid pII8, which
CC contains the coding region of AFP (see also AAT35173), was used as
CC template. Primer DomII3 (AAT35182) was used with primer DomII5 (AAT35181)
CC to amplify AFP domain II (AAR99224) cDNA, and with primer DomI25
CC (AAT35179) to amplify domain I+II (AAR99222) cDNA. The recombinant AFP
CC fragments have therapeutic appln
XX
XX Sequence 33 BP; 10 A; 6 C; 6 G; 11 T; 0 U; 0 Other;
SQ
Query Match 62.5%; Score 15; DB 2; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
Db ||||| || |||||
5 AAGGATCGCTTAGCTCTCTGGAT 27
RESULT 14
ABZ70298
ID ABZ70298 standard; DNA; 33 BP.
XX
XX AC ABZ70298;
XX
XX DT 25-APR-2003 (first entry)
XX
XX Dihydropyrroline-5-carboxylic acid reductase 8.91 PCR primer #4.
XX
XX Dihydropyrroline-5-carboxylic acid reductase 8.91; enzyme; cancer;
KW HIV infection; anti-HIV; cytostatic; PCR; primer; ss.
XX
XX Unidentified.
XX
XX CN1363661-A.
XX
XX 14-AUG-2002.
XX
XX 05-JAN-2001; 2001CN-00105030.
XX
XX 05-JAN-2001; 2001CN-00105030.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-751775/82.
XX
XX Polypeptide-dihydropyrroline-5-carboxylic acid reductase 8.91 and
PT polynucleotide for coding it.
XX
XX Example 4; Page 17 (Disclosure); 32pp; Chinese.
XX
XX The present invention relates to dihydropyrroline-5-carboxylic acid
CC reductase 8.91 (see AB59181). The protein can be used for treating
CC diseases such as cancer and HIV infection. The present sequence is a PCR
CC primer, which was used in an example from the invention
XX
XX Sequence 33 BP; 6 A; 10 C; 6 G; 11 T; 0 U; 0 Other;
SQ
Query Match 62.5%; Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db ||||| ||||| |||||
1 CATGGATCCCTACTTCTCTTGGGA 23
RESULT 15
AAQ04591/c
ID AAQ04591 standard; DNA; 36 BP.
```

```
XX AAQ04591;
XX AC
XX DT 27-SEP-1990 (first entry)
XX
XX DE Probe used to screen cDNA library of bovine heavy metal responsive
XX sequence.
XX
XX KW Metallothionein; bMT-II; operator; ds.
XX
XX OS Bos taurus.
XX
XX PN EP369458-A.
XX
XX PD 23-MAY-1990.
XX
XX PF 17-NOV-1989; 89EP-00121295.
XX
XX PR 18-NOV-1988; 88US-00274241.
XX
XX PA (PHIP ) PHILLIPS PETROLEUM CO.
XX
XX PI Williams ME, Murphy MF;
XX
XX DR WPI; 1990-157607/21.
XX
XX Bovine metallothionein regulatory region fragment - providing inducible
PT expression of polypeptide in presence of heavy metal.
XX
XX PS Example 5; Page 14; 9pp; English.
XX
XX CC Gene being screened is bovine metallothionein regulatory gene it can be
CC used as an operator linked to the coding region of an heterologous
CC sequence, and is induced in the presence of heavy metals esp. Cd and Zn
XX
XX SQ Sequence 36 BP; 6 A; 8 C; 16 G; 6 T; 0 U; 0 Other;
Query Match 62.5%; Score 15; DB 2; Length 36;
Best Local Similarity 78.3%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db ||||| ||||| |||||
28 CATGGATCCCACTGCTCTCTGCA 6
RESULT 16
ABQ01333
ID ABQ01333 standard; DNA; 24 BP.
XX
XX AC ABQ01333;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 1324.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX
XX PR 25-AUG-2000; 2000US-0227948P.
XX
XX PR 29-AUG-2000; 2000US-0228854P.
XX
XX PA (ILLU-) ILLUMINA INC.
XX
XX PI Gunderson K;
```

DR WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising

PT different specific capture probes.

XX Claim 1; Page 75; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

XX Sequence 24 BP; 1 A; 7 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GGATCGCTACGGCTCTGGAT 24
DB 2 GGTTCGCTACGGCGTGGTT 22

RESULT 17
ID ABQ06613 standard; DNA; 24 BP.
AC ABQ06613;
XX 11-JUN-2002 (first entry)
XX Oligonucleotide adapter/capture probe 6604.
XX Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
PA Gunderson K;
PI WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
XX Claim 1; Page 171; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

XX Sequence 24 BP; 1 A; 7 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GGATCGCTACGGCTCTGGAT 24
DB 2 GGTTCGCTACGGCGTGGTT 22

RESULT 17
ID ABQ06613 standard; DNA; 24 BP.
AC ABQ06613;
XX 11-JUN-2002 (first entry)
XX Oligonucleotide adapter/capture probe 6604.
XX Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
PA Gunderson K;
PI WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
XX Claim 1; Page 171; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

XX Sequence 24 BP; 1 A; 7 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 6; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GGATCGCTACGGCTCTGGAT 24
DB 2 GGTTCGCTACGGCGTGGTT 22

RESULT 19
ID ACK06282 standard; DNA; 25 BP.
AC ACK06282;


```

XX 09-FEB-2000; 2000WO-US003374.
XX PF
XX 09-FEB-1999; 99US-0119515P.
XX PR
XX 26-OCT-1999; 99US-0161699P.
XX PR
XX (POWD-) POWDERJECT VACCINES INC.
XX PA
XX Macklin MD, Fuller DL;
XX PI
XX WPI; 2000-524486/47.
XX DR
XX Nucleic acid immunization utilizing antigens from Mycobacterium
XX PT tuberculosis to protect against tuberculosis.
XX PR
XX Example 1; Page 31; 63pp; English.
XX PS
XX The present sequence is a PCR primer for the Mycobacterium tuberculosis
XX CC MPT 63 gene. Once amplified, the gene can be used in DNA vaccines to
XX CC elicit an immune response in humans, thus enabling immunisation against
XX CC the bacterium. This gives protection from tuberculosis (TB) either by DNA
XX CC vaccine alone or by combining the vaccine with the present BCG version to
XX CC give an enhanced immune response
XX CC
XX Sequence 36 BP; 9 A; 14 C; 6 G; 7 T; 0 U; 0 Other;
SQ
    Query Match      60.8%; Score 14.6; DB 3; Length 36;
    Best Local Similarity 81.0%; Pred. No. 4.8e+03;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| ||
Db 1 GGATCCCTACGGCTCCCAAT 21
    ||||| ||||| ||||| ||

RESULT 22
ACD54952
ID ACD54952 standard; DNA; 31 BP.
XX
AC ACD54952;
XX
XX 24-SEP-2003 (first entry)
DT
DE HBV DNazyme sequence #691.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; ss.
XX
XX Hepatitis B virus.
XX OS
XX
XX WO200281494-A1.
XX PN
XX 17-OCT-2002.
XX PD
XX
XX 26-MAR-2002; 2002WO-US009187.
XX PF
XX
XX 26-MAR-2001; 2001US-00817879.
XX PR
XX 08-JUN-2001; 2001US-00877478.
XX PR
XX 08-JUN-2001; 2001US-0296876P.
XX PR
XX 24-OCT-2001; 2001US-0335059P.
XX PR
XX 05-DEC-2001; 2001US-0337055P.
XX PF
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX (BLAT/) BLATT L.
XX PA (MACE/) MACEJAK D.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX PR
XX Example 1; Page 190; 387pp; English.
XX PS
XX The present invention relates to nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV
XX CC DNA. The nucleic acids may be used to modulate the expression of HBV
XX CC genes and HBV viral replication. Also disclosed is a method for screening
XX CC compounds and/or potential therapies directed against HBV, and compounds
XX CC that modulate the expression and/or replication of HCV. The compounds and
XX CC methods of the invention are useful for the treatment of degenerative and
XX CC disease states related to HBV and HCV infection, replication and gene
XX CC expression such as cirrhosis, liver failure, and hepatocellular
XX CC carcinoma. The present sequence represents one of the HBV ribozyme,
XX CC inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences disclosed in
XX CC the present invention
XX SQ
    Query Match      60.0%; Score 14.4; DB 8; Length 31;
    Best Local Similarity 75.0%; Pred. No. 5.9e+03;
    Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
    ||||| ||||| ||||| ||
Db 6 CAAGGCTAGCTACAACGACTGGAT 29
    ||||| ||||| ||||| ||

RESULT 23
ADM63061
ID ADM63061 standard; DNA; 31 BP.
XX
AC ADM63061;
XX
XX 03-JUN-2004 (first entry)
DT
DE Hepatitis B virus (HBV) enzymatic nucleic acid #2653.
XX
XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
XX hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
XX cirrhosis; liver failure; lamivudine; interferon; genetic drift;
XX virucide; hepatotropic; antiinflammatory; cytostatic.
XX
XX Hepatitis B virus.
XX OS
XX
XX US2004054156-A1.
XX PN
XX 18-MAR-2004.
XX PD
XX 15-JAN-2003; 2003US-00342902.
XX PF
XX 14-MAY-1992; 92US-00882712.
XX PR
XX 07-FEB-1994; 94US-00193627.
XX PR
XX 08-NOV-1999; 99US-00436430.
XX PR
XX 20-MAR-2000; 2000US-00531025.
XX PR

```

```
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00896347.
PR 08-JUN-2001; 2001US-00877478.
XX
XX (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
XX
XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 5195; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 31 BP; 8 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 12; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db ||||| ||||| ||||| ||||| |||||
6 CAAGGCTAGCTACACGACTGGAT 29
RESULT 24
AAX59667/c
ID AAX59667 standard; DNA; 32 BP.
XX
XX AAX59667;
AC
XX
XX 22-JUL-1999 (first entry)
DT
XX
XX Muragenic primer DA23 used to amplify termamyl-like alpha-amylase DNA.
DE
XX
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
KW saccharification process; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9923211-A1.
FN
XX
XX 14-MAY-1999.
PD
XX
XX 30-OCT-1998; 98WO-DK000471.
PF
XX
XX 30-OCT-1997; 97DK-00001240.
PR
XX 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO ) NOVO-NORDISK AS.
PA
XX
```

```
PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulff S;
XX
XX WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Example 5; Page 48; 115pp; English.
XX
XX The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present PCR primer was used to construct the variants of
CC the invention
XX
XX Sequence 32 BP; 12 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 2; Length 32;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db ||||| ||||| ||||| ||||| |||||
31 CATGTGCTGTAACGGGTCCTGGTT 8
RESULT 25
ABQ83921
ID ABQ83921 standard; DNA; 33 BP.
XX
XX ABQ83921;
AC
XX
XX 04-FEB-2003 (first entry)
DT
XX
XX Mouse polycomb gene enhancer 84-57.31 PCR primer 4 SEQ ID NO:6.
DE
XX
XX Mouse; polycomb gene enhancer 84-57.31; embryotic development deformity;
KW tumour; PCR primer; ss.
XX
XX Mus sp.
OS
XX
XX CNI342699-A.
FN
XX
XX 03-APR-2002.
PD
XX
XX 12-SEP-2000; 2000CN-00125168.
PF
XX
XX 12-SEP-2000; 2000CN-00125168.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-529776/57.
DR
XX
XX A novel mouse polycomb gene enhancer 84-57.31 polypeptide, and the
PT polynucleotide encoding it, useful for treating several diseases e.g.
PT embryotic development deformity and tumors.
XX
XX Example 5; Page 18 (Disclosure); 34pp; Chinese.
PS
XX
XX The present invention describes mouse polycomb gene enhancer 84-57.31
CC (I). Also described is a process for preparing (I) using DNA
CC recombination techniques. (I) can be used for treating several diseases
CC e.g. embryotic development deformity and tumours. The present sequence
CC
```

Qy

1 CAAGGATCGCTACGGCTCCTGGAT 24
||| ||| ||| ||| ||| ||| ||| |||

D6

1 CATGGATCCCTAAGGTCCCTGAAT 24

AA
PN
US2003104410-A1.

PT Cysteine noose antibody libraries and their production.

XX Example 6; Page 42; 64pp; English.

XX This invention describes the construction of libraries of antibody
CC variable domains containing modified complementarity determining regions
CC (CDRs) carrying a cysteine noose and which have cytokine agonist and
CC antagonist mechanisms of action. The method of the invention can be used
CC to obtain peptide ligand mimetics capable of binding a target antigen.
CC The binding members may also be used to provide agonists or antagonists
CC of targets such as cytokines. In particular specific binding members for
CC MIP-1 alpha receptors are useful for treatment of HIV infection and for
CC in vitro investigation of mechanisms of HIV infection. A selection of
CC peptide ligand mimetics from CDR3 cysteine noose libraries provide a
CC means to select a different and potentially more effective population of
CC peptide ligands than direct display of similar cysteine noose ligands on
CC the surface of bacteriophage. The products of the invention have anti-HIV
CC activity

XX SQ Sequence 30 BP; 5 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 30;

Best Local Similarity 77.3%; Pred. No. 9.1e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 23 CAAGGATCGCTACGGCTCTCTGG 2

RESULT 31

ADO43696

ID ADO43696 standard; DNA; 32 BP.

XX AC ADO43696;

XX DT 29-JUL-2004 (first entry)

XX DE PCR primer used to isolate cDNA encoding HINF-P.

XX KW cellular proliferation; histone nuclear factor P; HINF-P; bone disorder;
XX cancer; immune disorder; cardiovascular disorder; viral infection; PCR;
XX primer; ss.

XX OS Unidentified.

XX FN WO2004038008-A2.

XX PD 06-MAY-2004.

XX PF 27-OCT-2003; 2003WO-US034188.

XX PR 25-OCT-2002; 2002US-0421166P.

XX PA (UYMA-) UNIV MASSACHUSETTS.

XX PI Stein GS, Van Wijnen AJ, Xie R, Stein JL, Mitra P;

XX DR WPI; 2004-365515/34.

XX PT Modulating cellular proliferation using a Histone Nuclear Factor P (HINF-
XX P) or Nuclear Protein or Ataxia-Telangiectasia locus (NPAT) polypeptide,
XX useful for diagnosing or treating cancer, immune disorders and/or viral
XX infections.

XX FS Example 3; Page 72; 117pp; English.

XX The specification describes a method for enhancing cellular
CC proliferation. The method comprises introducing into a cell a compound
CC that alters the expression or activity of a Histone Nuclear Factor P
CC (HINF-P) polypeptide to enhance proliferation of the cell. The method of
CC the invention is useful for the diagnosis, prevention and treatment of
CC diseases or conditions associated with aberrant expression or activity of

CC the HINF-P polypeptide, such as bone disorders, cancer, immune disorders,
CC cardiovascular disorders and viral infections. PCR primers ADO43696-
CC ADO43697 were used to isolate cDNA encoding HINF-P.

XX SQ Sequence 32 BP; 5 A; 11 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 32;

Best Local Similarity 77.3%; Pred. No. 9.1e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 2 CAGGATCGCTACGGCTCTCTGG 23

RESULT 32

ABX14381

ID ABX14381 standard; DNA; 33 BP.

XX AC ABX14381;

XX DT 03-MAR-2003 (first entry)

XX DE PCR primer #2 for cDNA encoding human zinc finger protein 11.88.

XX KW Human; zinc finger protein 11.88; cancer; HIV infection; PCR;
XX human immunodeficiency virus infection; primer; ss.

XX OS Homo sapiens.

XX FN CN1359917-A.

XX PD 24-JUL-2002.

XX PF 20-DEC-2000; 2000CN-00135106.

XX PR 20-DEC-2000; 2000CN-00135106.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-733606/80.

XX PT Polypeptide-human zinc finger protein 11.88 and encoding polynucleotide.
XX Example 4; Page 17 (disclosure); 32pp; Chinese.

XX The present invention relates to the isolation of human zinc finger
XX protein 11.88, and the polynucleotide sequence encoding it. Also
XX described is the process for preparing the protein by DNA recombination
XX and the application of the polypeptide and polynucleotide in treating
XX various diseases such as cancer and human immunodeficiency virus (HIV)
XX infection. The present sequence represents a PCR primer used to clone
XX cDNA encoding human zinc finger protein 11.88

XX SQ Sequence 33 BP; 7 A; 8 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 33;

Best Local Similarity 77.3%; Pred. No. 9.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGG 22

Db 1 CATGGATCCCTACGGCAGTTGG 22

RESULT 33

AAZ35063/c

ID AAZ35063 standard; DNA; 22 BP.

XX AC AAZ35063;

XX

```

DT 28-FEB-2000 (first entry)
XX
DE Feline CD86 gene PCR primer 8/97.31.
XX
XX CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;
KW therapy; PCR; primer; ss.
XX
XX Synthetic.
OS Felis catus.
XX
XX WO9957295-A1.
XX
XX 11-NOV-1999.
PD
XX
XX 30-APR-1999; 99WO-US009504.
PF
XX
XX 01-MAY-1998; 98US-00071711.
PR
XX
XX (SCHE ) SCHERING-PLOUGH LTD.
PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX
XX Winslow BU, Cochran MD;
XX
XX WPI; 2000-062155/05.
XX
XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines.
XX
XX Example; Page 122; 230pp; English.
XX
XX This oligonucleotide represents primer 8/97.31 that was used in the PCR
CC amplification of the feline CD70 (B7-2) (see AAZ34838) cDNA. The
CC amplified gene was used in the construction of homology vector 1015.18.8A
CC (LP1-CD86/IRE5-CD80), which was used to create recombinant racoonpox
CC viruses (RPV) expressing feline CD80 and CD86. The invention relates to a
CC recombinant virus, e.g. RPV, that contains at least one foreign nucleic
CC acid, inserted into a nonessential genomic region, that encodes feline
CC CD28, CD80, CD86 or CTLA-4 protein (see AAY32283-87), or their
CC immunogenic fragments, and is expressed when the recombinant virus is
CC introduced into a suitable host. The recombinant virus may further
CC comprise a foreign nucleic acid encoding an immunogen derived from a
CC feline pathogen. It is used to modulate an immune response in a feline,
CC particularly as a vaccine
XX
XX Sequence 22 BP; 4 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
SQ
Query Match 57.5%; Score 13.8; DB 3; Length 22;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 CGCTACGGCTCTCTGGAT 24
Db 21 CGCTCCGGATCTCTGGAT 5
RESULT 34
AAT34298
ID AAT34298 standard; cDNA; 36 BP.
AC
XX
XX AAT34298;
XX
DT 24-OCT-1996 (first entry)
XX
XX HEK4 binding protein PCR primer 819-28.
XX
XX HEK4 binding protein; HEK4 receptor; EPH-like receptor;
KW protein tyrosine kinase; ligand; growth; differentiation; cancer;
XX nervous system disorder; therapy; polymerase chain reaction; PCR; primer;
KW antibody; ss.
XX
XX Synthetic.
OS
XX
XX WO9623000-A1.
PN

```

```

XX 01-AUG-1996.
PD
XX
XX 16-JAN-1996; 96WO-US001079.
PF
XX
XX 27-JAN-1995; 95US-00379802.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Bartley TD, Fox GM;
XX
XX WPI; 1996-362633/36.
XX
XX Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
PT modulate growth and differentiation of, e.g. liver and kidney cells, and
PT to treat cancer and nervous system disorders.
XX
XX Example 5; Page 31; 65pp; English.
XX
XX PCR primers 819-31 (AAT34297) and 819-28 (AAT34298) were used to amplify
CC a portion of HEK4 binding protein cDNA (see also AAT34292) coding for
CC amino acids 1-179 of the protein (see also AAW00035). The PCR fragment
CC was cloned into vector pCFM1656 and truncated HEK4 binding protein was
CC expressed in Escherichia coli FMS (ATCC 53911) transformants. The protein
CC was used as an antigen in rabbits. The antiserum recognised HEK4 binding
CC protein in CHO cells in Western blot analysis
XX
XX Sequence 36 BP; 9 A; 9 C; 10 G; 8 T; 0 U; 0 Other;
SQ
Query Match 57.5%; Score 13.8; DB 2; Length 36;
Best Local Similarity 88.2%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGCTC 18
Db 5 AAGGATCCCTATGCTC 21
RESULT 35
AAC69334/c
ID AAC69334 standard; DNA; 21 BP.
XX
XX AAC69334;
AC
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 gene intron 9 polymorphic site, SEQ ID NO:233.
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200055318-A2.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000; 2000WO-IB000532.
PF
XX
XX 15-MAR-1999; 99US-0124702P.
PR
XX 08-JUN-1999; 99US-0138048P.
PR
XX 17-JUN-1999; 99US-0139600P.
PR
XX 01-SEP-1999; 99US-0151977P.
PR
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
PA
XX

```

```

PI Hayden MR, Wilson AR, Pimstone SN;
XX WPI; 2000-587528/55.
XX
XX New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT cancer.
XX
XX Example; Fig 11; 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds. It
CC further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents a polymorphic site of the human ABC1 gene
XX
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 56.7%; Score 13.6; DB 3; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCT 20
DB 20 CAATGAGCGCTTTGGCTCCT 1
RESULT 36
AAF93000/c
ID AAF93000 standard; DNA; 21 BP.
XX
XX AAF93000;
XX
XX 17-MAY-2001 (first entry)
XX
XX Polymorphic sequence for ABC1 polymorphic site #19.
XX
XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
XX Homo sapiens.
XX
XX WO200115676-A2.
XX
XX 08-MAR-2001.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX WPI; 2001-244356/25.
XX
XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)
XX level, a higher than normal triglyceride level, or a cardiovascular
XX disease, by administering a compound that modulates LXR- or RXR-mediated
XX transcriptional activity.
XX
XX Disclosure; Fig 4; 317pp; English.
XX
XX The present invention relates to a method for treating a patient
XX diagnosed as having a lower than normal high density lipoprotein-
XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, involving administering a compound that modulates
XX LXR- or RXR-mediated transcriptional activity or ABC1 expression or
XX activity. The LXR gene product may be used in an assay to identify
XX compounds useful for the treatment of a disease or condition selected a
XX lower than normal HDL cholesterol level, a higher than normal
XX triglyceride level, and a cardiovascular disease
XX
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 56.7%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAAGGATCGCTACGGCTCCT 20
DB 20 CAATGAGCGCTTTGGCTCCT 1
RESULT 37
ACK06220/c
ID ACK06220 standard; DNA; 25 BP.
XX
XX ACK06220;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 106201.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT

```

PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 106201; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 9; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.4e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGAT 24

Db ||||| ||||| ||||| ||||| |||||
 25 GGTCTCTACGGGACCTGGAT 6

RESULT 38

AC104808/c

ID AC104808 standard; DNA; 25 BP.

XX AC104808;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 4799.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 4799; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 9; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.4e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTG 21

Db ||||| ||||| ||||| ||||| |||||
 23 AAGGAGGCAACGGTCTG 4

RESULT 39

ACK05594/c

ID ACK05594 standard; DNA; 25 BP.

XX ACK05594;

XX 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 105575.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 105575; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used CC in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled CC compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying allelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 GATCGCTACGGCTCTCGAT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GGTCCCTACGGGACCTGGAT 6

RESULT 40
AAZ35681
ID AAZ35681 standard; DNA; 28 BP.
XX
AC AAZ35681;
XX
DT 26-JAN-2000 (first entry)
XX
DE IL-2/GM-CSF fusion protein construction oligonucleotide P4.
XX
KW IL-2; interleukin 2; granulocyte macrophage colony stimulating factor;
KW GM-CSF; fusion protein; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN CN1225368-A.
XX
PD 11-AUG-1999.
XX
PF 05-FEB-1999; 99CN-00113461.
XX
PR 05-FEB-1999; 99CN-00113461.
XX
XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
XX
XX Wang X, Huang S, Gao J;
XX WPI; 1999-581110/50.
XX
XX Interleukin -2/granulocyte-macrophage colony stimulating factor fusion
XX protein.
XX
XX Claim 5; Page 1; 17pp; Chinese.
XX
XX The present invention describes an interleukin-2/granulocyte-macrophage
XX colony stimulating factor fusion protein (IL-2/GM-CSF fusion protein).

CC The fusion protein is produced by genetic engineering technology by
CC subcloning against IL-2 and end reform and a GM-CSF connection IL-2/GM-
CC CSF expression plasmid is constructed. The fusion protein can be used to
CC convert *Escherichia coli* obtaining high effect expression. The fused
CC protein possesses IL-2 and GM-CSF dual activity. The present sequence
CC represent an oligonucleotide used in the construction of the IL-2/GM-CSF
XX fusion protein

SQ Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 2; Length 28;
Best Local Similarity 80.0%; Pred. NO. 1.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4 GGATCGCTACGGCTCTCGGA 23
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GGATCCTTATCGCTCTCGGA 21

Search completed: November 18, 2005, 11:52:17
Job time : 169.262 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGTACGGCTCTCGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	73.3	50	1	AU103062
2	15.2	63.3	41	9	CG716757
3	15	62.5	24	8	AZ812591
4	15	62.5	50	1	AU103061
5	15	62.5	50	1	AU103068
6	14.6	60.8	50	1	AU103064
7	14.6	60.8	50	1	AU103067
8	14.2	59.2	50	1	AU107042
9	14	58.3	44	8	AZ476398
10	14	58.3	50	1	AU102662
11	13.6	56.7	50	1	AU103063
12	13.4	55.8	40	1	A1317060
13	13	54.2	39	9	AJ594860
14	13	54.2	44	5	B0589685
15	13	54.2	50	1	AU103069
16	13	54.2	50	1	AU104866
17	12.8	53.3	31	7	N94283
18	12.8	53.3	35	9	CL665533
19	12.8	53.3	50	1	AU107276
20	12.6	52.5	34	8	BJ064678
21	12.6	52.5	42	8	CC027439
22	12.6	52.5	50	1	AU103065
23	12.6	52.5	50	1	AU105726
24	12.6	52.5	50	1	AU105728

C 25	12.4	51.7	38	1	AJ655775
C 26	12.4	51.7	46	9	AG213917
C 27	12.4	51.7	47	8	AZ820416
C 28	12.4	51.7	49	1	A1159805
C 29	12.2	50.8	45	7	CF277394
30	12.2	50.8	48	8	BH907825
31	12.2	50.8	50	1	AU104805
32	12.2	50.8	50	1	AU104807
C 33	12.2	50.8	50	1	AU107142
C 34	12	50.0	30	9	AG195132
C 35	12	50.0	38	8	AZ492391
36	12	50.0	42	8	BH804014
37	12	50.0	49	1	AA087268
38	12	50.0	50	1	AU103066
C 39	12	50.0	50	1	AU104834
40	12	50.0	50	1	AU106612
41	12	50.0	50	1	AU106614
C 42	12	50.0	50	1	AU107039
C 43	11.8	49.2	23	8	AZ858813
C 44	11.8	49.2	34	9	CL522317
C 45	11.8	49.2	37	1	AA518952

ALIGNMENTS

RESULT 1
LOCUS AU103062 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103062 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP19487, mRNA sequence.
ACCESSION AU103062
VERSION AU103062.1 GI:13552583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Seese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP19487"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 73.3%; Score 17.6; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CAAGGATCGTACGGCTCTCGAT 24
Db 10 CTAGGATCGGACGGTCTCGAT 33

```

RESULT 2
CG716757
LOCUS
DEFINITION
1119046B12.1EL.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION
CG716757
KEYWORDS
CG716757.1 GI:37745389
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 41)

REFERENCE
AUTHORS
Walbot,V.
TITLE
Maize genomic sequences found using engineered RescueMu transposon
JOURNAL
Unpublished (2001)
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119046 row: 7
Class: transposon-tagged.
FEATURES
source
1..41
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 63.3%; Score 15.2; DB 9; Length 41;
Best Local Similarity 85.0%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTG 21
|||||
Db 13 AAGGATCGATCGCGCACCTG 32

RESULT 3
AZ812591
LOCUS
DEFINITION
2M0079D21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0079D21 F, genomic survey sequence.
ACCESSION
AZ812591
KEYWORDS
AZ812591.1 GI:12981989
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: D column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0079D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWB42 (GI4732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 62.5%; Score 15; DB 8; Length 24;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTCGAT 24
|||||
Db 1 ATGATCGCCATGGCTCTCGAT 23

RESULT 4
AUI03061
LOCUS
DEFINITION
AUI03061 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLFI1890, mRNA sequence.
ACCESSION
AUI03061
KEYWORDS
AUI03061.1 GI:13552582
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES
    source
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="COLF1890"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGA 23
    |||||
Db 28 CTAGATCGGACGGGAAGTGG 50

RESULT 5
AUI03068
LOCUS
DEFINITION
AUI03068 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI02929, mRNA sequence.
ACCESSION
AUI03068
VERSION
AUI03068.1 GI:13552589
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES
    source
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HSI02929"

```

```

/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGA 23
    |||||
Db 18 CTAGATCGGACGGGAAGTGG 40

RESULT 6
AUI03064
LOCUS
DEFINITION
AUI03064 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC00745, mRNA sequence.
ACCESSION
AUI03064
VERSION
AUI03064.1 GI:13552585
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Taunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
FEATURES
    source
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HRC00745"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      60.8%; Score 14.6; DB 1; Length 50;
Best Local Similarity 81.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGGA 23
    |||||
Db 1 AGGATCGGACGGGAAGTGG 21

RESULT 7
AUI03067
LOCUS
DEFINITION
AUI03067 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC09549, mRNA sequence.
ACCESSION
AUI03067
VERSION
AUI03067.1 GI:13552588
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

```

AUTHORS
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isoqai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. fine, large-scale
 mapping of mRNA start sites

TITLE
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE
 21270072

PUBMED
 11375929

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC09549"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 60.8%; Score 14.6; DB 1; Length 50;
 Best Local Similarity 81.0%; Pred. No. 4.9e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGGA 23
 |||||
 Db 1 AGGATCGCGACGGGAAGTGG 21
 |||||

RESULT 8
 AUI07042/c

LOCUS
 AUI07042 50 bp mRNA linear EST 28-JAN-2004

DEFINITION
 AUI07042 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 KAT06852, mRNA sequence.

ACCESSION
 AUI07042

VERSION
 AUI07042.1 GI:13556563

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 50)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isoqai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL
 EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE
 21270072

PUBMED
 11375929

COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KAT06852"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 59.2%; Score 14.2; DB 1; Length 50;
 Best Local Similarity 84.2%; Pred. No. 7.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGA 23
 |||||
 Db 34 GATAACTAGGCTCCTGGA 16
 |||||

RESULT 9
 AZ476398

LOCUS
 AZ476398 44 bp DNA linear GSS 04-OCT-2000

DEFINITION
 IM0295B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0295B16 F, genomic survey sequence.

ACCESSION
 AZ476398

VERSION
 AZ476398.1 GI:10634523

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
 1 (bases 1 to 44)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0295 row: B column: 16
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES
 Location/Qualifiers
 1..44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0295B16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

```

Query Match      58.3%; Score 14; DB 8; Length 44;
Best Local Similarity 77.3%; Pred. NO. 9.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGG 22
    ||||| ||||| ||||| |||||
Db 23 CAAGCATCACTCCGGTGCCTGG 44

RESULT 10
AUI02662/c
LOCUS
DEFINITION
AUI02662 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS07035, mRNA sequence.
ACCESSION
AUI02662
VERSION
AUI02662.1 GI:13552183
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
21270072
MEDLINE
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Sakaki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS07035"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      58.3%; Score 14; DB 1; Length 50;
Best Local Similarity 77.3%; Pred. NO. 9.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCTGG 23
    ||||| ||||| ||||| |||||
Db 49 AAGTCTCGCATTCGCTCCTGG 28

RESULT 11
AUI03063
LOCUS
DEFINITION
AUI03063 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC00126, mRNA sequence.
ACCESSION
AUI03063
VERSION
AUI03063.1 GI:13552584
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
21270072
MEDLINE
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Sakaki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS07035"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      58.3%; Score 14; DB 1; Length 50;
Best Local Similarity 77.3%; Pred. NO. 9.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGG 22
    ||||| ||||| ||||| |||||
Db 23 CAAGCATCACTCCGGTGCCTGG 44

RESULT 12
AUI07060
LOCUS
DEFINITION
AUI07060 Schiller mouse At720 Mus musculus cDNA clone
IMAGE:1974506 5' similar to SW:HEMN SYN3 P73245 PROBABLE
OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE ; mRNA sequence.
ACCESSION
AUI07060
VERSION
AUI07060.1 GI:4032327
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:991246
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1974506"

```

```

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00126"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      56.7%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. NO. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
    ||||| ||||| ||||| |||||
Db 1 GGATCGCGACGGGAACCTGGA 20

RESULT 12
AUI37060
LOCUS
DEFINITION
AUI37060 Schiller mouse At720 Mus musculus cDNA clone
IMAGE:1974506 5' similar to SW:HEMN SYN3 P73245 PROBABLE
OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE ; mRNA sequence.
ACCESSION
AUI37060
VERSION
AUI37060.1 GI:4032327
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:991246
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1974506"

```

/cell_line="pituitary cell line"
 /lab_host="SOUR"
 /clone_lib="Schiller mouse Att20"
 /note="Organ: pituitary; Vector: pBluescript SK-
 (Stratagene); Site 1: EcoRI; Site 2: XhoI; Double-stranded
 cDNA was prepared from cell line Att-20 using primer
 5'-CAGAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An SCORI
 adaptor was used on the 5' end of the cDNA as follows:
 5'-AATTGGCAGAG-3'. The library was size-selected and
 went through one round of amplification. Average insert
 size is 1.7 kb, with a range from 0.4-12 kb. This library
 was constructed by Dr. Martin Schiller (Johns Hopkins
 University)."

ORIGIN

Query Match 55.8%; Score 13.4; DB 1; Length 40;
 Best Local Similarity 73.9%; Pred. No. 1.7e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGATCGTACGGCTCTCGA 23
 ||||| ||||| ||||| ||||| |||||
 Db 13 CAAGAAACGCTGCAGTACTGCA 35

RESULT 13

AJ594860/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 406G07, genomic survey sequence.

AJ594860

AJ594860

AJ594860.1 GI:37944484

VERSION GSS; left border; T-DNA flanking sequence.

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (http://www.genoplante.com and
 http://genoplante-info.infobiogen.fr).

FEATURES

source

1. .39

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassilewskija"

/db_xref="taxon:3702"

/clone="406G07"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature

1. .39

/note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 39;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGATCGTACGGCTCTCTG 21
 ||||| ||||| ||||| ||||| |||||
 Db 22 CAAGCATCTTTCAGTCTCATG 2

RESULT 14

BQ589685

LOCUS

DEFINITION BQ589685 44 bp mRNA linear EST 06-DEC-2002
 E012680-024-020-L13-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-020-L13 5-PRIME, mRNA sequence.

ACCESSION

BQ589685

VERSION

BQ589685.1

KEYWORDS

EST.

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weissshaar@mpiz-koeln.mpg.de
 Insert Length: 44 Std Error: 0.00
 Plate: 20 row: 1 column: 13
 Seq primer: SP6, CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1. .44
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:190477"
 /db_xref="taxon:161934"
 /clone="024-020-L13"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 54.2%; Score 13; DB 5; Length 44;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGATCGTACGGCTCTCTG 21
 ||||| ||||| ||||| ||||| |||||
 Db 5 CACTGATGCCACGGCTCCGG 25

RESULT 15
 AUI03069
 LOCUS
 DEFINITION AUI03069 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HUV00521, mRNA sequence.
 ACCESSION AUI03069
 VERSION AUI03069
 KEYWORDS EST.
 SOURCE AUI03069.1 GI:13552590
 ORGANISM Homo sapiens (human)
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Hataki, Y., Ota, T., Isogai, T., Tanaka, T., Mizushima-Sugano, J., Sese, J.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HUV00521"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 AGGATCGCTACGGCTCTGGA 23
 Db 1 AGGATCGCGACTGGAACTGGA 21

RESULT 16
 AUI04866
 LOCUS
 DEFINITION AUI04866 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 CAS03624, mRNA sequence.
 ACCESSION AUI04866
 VERSION AUI04866
 KEYWORDS EST.
 SOURCE AUI04866.1 GI:13554387
 ORGANISM Homo sapiens (human)
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Hataki, Y., Ota, T., Isogai, T., Tanaka, T., Mizushima-Sugano, J., Sese, J.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology

Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS03624"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 2.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CAAGGATCGCTACGGCTCTG 21
 Db 25 CAAGGATCATTTACTTTTCTG 45

RESULT 17

N94283
 LOCUS
 DEFINITION N94283 31 bp mRNA linear EST 05-APR-1996
 zz26f01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:293689 5' similar to gb:X56807_cds2 DESMOCOLLIN 3A/3B
 PRECURSOR (HUMAN); mRNA sequence.

ACCESSION N94283
 VERSION N94283.1 GI:1266592
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 31)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Ruchling, T., Soares, M., Tan, F.,
 Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Willson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

TITLE
 JOURNAL
 COMMENT
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: mob.REGA+ET
 High quality sequence stop: 1.

FEATURES
 source
 1..31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="CDB:3801536"
 /db_xref="taxon:9606"
 /clone="IMAGE:293689"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /notes="Organ: Liver and Spleen; Vector: pTV73D (Pharmacia)
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5' AACTGGAAGAATTAATAAGATCTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors


```

/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"

ORIGIN
Query Match      52.5%; Score 12.6; DB 4; Length 34;
Best Local Similarity 68.2%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AAGGATCGTACGGCTCTCGGA 23
|||||
Db 10 AAGNTCCCTTNGCCACTTGA 31

RESULT 21
LOCUS CC027439
DEFINITION 3591_1_5_1_D10.1EL_Y_1 3591 - RescueMu Grid P Zee may's genomic,
ACCESSION CC027439
VERSION CC027439
KEYWORDS GSS.
SOURCE CC027439.1 GI:29442296
ORGANISM Zee may's
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE clade; Panicoideae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 42)
COMMENT Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591_1_5_1 row: 4
Class: transposon-tagged.
Location/Qualifiers
1. 42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmhd.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match      52.5%; Score 12.6; DB 8; Length 42;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCC 19
|||||

```

```

Db 23 CAAGAATCGCTTCGTTCC 41

RESULT 22
LOCUS AU103065
DEFINITION AU103065 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION HRC01582, mRNA sequence.
VERSION AU103065
KEYWORDS AU103065.1 GI:13552586
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC01582"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES
source
Query Match      52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCGGA 23
|||||
Db 1 GATCGGACGGGAAGTCTGA 19

RESULT 23
LOCUS AU105726
DEFINITION AU105726 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION HST05236, mRNA sequence.
VERSION AU105726
KEYWORDS AU105726.1 GI:13555247
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki

```

REFERENCE
AUTHORS
TITLE
1 Miyao, A., Tanaka, K., Murata, K., Sawaki, H., Takeda, S., Abe, K.,
Shinozuka, Y., Onosato, K. and Hirochika, H.
Target Site Specificity of the Tos17 Retrotransposon Shows a
Preference for Insertion within Genes and against Insertion in
Retrotransposon-Rich Regions of the Genome
Spermatophytica; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriophoraceae; Oryzoideae; Oryzaceae; Oryza.

```

MEDLINE      22779046
PUBMED       12897251
REFERENCE    2 (bases 1 to 46)
AUTHORS      Miyao,A., Kato,M. and Hirochika,H.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Akio Miyao, National Institute of
              Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,
              Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
              URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
              Fax:81-298-38-7020)
FEATURES
  source
    1..46
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="genomic DNA"
    /strain="ND9022"
    /cultivar="Nipponbare"
    /db_xref="taxon:39947"
    /clone="T11738T"
    /clone_lib="PCR product directly amplified from rice
    genomic DNA"
    /note="The 3' end of retrotransposon Tos17 was found
    immediately upstream of this sequence."
ORIGIN
Query Match      51.7%; Score 12.4; DB 9; Length 46;
Best Local Similarity 72.7%; Pred. No. 4.9e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  2  AAGGATCGCTACGGCTCTGGA 23
      |||||
DB   44 AGGGATTGATGAGGCTCATGGA 23

RESULT 27
AZ820416/c
LOCUS      AZ820416              47 bp  DNA  linear  GSS 20-FEB-2001
DEFINITION 2M0092F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0092F16 R, genomic survey sequence.
ACCESSION  AZ820416
VERSION     AZ820416.1  GI:12990420
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 47)
REFERENCE   1
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112 USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dduun@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0092 row: F column: 16
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 47.
            Location/Qualifiers
              1..47
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0092F16"

/ssex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      51.7%; Score 12.4; DB 8; Length 47;
Best Local Similarity 92.9%; Pred. No. 4.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  9  GCTACGGCTCTCTGG 22
      |||||
DB   31 GCTTCGGCTCTCTGG 18

RESULT 28
A1159805/c
LOCUS      A1159805              49 bp  mRNA  linear  EST 28-OCT-1998
DEFINITION qc73c05.x1 Soares_placenta 8to9weeks 2NBP8to9w Homo sapiens cDNA
clone IMAGE:1715240 3' similar to TR:Q15726 Q15726 MALIGNANT
MELANOMA METASTASIS-SUPPRESSOR. ; mRNA sequence.
ACCESSION  A1159805
VERSION     A1159805.1  GI:3693164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 49)
REFERENCE   1
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-remail.nih.gov
            This clone is available royalty-free through LNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 545 Std Error: 0.00
            Seq primer: -40ml3 fwd. ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
              1..49
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:1715240"
              /dev stage="two placenta: one from 8 weeks and another
              from 9 weeks post conception"
              /lab host="DH10B (ampicillin resistant)"
              /clone_lib="Soares_placenta 8to9weeks 2NBP8to9w"
              /note="Organ: placenta; Vector: p77T3D (Pharmacia) with a
              modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
              strand cDNA was primed with a Not I - oligo(dT) primer (5',
              TGTTACCAATCTGAAGTGGGCGCGCGATTTTTCCTTTT 3'),

```

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pYT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 51.7%; Score 12.4; DB 1; Length 49;
Best Local Similarity 72.7%; Pred. No. 5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCCTCG 22
|||||

Db 34 CTAGATCCCTGGGCTCCTCG 13
|||||

RESULT 29

CF277394

LOCUS

DEFINITION 14ETL--02-O14.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-O14,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

ORyza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 45)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..45

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ETL--02-O14"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

ORIGIN

Query Match 50.8%; Score 12.2; DB 7; Length 45;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCT 20
|||||

Db 8 GGATCGCGCCGGCTCCT 24
|||||

RESULT 30

BH907825

LOCUS

DEFINITION SALK_044281.17.00.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044281.17.00.n, genomic

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 48)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jecke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At5g08240.

Class: TDNA tagged.

FEATURES

Location/Qualifiers

1..48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_044281.17.00.n"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.8%; Score 12.2; DB 8; Length 48;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGATCGCTACGGCTC 18
|||||

Db 21 AAGATCCTCAGGCTC 37
|||||

RESULT 31

AU104805

LOCUS

DEFINITION

AU104805 Sugano Homo sapiens CDNA library Homo sapiens cDNA clone

CASI0961, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="SUGANO Homo sapiens cDNA library"

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 33 AGCCTCGCTATGGCTCC 49

RESULT 32
AUI04807
LOCUS
DEFINITION
HRC08216, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="SUGANO Homo sapiens cDNA library"

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 32 AGCCTCGCTATGGCTCC 48

RESULT 32
AUI04807
LOCUS
DEFINITION
HRC08216, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="SUGANO Homo sapiens cDNA library"

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCC 19
Db 32 AGCCTCGCTATGGCTCC 48

RESULT 32
AUI04807
LOCUS
DEFINITION
HRC08216, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

RESULT 33
AUI07142/c
LOCUS
DEFINITION
ZRV6C680, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="ZRV6C680"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTG 21
Db 22 GACAGCTACGGCTCCG 6

RESULT 34
AG195132
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-073N21.T7, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes
Pan troglodytes (chimpanzee)
REFERENCE
AUTHORS
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 30)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .30
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clones="RP43-073N21.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGATCGCTACGGCTCTCTG 21

|||||

Db 4 AGGAATCCCTGCTGCTCTG 23

RESULT 35

AZ492391

LOCUS

DEFINITION lM0326D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0326D04 R, genomic survey sequence.

ACCESSION AZ492391

VERSION AZ492391.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 38)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0326 row: D column: 04

Seq primer: CACACAGGAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 38.

Location/Qualifiers

1. .38

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0326D04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 12; DB 8; Length 38;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTCTG 22

|||||

Db 3 AGGACACTACTGCTCTG 22

RESULT 36

BH804014

LOCUS

DEFINITION BH804014 42 bp DNA linear GSS 25-APR-2002
1008097B08.2EL_x2 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.

ACCESSION BH804014

VERSION BH804014.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 42)

AUTHORS Walbot, V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008097 row: 13

Class: transposon-tagged.

Location/Qualifiers

1. .42

/organism="Zea mays"

/mol_type="genomic DNA"

/culturivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1008 - RescueMu Grid I"

/notes="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 50.0%; Score 12; DB 8; Length 42;
Best Local Similarity 75.0%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGG 22
|||||
Db 8 AGGTACGGTACGGCGCTGG 27
|||||

RESULT 37
AA087268
LOCUS
DEFINITION
mol2g10.r1 Life Tech mouse embryo 10 5dpc 10665016 Mus musculus
CDNA clone IMAGE:553410 5', similar to TR:G285961 G285961 MRNA ,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:334202

Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 1.

FEATURES
source
Location/Qualifiers
1. .49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:553410"
/tissue_type="embryo"
/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 10 5dpc 10665016"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site: 1; SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. 10.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN
Query Match 50.0%; Score 12; DB 1; Length 49;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GATCGTACGGCTCCTGGAT 24
|||||
Db 21 GACCGGTACGGCTCCTGGTT 40
|||||

RESULT 38
AU103066
LOCUS

DEFINITION
AU103066 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC03739, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC03739"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
|||||
Db 12 GGATCGGACGGGAACCTGGA 31
|||||

RESULT 39
AU104834/c
LOCUS

DEFINITION
AU104834 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG00343, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
JOURNAL
MEDLINE
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072

PUBMED 11375929 Db

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG00343"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGAT 24
||| ||| ||| ||| |||
Db 48 GAAGGCTTCAGCACCTGGAT 29

RESULT 40
AU106612 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU106612 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC00105, mRNA sequence.
ACCESSION AU106612
VERSION AU106612.1 GI:13556133
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyana,A. and Sugano.S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00105"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 50.0%; Score 12; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 7.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCTGG 22
||||| ||| ||| ||| |||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGGATCGTACGGCTCCTGGAT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-07-989-160-1
2	16.2	67.5	25	4	US-09-396-196G-60856
3	15	62.5	33	2	US-08-377-309-12
4	15	62.5	33	3	US-09-186-723-12
5	15	62.5	33	3	US-08-505-012-17
6	15	62.5	33	3	US-08-186-949A-13
7	15	62.5	33	4	US-08-758-757-12
8	15	62.5	33	4	US-09-187-978-12
9	15	62.5	33	4	US-10-115-701A-12
10	15	62.5	33	4	US-09-940-308A-12
11	15	62.5	33	4	US-09-940-308A-12
12	15	62.5	33	5	PCT-US96-00996-17
13	14.6	60.8	32	4	US-09-152-361A-5
14	14.4	60.0	32	3	US-09-183-412-44
15	14.4	60.0	32	4	US-09-769-864-44
16	14.2	59.2	25	4	US-09-396-196G-70013
17	14.2	59.2	25	4	US-09-396-196G-70024
18	14	58.3	25	4	US-08-396-196G-4290
19	13.8	57.5	36	3	US-08-379-802-11
20	13.8	57.5	36	3	US-09-048-129-11
21	13.8	57.5	36	3	US-09-048-079-11
22	13.6	56.7	21	4	US-09-526-191A-233
23	13.6	56.7	25	4	US-09-396-196G-108958
24	13.6	56.7	25	4	US-08-396-196G-108959
25	13.6	56.7	40	3	US-08-827-336-3
26	13.6	56.7	40	3	US-09-357-905-3
27	13.6	56.7	49	2	US-08-960-756-17

28	13.4	55.8	24	3	US-08-506-296B-8	Sequence 8, Appl
29	13.4	55.8	30	2	US-08-465-095-11	Sequence 11, Appl
30	13.4	55.8	30	4	US-08-179-656A-11	Sequence 11, Appl
31	13.4	55.8	30	5	PCT-US94-00300-11	Sequence 11, Appl
32	13.2	55.0	19	4	US-09-696-791-1126	Sequence 1126, Ap
33	13.2	55.0	25	4	US-09-396-196G-126395	Sequence 126395,
34	13.2	55.0	27	3	US-09-347-878-72	Sequence 72, Appl
35	13.2	55.0	27	4	US-09-546-013-91	Sequence 91, Appl
36	13.2	55.0	31	3	US-09-134-078-38	Sequence 38, Appl
37	13	54.2	18	3	US-08-211-882-15	Sequence 15, Appl
38	13	54.2	18	3	US-09-633-659-15	Sequence 15, Appl
39	13	54.2	18	4	US-10-073-718-15	Sequence 15, Appl
40	13	54.2	25	4	US-09-396-196G-22766	Sequence 22766, A
41	13	54.2	25	4	US-09-396-196G-41969	Sequence 41969, A
42	13	54.2	25	4	US-09-396-196G-62126	Sequence 62126, A
43	13	54.2	27	4	US-09-788-319-1	Sequence 1, Appl
44	13	54.2	30	3	US-09-067-091-4	Sequence 4, Appl
45	13	54.2	30	3	US-09-230-222-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-1
; Sequence 1, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-989-160-1

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGGATCGTACGGCTCCTGGAT 24
|||||

```
Db      1 CAAGGATCGCTACGGCTCCTGGAT 24

RESULT 2
US-09-396-196G-60856
; Sequence 60856, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60856
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60856

Query Match      67.5%; Score 16.2; DB 4; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GGATCGCTACGGCTCCTGGAT 24
        ||||| ||||| ||||| |||||
Db      1 GCATGGCTATGGCTCCTGGAT 21

RESULT 3
US-08-377-309-12
; Sequence 12, Application US/08377309A
; Patent No. 5965528
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
; FILE REFERENCE: 06727/005001
; CURRENT APPLICATION NUMBER: US/08/377,309A
; CURRENT FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-377-309-12

Query Match      62.5%; Score 15; DB 2; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGCTACGGCTCCTGGAT 24
        ||||| ||||| ||||| |||||
Db      5 AAGGATCCTTAGCTCTCTGGAT 27

RESULT 4
US-09-186-723-12
; Sequence 12, Application US/09186723
; Patent No. 6288034
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS
; TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
; FILE REFERENCE: 06727/005002
; CURRENT APPLICATION NUMBER: US/09/186,723
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-186-723-12

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGCTACGGCTCCTGGAT 24
        ||||| ||||| ||||| |||||
Db      5 AAGGATCCTTAGCTCTCTGGAT 27

; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/377,309
; EARLIER FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-186-723-12

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGCTACGGCTCCTGGAT 24
        ||||| ||||| ||||| |||||
Db      5 AAGGATCCTTAGCTCTCTGGAT 27

RESULT 5
US-08-505-012-17
; Sequence 17, Application US/08505012
; Patent No. 6331611
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
; TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/505,012
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/377,317
; FILING DATE: 24-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06727/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-505-012-17

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGCTACGGCTCCTGGAT 24
        ||||| ||||| ||||| |||||
Db      5 AAGGATCCTTAGCTCTCTGGAT 27
```

RESULT 6
US-09-186-949A-13
; Sequence 13, Application US/09186949A
; Patent No. 6416734
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Alpha-Fetoprotein For
; TITLE OF INVENTION: Treating and Diagnosing Cancers
; FILE REFERENCE: 06727/004002
; CURRENT APPLICATION NUMBER: US/09/186,949A
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/758,757
; PRIOR FILING DATE: 1996-12-03
; PRIOR APPLICATION NUMBER: US 08/377,311
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Based on Homo sapiens
US-09-186-949A-13

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 7
US-08-758-757-12
; Sequence 12, Application US/08758757
; Patent No. 6534479
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: RECOMBINANT ALPHA-FETOPROTEIN FOR
; TITLE OF INVENTION: TREATING AND DIAGNOSIS
; FILE REFERENCE: 06727/004001
; CURRENT APPLICATION NUMBER: US/08/758,757
; CURRENT FILING DATE: 1996-12-03
; EARLIER APPLICATION NUMBER: 08/377,311
; EARLIER FILING DATE: 1995-01-24
; EARLIER APPLICATION NUMBER: 08/758,757
; EARLIER FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-758-757-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 8
US-09-187-978-12
; Sequence 12, Application US/09187978A
; Patent No. 6627440
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.

; TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A
; TITLE OF INVENTION: CELL PROLIFERATIVE AGENT
; FILE REFERENCE: 06727/006002
; CURRENT APPLICATION NUMBER: US/09/187,978A
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: 08/377,316
; EARLIER FILING DATE: 1995-01-24
; EARLIER APPLICATION NUMBER: 08/879,469
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-187-978-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 9
US-10-115-701A-12
; Sequence 12, Application US/10115701A
; Patent No. 6630445
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Alpha-Fetoprotein for
; TITLE OF INVENTION: Treating and Diagnosing Cancers
; FILE REFERENCE: 06727/004003
; CURRENT APPLICATION NUMBER: US/10/115,701A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 08/758,757
; PRIOR FILING DATE: 1996-12-03
; PRIOR APPLICATION NUMBER: 08/377,311
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-701A-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| ||| |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 10
US-09-940-308A-12
; Sequence 12, Application US/09940308A
; Patent No. 6656909
; GENERAL INFORMATION:
; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; TITLE OF INVENTION: an Immunosuppressive Agent
; FILE REFERENCE: 06727/005003
; CURRENT APPLICATION NUMBER: US/09/940,308A
; CURRENT FILING DATE: 2001-08-27

; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-940-308A-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 11

US-09-940-308A-12
; Sequence 12, Application US/09940308A
; Patent No. 6774108
; GENERAL INFORMATION:

; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: Recombinant Human Alpha-Fetoprotein as
; FILE REFERENCE: an Immunosuppressive Agent
; CURRENT APPLICATION NUMBER: US/09/940,308A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 09/186,723
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 08/377,309
; PRIOR FILING DATE: 1995-01-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-940-308A-12

Query Match 62.5%; Score 15; DB 4; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 12

PCT-US96-00996-17
; Sequence 17, Application PC/TUS9600996
; GENERAL INFORMATION:

; APPLICANT: Murgita, Robert A.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF CLONED
; TITLE OF INVENTION: HUMAN ALPHA-FETOPROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00996
; FILING DATE: 24-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,317
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,311
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,309
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/377,316
; FILING DATE: 24-JAN-1995
; CLASSIFICATION:
; APPLICATION NUMBER: 08/505,012
; FILING DATE: 21-JULY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06727/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-00996-17

Query Match 62.5%; Score 15; DB 5; Length 33;
Best Local Similarity 78.3%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTCTGGAT 24
||||| || |||||
Db 5 AAGGATCCTTAGCTCTCTCTGGAT 27

RESULT 13

US-09-152-361A-5
; Sequence 5, Application US/09152361A
; Patent No. 6656735
; GENERAL INFORMATION:

; APPLICANT: Wurst, Wolfgang
; APPLICANT: Prochaintz, Alain
; APPLICANT: GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH
; APPLICANT: Centre National de la Recherche Scientifique
; TITLE OF INVENTION: Method for Identification of Target Genes of
; TITLE OF INVENTION: Transcription Factors
; FILE REFERENCE: 080314-000000US
; CURRENT APPLICATION NUMBER: US/09/152,361A
; CURRENT FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: DE 197 40 578.9
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer for
; OTHER INFORMATION: Isolation of 60 amino acid homeodomain of chicken
; OTHER INFORMATION: Engrailed 2 (EnHD) protein from plasmid containing
; OTHER INFORMATION: chicken cDNA sequence

US-09-152-361A-5

Query Match 60.8%; Score 14.6; DB 4; Length 32;
Best Local Similarity 81.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||| |||
Db 4 GGATCCCTACGGCTTCTTGGAT 24

RESULT 14

US-09-183-412-44/c
; Sequence 44, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-183-412-44

Query Match 60.0%; Score 14.4; DB 3; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGTCCTGGTT 8

RESULT 15

US-09-769-864-44/c
; Sequence 44, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44

; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-769-864-44

Query Match 60.0%; Score 14.4; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGAT 24
||| ||||| ||||| |||||
Db 31 CATTGATCGTAACGGGTCCTGGTT 8

RESULT 16

US-09-396-196G-70013
; Sequence 70013, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70013
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70013

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCTGGA 23
||| ||||| ||||| |||||
Db 6 GATCGGACTGCTCGGGA 24

RESULT 17

US-09-396-196G-70024
; Sequence 70024, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70024

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTCGGA 23
|||||
Db 4 GATCGGACTGCTCGGGA 22

RESULT 18

US-09-396-196G-4290/c
; Sequence 4290, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4290

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-4290

Query Match 58.3%; Score 14; DB 4; Length 25;

Best Local Similarity 77.3%; Pred. No. 1.9e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCGG 22

|||||

Db 22 CTAGGATCTCGGAGGCTGG 1

RESULT 19

US-08-379-802-11

; Sequence 11, Application US/08379802

; Patent No. 6057124

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/379, 802

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-325

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

US-08-379-802-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;

Best Local Similarity 88.2%; Pred. No. 2.6e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18

|||||

Db 5 AAGGATCCCTATGGCTC 21

RESULT 20

US-09-048-129-11

; Sequence 11, Application US/09048129

; Patent No. 6063903

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/048,129

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/379,802

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-325

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

US-09-048-129-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;

Best Local Similarity 88.2%; Pred. No. 2.6e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTC 18

|||||

Db 5 AAGGATCCCTATGGCTC 21

RESULT 21

US-09-048-079-11

; Sequence 11, Application US/09048079

; Patent No. 6169167

GENERAL INFORMATION:

; APPLICANT: Bartley, Timothy D.

; APPLICANT: Fox, Gary M.

; TITLE OF INVENTION: Ligands for EPH-Like Receptor

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,079
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,802
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-325
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-048-079-11

Query Match 57.5%; Score 13.8; DB 3; Length 36;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGATCGCTACGGCTC 18
|||||
Db 5 AAGATCGCTACGGCTC 21

RESULT 22
US-09-526-193A-233/c
; Sequence 233, Application US/09526193A
; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pinstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; TITLE OF INVENTION: CHOLESTEROL LEVELS
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-233

Query Match 56.7%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCCT 20
|||||
Db 20 CAATGAGCGCTTGGCTCCT 1

RESULT 23
US-09-396-196G-108958
; Sequence 108958, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108958

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
|||||
Db 4 GAATCGCTACGGTCCAGGA 23

RESULT 24
US-09-396-196G-108959
; Sequence 108959, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108959

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGA 23
|||||
Db 1 GAATCGCTACGGTCCAGGA 20

RESULT 25
US-08-827-336-3/c
; Sequence 3, Application US/08827336
; Patent No. 6004780
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL
; TITLE OF INVENTION: GROWTH FACTOR HTER36

;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/827,336
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROOKES, ANDY, A.
;; REGISTRATION NUMBER: 36,373
;; REFERENCE/DOCKET NUMBER: PF230
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8504
;; TELEFAX: 301-309-8512
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-827-336-3

Query Match 56.7%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%; Pred.No.3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
Db 23 CAGGGATGGCTGCGGATCCT 4

RESULT 26
US-09-357-905-3/c
; Sequence 3, Application US/09357905
; Patent No. 6413933
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL
; TITLE OF INVENTION: GROWTH FACTOR HTT36
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,905
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,336
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDY, A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF230

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8504
;; TELEFAX: 301-309-8512
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 40 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-357-905-3

Query Match 56.7%; Score 13.6; DB 3; Length 40;
Best Local Similarity 80.0%; Pred.No.3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20
Db 23 CAGGGATGGCTGCGGATCCT 4

RESULT 27
US-08-960-756-17/c
; Sequence 17, Application US/08960756
; Patent No. 5866422
; GENERAL INFORMATION:
; APPLICANT: WAYNE, JAY
; APPLICANT: XU, SHUANG-YONG
; TITLE OF INVENTION: METHOD FOR CLONING AND
; TITLE OF INVENTION: PRODUCING THE Tsp45I RESTRICTION ENDONUCLEASE IN E. COLI
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,756
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Synthetic DNA
US-08-960-756-17

Query Match 56.7%; Score 13.6; DB 2; Length 49;
Best Local Similarity 80.0%; Pred.No.3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCT 20

Db 45 CCAGGCTAGCTACGGCTCAT 26
|||||

RESULT 28
US-08-506-296B-8

; Sequence 8, Application US/08506296B
; Patent No. 6313265

; GENERAL INFORMATION:

; APPLICANT: Phillips, Greg

; APPLICANT: Cunningham, Bruce A.

; APPLICANT: Crossin, Kathryn L.

; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES

; TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute

; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8

; CITY: La Jolla

; STATE: California

; COUNTRY: U.S.

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/506,296B

; FILING DATE: 24-JUL-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: TSRI 488.0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 554-2937

; TELEFAX: (619) 554-6312

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-506-296B-8

Query Match 55.8%; Score 13.4; DB 3; Length 24;

Best Local Similarity 73.9%; Pred. No. 3.8e+03;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCTGGAT 24

Db 2 AAGGATCGCTACCGCCCTTGT 24

RESULT 29

US-08-465-095-11

; Sequence 11, Application US/08465095

; Patent No. 5849534

; GENERAL INFORMATION:

; APPLICANT: Grotendorst, Gary R.

; APPLICANT: Iida, Naoka

; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,095

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/179,656

; FILING DATE: 07-JAN-1994

; APPLICATION NUMBER: 08/001,177

; FILING DATE: 07-JAN-1993

; APPLICATION NUMBER: 07/472,377

; FILING DATE: 01-FEB-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Elizabeth A. Hanley

; REGISTRATION NUMBER: 33,505

; REFERENCE/DOCKET NUMBER: GZI-003C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-465-095-11

Query Match 55.8%; Score 13.4; DB 2; Length 30;

Best Local Similarity 73.9%; Pred. No. 3.9e+03;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTGGGA 23

Db 4 CGACGTGGCGACGACTCTGGGA 26

RESULT 30

US-08-179-656A-11

; Sequence 11, Application US/08179656A

; Patent No. 6673893

; GENERAL INFORMATION:

; APPLICANT: Grotendorst, Gary R.

; APPLICANT: Iida, Naoka

; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/179,656A

; FILING DATE: 07-JAN-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/001,177

; FILING DATE: 07-JAN-1993

; APPLICATION NUMBER: 07/472,377

; FILING DATE: 01-FEB-1990

; ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: G21-003C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-179-656A-11

Query Match 55.8%; Score 13.4; DB 4; Length 30;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 31
PCT-US94-00300-11
Sequence 11, Application PC/TUS9400300
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Iida, Naoka
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00300
FILING DATE: 07-JAN-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/001,177
FILING DATE: 07-JAN-1993
APPLICATION NUMBER: 07/472,377
FILING DATE: 01-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: G21-003C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US94-00300-11

Query Match 55.8%; Score 13.4; DB 5; Length 30;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCTCTGGA 23
Db 4 CGACGGTGGCGACGACTCTCTGGA 26

RESULT 32
US-09-696-791-1126
Sequence 1126, Application US/09696791
Patent No. 6770633
GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1126
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1126

Query Match 55.0%; Score 13.2; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCCT 20
Db 1 AGGAGGCTTCGGCTCCT 18

RESULT 33
US-09-396-196G-126395
Sequence 126395, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 126395
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-126395

Query Match 55.0%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATCGCTACGGCTCTCTGGA 23
Db 1 ATAGCTACAGTTCTCTGGA 18

RESULT 34
US-09-347-878-72
Sequence 72, Application US/09347878C
Patent No. 6376210
GENERAL INFORMATION:

```
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
; OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (13)..(15)
; OTHER INFORMATION: Codon change from CGC to GCC
US-09-347-878-72

Query Match          55.0%; Score 13.2; DB 3; Length 27;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  GGATCGCTACGGCTCCTG 21
        ||||| ||||| |||||
Db      3  GGATCACTACGCCTACTG 20

RESULT 35
US-09-546-013-91
; Sequence 91, Application US/09546013
; Patent No. 6610504
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong-Shen
; TITLE OF INVENTION: METHODS FOR ASSAYING S-ADENOSYLMETHIONINE-DEPENDENT Methyltransfe
; FILE REFERENCE: 10937-1652
; CURRENT APPLICATION NUMBER: US/09/546,013
; CURRENT FILING DATE: 2000-04-10
; EARLIER APPLICATION NUMBER: 09/347,878
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 09/457,205
; EARLIER FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
; OTHER INFORMATION: of Human SAH hydrolase (mutant R431A)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (13)..(15)
; OTHER INFORMATION: Codon change from CGC to GCC
US-09-546-013-91

Query Match          55.0%; Score 13.2; DB 4; Length 27;
Best Local Similarity 83.3%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  GGATCGCTACGGCTCCTG 21
        ||||| ||||| |||||
Db      3  GGATCACTACGCCTACTG 20

RESULT 36
US-09-134-078-38
; Sequence 38, Application US/09134078
; Patent No. 6368844
```

```
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lies A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-134-078-38

Query Match          55.0%; Score 13.2; DB 3; Length 31;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  AGGATCGCTACGGCTCCT 20
        ||||| ||||| |||||
Db      4  AGGATCCCTACCCCTCCT 21

RESULT 37
US-08-211-882-15/c
; Sequence 15, Application US/08211882
; Patent No. 6153737
; GENERAL INFORMATION:
; APPLICANT: Manoharan et al.
; TITLE OF INVENTION: Derivatized Oligonucleotides Having
; TITLE OF INVENTION: Improved Uptake And Other Properties
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6153737ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,882
```

```
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,374
; FILING DATE: 24-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-0649
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-211-882-15

Query Match 54.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 38
US-09-633-659-15/c
; Sequence 15, Application US/09633659
; Patent No. 6395492
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Bennett, Clarence Frank
; TITLE OF INVENTION: Derivatized Oligonucleotides Having Improved Uptake And
; TITLE OF INVENTION: Other Properties
; FILE REFERENCE: ISIS4470
; CURRENT APPLICATION NUMBER: US/09/633,659
; CURRENT FILING DATE: 2000-08-07
; PRIOR FILING DATE: 08/211,882
; PRIOR FILING DATE: 1994-04-22
; PRIOR APPLICATION NUMBER: 07/782,374
; PRIOR FILING DATE: 1991-10-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6395492e1 Sequence
US-09-633-659-15

Query Match 54.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 39
US-10-073-718-15/c
; Sequence 15, Application US/10073718
; Patent No. 6831166
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Bennett, Clarence Frank
```

```
; TITLE OF INVENTION: Derivatized Oligonucleotides Having Improved Uptake and Other Pro
; FILE REFERENCE: ISIS-5024
; CURRENT APPLICATION NUMBER: US/10/073,718
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 09/633659
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 6153737
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/211882
; PRIOR FILING DATE: 1994-04-22
; PRIOR APPLICATION NUMBER: PCT/US92/09196
; PRIOR FILING DATE: 1992-10-23
; PRIOR APPLICATION NUMBER: 07/782374
; PRIOR FILING DATE: 1991-10-24
; PRIOR APPLICATION NUMBER: 07/566977
; PRIOR FILING DATE: 1990-08-13
; PRIOR APPLICATION NUMBER: PCT/US91/000243
; PRIOR FILING DATE: 1991-01-11
; PRIOR APPLICATION NUMBER: 08/463359
; PRIOR FILING DATE: 1990-01-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6831166e1 Sequence
US-10-073-718-15

Query Match 54.2%; Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TCGCTACGGCTCC 19
Db 15 TCGCTACGGCTCC 3

RESULT 40
US-09-396-196G-22766/c
; Sequence 22766, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22766
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-22766

Query Match 54.2%; Score 13; DB 4; Length 25;
Best Local Similarity 76.2%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTG 21
Db 21 CACGGGTGGCTATAGCTCCTG 1

Search completed: November 18, 2005, 11:21:57
Job time : 47.6312 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-1

Perfect score: 24

Sequence: 1 CAAGATCGTACGCTCTCGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
13:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
14:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
17:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
18:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
19:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
20:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq*
21:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq*
22:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
23:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
24:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
25:	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
26:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
27:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
28:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	US-08-469-172-1	Sequence 1, Appli
2	24	100.0	24	US-10-788-779-1	Sequence 1, Appli
3	16.2	67.5	25	US-10-809-189-60856	Sequence 60856, A
4	16.2	67.5	26	US-10-938-249-375	Sequence 375, App
5	16.2	67.5	26	US-11-131-054-362	Sequence 362, App

6	16.2	67.5	26	US-11-131-042-362	Sequence 362, App
7	15.8	65.8	25	US-11-036-317-219546	Sequence 219546,
8	15.2	63.3	24	US-10-484-989-79	Sequence 79, Appl
9	15.2	63.3	25	US-10-098-263B-105576	Sequence 105576,
10	15.2	63.3	25	US-10-098-263B-106202	Sequence 106202,
11	15.2	63.3	25	US-10-719-900-572806	Sequence 572806,
12	15.2	63.3	25	US-10-719-956-368379	Sequence 368379,
13	15	62.5	24	US-10-719-956-44525	Sequence 44525, A
14	15	62.5	25	US-10-719-956-44526	Sequence 44526, A
15	15	62.5	25	US-11-036-317-783296	Sequence 783296,
16	15	62.5	25	US-11-036-317-869432	Sequence 869432,
17	15	62.5	33	US-09-940-308-12	Sequence 12, Appl
18	15	62.5	33	US-09-940-308-12	Sequence 12, Appl
19	15	62.5	33	US-10-115-701A-12	Sequence 12, Appl
20	15	62.5	33	US-10-838-476-12	Sequence 166635,
21	14.8	61.7	25	US-11-036-317-166635	Sequence 1340, Ap
22	14.6	60.8	24	US-09-940-185-1340	Sequence 106263,
23	14.6	60.8	25	US-10-098-263B-106263	Sequence 72142, A
24	14.6	60.8	25	US-11-036-317-72142	Sequence 421165,
25	14.6	60.8	25	US-11-036-317-421165	Sequence 936457,
26	14.6	60.8	25	US-11-036-317-936457	Sequence 238398,
27	14.4	60.0	25	US-10-719-900-298398	Sequence 298476,
28	14.4	60.0	25	US-10-719-900-298476	Sequence 564538,
29	14.4	60.0	25	US-10-956-157-177036	Sequence 177036,
30	14.4	60.0	31	US-09-877-478-5195	Sequence 5195, Ap
31	14.4	60.0	31	US-10-342-902-5195	Sequence 5195, Ap
32	14.4	60.0	31	US-10-669-841-10086	Sequence 10086, A
33	14.4	60.0	32	US-09-769-864-44	Sequence 44, Appl
34	14.4	60.0	32	US-10-665-667-44	Sequence 44, Appl
35	14.4	60.0	32	US-10-980-923-44	Sequence 28357, A
36	14.4	60.0	25	US-10-098-263B-28357	Sequence 70013, A
37	14.2	59.2	25	US-10-809-189-70013	Sequence 70024, A
38	14.2	59.2	25	US-10-809-189-70024	Sequence 168189,
39	14.2	59.2	25	US-10-956-157-168189	Sequence 230829,
40	14.2	59.2	25	US-10-719-956-260417	Sequence 260417,
41	14.2	59.2	25	US-10-719-956-260417	Sequence 488626,
42	14.2	59.2	25	US-10-719-956-488626	Sequence 276920,
43	14.2	59.2	25	US-11-036-317-276920	Sequence 334044,
44	14.2	59.2	25	US-11-036-317-334044	
45	14.2	59.2	25	US-11-036-317-334044	

ALIGNMENTS

RESULT 1

US-08-469-172-1

; Sequence 1, Application US/08469172

; Publication No. US20030054343A1

GENERAL INFORMATION:

APPLICANT: SEIDMAN, CHRISTINE

APPLICANT: SEIDMAN, JOHN

APPLICANT: WATKINS, HUGH

APPLICANT: ROSENZWEIG, ANTHONY

TITLE OF INVENTION: A METHOD FOR DETECTING

TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, Suite 510

CITY: BOSTON

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,172

FILING DATE:

CLASSIFICATION:

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-1

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCCTGGAT 24
Db 1 CAAGATCGCTACGGCTCCTGGAT 24

RESULT 2
US-10-788-779-1
; Sequence 1, Application US/10788779
; Publication No. US2004015121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-788-779-1

Query Match 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGATCGCTACGGCTCCTGGAT 24
Db 1 CAAGATCGCTACGGCTCCTGGAT 24

RESULT 3
US-10-809-189-60856
; Sequence 60856, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60856
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-60856

Query Match 67.5%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCCTGGAT 24
Db 1 GCATGGCTATGGCTCCTGGAT 21

RESULT 4
US-10-938-249-375
; Sequence 375, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; Cells
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
```

```
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: forward primer 158KIF
US-10-938-249-375
```

```
Query Match          67.5%; Score 16.2; DB 22; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCGG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCTCG 22
```

```
RESULT 5
; Sequence 362, Application US/11131054
; Publication No. US20050214869A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,054
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 362
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 158KIF forward primer
US-11-131-054-362
```

Remaining Prior Application data removed - See File Wrapper or PALM.

```
Query Match          67.5%; Score 16.2; DB 26; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCTCG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCTCG 22
```

```
RESULT 6
US-11-131-042-362
; Sequence 362, Application US/11131042
; Publication No. US20050221388A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 020054-001110US
; CURRENT APPLICATION NUMBER: US/11/131,042
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: US/09/688,017
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 383
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 362
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 158KIF forward primer
US-11-131-042-362
```

```
Query Match          67.5%; Score 16.2; DB 26; Length 26;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAGGATCGCTACGGCTCTCTCG 22
    ||||| || ||||| ||
Db 2 AAGGATCCCTCCGGCTCTCTCG 22
```

```
RESULT 7
US-11-036-317-219546
; Sequence 219546, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
```

```
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-219546

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCC 19
Db 1 CAAGGACCGCTACAGTCC 19

RESULT 8
US-10-484-989-79
; Sequence 79, Application US/10484989
; Publication No. US20040171154A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Storici, Francesca
; APPLICANT: Resnick, Michael A.
; APPLICANT: Lewis, Lysle Kevin
; TITLE OF INVENTION: SYSTEMS FOR IN VIVO SITE-DIRECTED MUTAGENESIS USING
; FILE REFERENCE: 4239-67608
; CURRENT APPLICATION NUMBER: US/10/484,989
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/308,426
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/23634
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-484-989-79

Query Match      63.3%; Score 15.2; DB 20; Length 24;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGGATCGCTACGGCTCTCGG 22
Db 3 AGGATCGCGCGGCTCCGG 22

RESULT 9
US-10-098-263B-105576/c
; Sequence 105576, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-105576

Query Match      63.3%; Score 15.2; DB 16; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTGGAT 24
Db 25 GGTCCTACGGGTCTGGAT 6

RESULT 10
US-10-098-263B-106202/c
; Sequence 106202, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-106202

Query Match      63.3%; Score 15.2; DB 16; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCTGGAT 24
Db 25 GGTCCTACGGGTCTGGAT 6

RESULT 11
US-10-719-900-572806
; Sequence 572806, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 572806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-572806

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGATCGCTACGGCTCTGGA 23
Db 5 GGACCGCTACGGCCCCAGGA 24
```

```
RESULT 12
US-10-719-956-368379
; Sequence 368379, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 368379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-368379

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 GATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 GATGCTACCGCTTCTGGAT 20

RESULT 13
US-10-719-956-44525
; Sequence 44525, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44525

Query Match      62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 AAGGACCGCTACATCTCCAAGAT 23

RESULT 14
US-10-719-956-44526
; Sequence 44526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-44526

Query Match      62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCGGAT 24
      ||| |||| |||| |||| ||||
Db      1 AAGGACCGCTACATCTCCAAGAT 23

RESULT 15
US-11-036-317-783296/c
; Sequence 783296, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 783296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-783296

Query Match      62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAAGATCGTACGGCTCTCTGGA 23
      ||| |||| |||| |||| ||||
Db      23 CAAGACCTCTCCGGCTCCTAGA 1

RESULT 16
US-11-036-317-869432
; Sequence 869432, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 869432
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-869432

Query Match      62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAGGATCGTACGGCTCTCTGAT 24
      ||| |||| |||| |||| ||||
Db      3 AAGGCAAGCTTCGGCTCTCGCT 25
```

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

```

; NAME OF SEQ ID NO.: 110608
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106263
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-106263

```

```

Query Match      60.8%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  CAAGGATCGCTACGGCTCTCG 21
      ||| ||| ||| ||| ||| |||
Db       2  CATGGACGGACGGCTCCAG 22

RESULT 26
US-11-036-317-936457
; Sequence 936457, Application US/11036317

```

```
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 936457
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-936457

Query Match      60.8%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAGGATCGCTACGGCTCTCTGG 22
    ||||| ||||| ||||| |||||
Db  5 AAGGCAAGCTTCGGCTCTCTGG 25

RESULT 27
US-10-719-900-298398
; Sequence 298398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 298398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-298398

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGAGCTCTTCGGCTCTGTGGAT 24

RESULT 28
US-10-719-900-298476
; Sequence 298476, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 298476
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-298476

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGAGCTCTTCGGCTCTGTGGAT 24
```

```
; ORGANISM: Mus musculus
US-10-719-900-298476

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAAGGATGGCGACGTTTACTGCGAT 24

RESULT 29
US-10-719-900-564538
; Sequence 564538, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 564538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-564538

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  2 CTATGATGGCTACCGCATCTGGAT 25

RESULT 30
US-10-956-157-177036
; Sequence 177036, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 177036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-177036

Query Match      60.0%; Score 14.4; DB 22; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 CAAGATCGCTACGGCTCTCTGGAT 24
    ||||| ||||| ||||| |||||
Db  1 CAGTGATCGCTACTGCACTTGAT 24

RESULT 31
US-09-877-478-5195
; Sequence 5195, Application US/09877478
```


Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5195
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-5195

Query Match 60.0%; Score 14.4; DB 10; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAGGATCGTACGGCTCTGGAT 24
||||| ||||| ||||| |||||
DB 6 CAAGGCTAGCTACAACGACTGGAT 29

RESULT 32
US-10-342-902-5195
Sequence 5195, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MEH00-845-I)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5195
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-5195

Query Match 60.0%; Score 14.4; DB 19; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAAGGATCGTACGGCTCTGGAT 24
||||| ||||| ||||| |||||
DB 6 CAAGGCTAGCTACAACGACTGGAT 29

RESULT 33
US-10-669-841-10086
Sequence 10086, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patrice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MBH02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10086
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-669-841-10086

Query Match 60.0%; Score 14.4; DB 20; Length 31;
Best Local Similarity 75.0%; Pred. No. 9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 6 CAAGGATCGTACAAAGACTGGAT 29

RESULT 34
US-09-769-864-44/c
; Sequence 44, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-769-864-44

Query Match 60.0%; Score 14.4; DB 9; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 31 CATTGATCGTAACGGGCTCTGGTT 8

RESULT 35
US-10-665-667-44/c
; Sequence 44, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-665-667-44

Query Match 60.0%; Score 14.4; DB 19; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 31 CATTGATCGTAACGGGCTCTGGTT 8

RESULT 36
US-10-980-923-44/c
; Sequence 44, Application US/10980923
; Publication No. US20050084937A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/980,923
; CURRENT FILING DATE: 2004-11-04
; PRIOR FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-980-923-44

Query Match 60.0%; Score 14.4; DB 22; Length 32;
Best Local Similarity 75.0%; Pred. No. 8.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGGATCGCTACGGCTCCTGGAT 24
Db 31 CATTGATCGTAACGGGCTCTGGTT 8

RESULT 37
US-10-098-263B-28357
; Sequence 28357, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-28357

Query Match 59.2%; Score 14.2; DB 16; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTGGA 23
||||| ||||| ||||| |||
```

Db 1 GATCTTAAGGCTCCAGGA 19

RESULT 38

US-10-809-189-70013
; Sequence 70013, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70013
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-70013

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTCGGA 23

Db 6 GATCGGAGTGTCTCGGGA 24

RESULT 39

US-10-809-189-70024
; Sequence 70024, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-70024

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GATCGCTACGGCTCCTCGGA 23

Db 4 GATCGGAGTGTCTCGGGA 22

RESULT 40

US-10-956-157-168189/c

; Sequence 168189, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168189
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-168189

Query Match 59.2%; Score 14.2; DB 22; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGATCGCTACGGCTCCT 20

Db 21 AAGGATCGCTACGGCTACT 3

Search completed: November 18, 2005, 15:41:02
Job time : 324.586 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30
Sequence: 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	30	I12895	I12895 Sequence 2
C 2	16.6	55.3	34	E59888	E59888 Method for
C 3	15.6	52.0	23	AX59517	AX59517 Sequence
4	15.6	52.0	41	AR359198	AR359198 Sequence
C 5	15.6	52.0	45	E31326	E31326 Process for
C 6	15.6	52.0	45	AR301265	AR301265 Sequence
7	15.6	52.0	50	E31327	E31327 Process for
8	15.6	52.0	50	AR301266	AR301266 Sequence
9	15.4	51.3	29	BD222501	BD222501 Novel met
10	15.4	51.3	29	AX647902	AX647902 Sequence
C 11	15.4	51.3	30	BD103433	BD103433 A carcino
12	15.4	51.3	33	AX453416	AX453416 Sequence
13	15.2	50.7	42	E51173	E51173 Method for
14	15.2	50.7	42	E51191	E51191 Process for
15	15.2	50.7	42	AR399392	AR399392 Sequence
16	15.2	50.7	42	AX137508	AX137508 Sequence
17	15	50.0	29	BD240955	BD240955 A novel h
18	15	50.0	29	AR437642	AR437642 Sequence
19	14.8	49.3	25	AR173178	AR173178 Sequence

20	14.8	49.3	37	6	AR183091	Sequence
21	14.6	48.7	24	6	AX956456	Sequence
22	14.6	48.7	31	6	AR137780	Sequence
23	14.6	48.7	31	6	BD192813	Improved
24	14.6	48.7	44	6	AX955017	Sequence
25	14.4	48.0	27	6	AX033626	Sequence
26	14.4	48.0	31	6	AR071455	Sequence
27	14.4	48.0	33	6	AR071444	Sequence
28	14.4	48.0	40	6	AR152460	Sequence
29	14.4	48.0	40	6	AX456419	Sequence
C 30	14.4	48.0	44	6	AR143578	Sequence
C 31	14.4	48.0	44	6	AR168947	Sequence
C 32	14.4	48.0	44	6	AR232695	Sequence
C 33	14.4	48.0	44	6	AR262637	Sequence
C 34	14.4	48.0	44	6	AR316574	Sequence
C 35	14.4	48.0	45	6	BD188256	BHLH-PAS
C 36	14.4	48.0	45	6	AX456402	Sequence
37	14.2	47.3	20	6	AX477123	Sequence
38	14.2	47.3	20	6	AX526499	Sequence
39	14.2	47.3	28	6	CQ878078	Sequence
40	14.2	47.3	28	6	AR184482	Sequence
41	14.2	47.3	30	6	I36158	Sequence 42
42	14.2	47.3	31	6	CQ855152	Sequence
43	14.2	47.3	34	6	E10783	PCR primer
44	14.2	47.3	39	6	AR121200	Sequence
45	14.2	47.3	39	6	AR160328	Sequence

ALIGNMENTS

RESULT 1
LOCUS I12895 I12895 30 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 2 from patent US 5429923.
ACCESSION I12895
VERSION I12895.1 GI:910872
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 2 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 2
LOCUS E59888/c E59888 34 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting micromutated DNA.
ACCESSION E59888
VERSION E59888.1 GI:18622724
KEYWORDS JP 2000308489-A/4.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 34)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

```

AUTHORS      Yokota, H. and Goto, K.
TITLE        Method for detecting microtutated DNA
JOURNAL      DAI ICHI SEIYAKU CO LTD
COMMENT      OS Pseudomonas aeruginosa
              PD 07-NOV-2000
              PF 28-APR-1999 JP 1999121957
              PI HIROSHI YOKOTA, KOSHICHI GOTO
              PC
C12N15/09, C12Q1/68// (C12N15/09, C12R1:385), (C12Q1/68, C12R1:385), PC
C12N15/00, C12N15/00, C12R1:385)
PC          (C12N15/00, C12R1:385)
CC          Key Location/Qualifiers
FH          1..34
FT          source
FEATURES     Location/Qualifiers
              1..34
              /organism="Pseudomonas aeruginosa"
              /mol_type="genomic DNA"
              /db_xref="taxon:287"
ORIGIN
Query Match      55.3%; Score 16.6; DB 6; Length 34;
Best Local Similarity 82.6%; Pred. No. 1.4e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      8 CAGGTAGGCAGACTTGTGCAGCCT 30
        ||| ||| ||| ||| ||| ||| |||
Db      27 CAGGAGGCAGACTTGTGCAGCCT 5

RESULT 3
AX659517/c
LOCUS      AX659517      23 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 72 from Patent WO03000897.
ACCESSION  AX659517
VERSION     AX659517.1 GI:29161733
KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
AUTHORS     Paszkowski, U., Briggs, S., Cooper, B., Goff, S., Moughamer, T.,
            Glazebrook, J., Katagiri, F., Kreps, J., Provart, N., Riecke, D. and
            Zhu, T.
TITLE       Identification and characterization of phosphate transporter genes
JOURNAL     Syngenta Participations AG (CH)
FEATURES     Location/Qualifiers
              1..23
              /organism="Oryza sativa"
              /mol_type="unassigned DNA"
              /db_xref="taxon:4530"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 23;
Best Local Similarity 81.8%; Pred. No. 4.5e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      8 CAGGTAGGCAGACTTGTGCAGC 29
        ||| ||| ||| ||| ||| ||| |||
Db      23 CAATAGGCAGACTTGTGACC 2

RESULT 4
AR359198
LOCUS      AR359198      41 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6593124.

```

```

ACCESSION    AR359198
VERSION      AR359198.1 GI:33765364
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unidentified.
REFERENCE    1 (bases 1 to 41)
AUTHORS      Lupton, S.D., Allen, J.M. and Feldhaus, A.L.
TITLE        Hybrid genes for expression of stimulatory factors in activated T
              cells
JOURNAL      Patent: US 6593124-A 14 15-JUL-2003;
FEATURES     Location/Qualifiers
              1..41
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 41;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CGGATCCAGGTAGGCAGACTTG 23
        ||| ||| ||| ||| ||| ||| |||
Db      8 CGGATCCAGGAGGCTGCCCTG 29

RESULT 5
E31326/c
LOCUS      E31326      45 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Process for producing novel microbial transglutaminase.
ACCESSION  E31326
VERSION     E31326.1 GI:13025716
KEYWORDS    JP 1999075876-A/25.
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
            1 (bases 1 to 45)
            Keiichi, Y., Nami, N., Tetsuya, M. and Katsuya, S.
            Process for producing novel microbial transglutaminase
            Patent: JP 1999075876-A 25 23-MAR-1999;
            AJINOMOTO CO INC
COMMENT      OS Unidentified
            PN JP 1999075876-A/25
            PD 23-MAR-1999
            PF 29-JUN-1998 JP 1998181951
            PR
            PI KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUYA MIWA, KATSUYA SEGURO PC
            C12N15/09, C12N1/21, C12N9/10// (C12N1/21, C12R1:19), (C12N9/10, PC
            C12R1:19),
PC          C12N15/00
CC          Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source 1..45
            FT /organism='Unidentified'.
FEATURES     Location/Qualifiers
              1..45
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC 26
        ||| ||| ||| ||| ||| ||| |||
Db      42 ATCCAGGTAGGCAGATTCATCA 21

RESULT 6
AR301265/c

```

```
LOCUS       AR301265               45 bp    DNA             linear     PAT 12-JUN-2003
DEFINITION   Sequence 26 from patent US 6538122.
ACCESSION   AR301265
VERSION     AR301265.1   GI:31689038
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 45)
AUTHORS   Yokoyama,K., Nakamura,N., Miwa,T. and Seguro,K.
TITLE     Process for producing microbial transglutaminase
JOURNAL   Patent: US 6538122-A 26 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
        ||||| ||||| ||||| |||||
Db      42 ATCCAGGTAAGCAGATTCATCA 21

RESULT 7
E31327
LOCUS       E31327               50 bp    DNA             linear     PAT 18-JUN-2001
DEFINITION   Process for producing novel microbial transglutaminase.
ACCESSION   E31327
VERSION     E31327.1   GI:13025717
KEYWORDS    JP 199075876-A/26.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS   Keiichi,Y., Nami,N., Tetsuya,M. and Katsuya,S.
TITLE     Process for producing novel microbial transglutaminase
JOURNAL   Patent: JP 199075876-A 26 23-MAR-1999;
COMMENT    AJINOMOTO CO INC
OS      Unidentified
PN      JP 199075876-A/26
PD      23-MAR-1999
PE      23-JUN-1998   JP 1998181951
PR
PI      KEIICHI YOKOYAMA, NAMI NAKAMURA, TETSUYA MIWA, KATSUYA SEGURO PC
        C12N15/09,C12N1/21,C12N9/10//C12N1/21,C12R1:19), (C12N9/10, PC
        C12R1:19),
PC      C12N15/00
CC      Strandedness: Single;
CC      Topology: Linear;
FH      Key      Location/Qualifiers
FT      source   1..50
        FT      /organism='Unidentified'.
        FEATURES             Location/Qualifiers
     source          1..50
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

ORIGIN
Query Match      52.0%; Score 15.6; DB 6; Length 50;
Best Local Similarity 81.8%; Pred. No. 4.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
        ||||| ||||| ||||| |||||
Db      13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 8
LOCUS       AR301266               50 bp    DNA             linear     PAT 12-JUN-2003
DEFINITION   Sequence 27 from patent US 6538122.
ACCESSION   AR301266
VERSION     AR301266.1   GI:31689039
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 50)
AUTHORS   Yokoyama,K., Nakamura,N., Miwa,T. and Seguro,K.
TITLE     Process for producing microbial transglutaminase
JOURNAL   Patent: US 6538122-A 27 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1..50
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN
Query Match      51.3%; Score 15.4; DB 6; Length 29;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      3 GGATCCAGGTAGGCAGACTTGTCAG 27
        ||||| ||||| ||||| |||||
Db      3 GGATCCATGAAGACAGAGATGCCAG 27
```

RESULT 10
AX647902
LOCUS AX647902 29 bp DNA linear PAT 03-MAR-2003
DEFINITION Sequence 18 from Patent EP1270746.
ACCESSION AX647902
VERSION AX647902.1 GI:28802733
SOURCE
KEYWORDS
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Jensen, A., Halkier, T. and Jespersen, L.
TITLE Methods for the identification of ligand and target biomolecules
JOURNAL Patent: EP 1270746-A 18 02-JAN-2003;
Inoxell A/S (DK)
FEATURES
source
location/Qualifiers
1. 29
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA primer"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 29;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGATCCAGGTAGCGACACTTGTGCAG 27
||||| | | | | | | | | |
Db 3 GGATCCATGAAGACAGAGTGCCAG 27
||||| | | | | | | | | |
RESULT 11
BD103433/c
LOCUS BD103433 30 bp DNA linear PAT 27-AUG-2002
DEFINITION A carcinostatic or antiviral agent containing IRG27 protein or gene.
ACCESSION BD103433
VERSION BD103433.1 GI:22649007
KEYWORDS WO 0187349-A/5.
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS Enjoji, T., Todo, N. and Imamura, M.
TITLE A carcinostatic or antiviral agent containing IRG27 protein or gene
JOURNAL Patent: WO 0187349-A 5 22-NOV-2001;
SUMITOMO PHARMACEUTICALS CO LTD, TAKASHI ENJOJI, NAOKI TODO, MOTOAKI IMAMURA
COMMENT OS Artificial Sequence
PN WO 0187349-A/5
PD 22-NOV-2001
PF 18-MAY-2001 WO 2001JP004155
PR 19-MAY-2000 JP 00P 149097
PI TAKASHI ENJOJI, NAOKI TODO, MOTOAKI IMAMURA
PC A61K48/00, A61K38/17, A61P31/12, A61P35/00//C12N15/12, C07K16/18
CC Description of Artificial Sequence: a sequence of primer 4U
CC a sequence of 5'-upstream region for IRG27 gene. FH Key
CC Location/Qualifiers
FT source
1. 30
Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES
source
1. 30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 30;
Best Local Similarity 94.1%; Pred. No. 5.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GGATCCAGGTAGCGACACTTGTGCAG 27
||||| | | | | | | | | |
Db 3 GGATCCATGAAGACAGAGTGCCAG 27
||||| | | | | | | | | |
RESULT 12
AX453416
LOCUS AX453416 33 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent WO0244212.
ACCESSION AX453416
VERSION AX453416.1 GI:21712729
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Deleersnijder, W., Blockx, H. and de Moor, L.
TITLE Human g-protein coupled receptor and uses thereof
JOURNAL Patent: WO 0244212-A 5 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
source
location/Qualifiers
1. 33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGATCCAGGTAGCGACACTTGTGCAG 27
||||| | | | | | | | | |
Db 3 GGATCCAGCTCTGAAAGCTTGTGCAG 27
||||| | | | | | | | | |
RESULT 13
E51173
LOCUS E51173 42 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION E51173
VERSION E51173.1 GI:18629490
KEYWORDS JP 2001046073-A/10.
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 42)
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Method for transforming plant and transformed plant
JOURNAL Patent: JP 2001046073-A 10 20-FEB-2001;
RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT OS Artificial Sequence
PN JP 2001046073-A/10
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225832
PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC
C12N15/00, C12N5/00
CC
FH Key
FT source
1. 42
Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES
source
1. 42
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 42;
Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Qy 14 GGCGAGCTTGTGCAGCCT 30
||||| | | | | | | | | |
Db 22 GGCAAACTTGTGCAGCCT 6
||||| | | | | | | | | |
RESULT 12
AX453416
LOCUS AX453416 33 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 5 from Patent WO0244212.
ACCESSION AX453416
VERSION AX453416.1 GI:21712729
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Deleersnijder, W., Blockx, H. and de Moor, L.
TITLE Human g-protein coupled receptor and uses thereof
JOURNAL Patent: WO 0244212-A 5 06-JUN-2002;
SOLVAY PHARMACEUTICALS B V (NL)
FEATURES
source
location/Qualifiers
1. 33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGATCCAGGTAGCGACACTTGTGCAG 27
||||| | | | | | | | | |
Db 3 GGATCCAGCTCTGAAAGCTTGTGCAG 27
||||| | | | | | | | | |
RESULT 13
E51173
LOCUS E51173 42 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for transforming plant and transformed plant.
ACCESSION E51173
VERSION E51173.1 GI:18629490
KEYWORDS JP 2001046073-A/10.
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 42)
AUTHORS Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE Method for transforming plant and transformed plant
JOURNAL Patent: JP 2001046073-A 10 20-FEB-2001;
RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT OS Artificial Sequence
PN JP 2001046073-A/10
PD 20-FEB-2001
PF 09-AUG-1999 JP 1999225832
PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI
PC C12N15/09, A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC
C12N15/00, C12N5/00
CC
FH Key
FT source
1. 42
Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES
source
1. 42
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 50.7%; Score 15.2; DB 6; Length 42;
Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGAATCATGGCGACC 30

RESULT 14
 AX137508
 LOCUS AX137508 42 bp DNA linear PAT 31-JAN-2002
 DEFINITION Process for producing polyester.
 ACCESSION E51191
 VERSION E51191.1 GI:18629508
 KEYWORDS JP 2001046074-A/10.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 42)
 AUTHORS Nakashita,H., Yamaguchi,I., Yoshioka,K. and Doi,Y.
 TITLE Process for producing polyester
 JOURNAL Patent: JP 2001046074-A 10 20-FEB-2001;
 RIKAGAKU KENKYUSHO
 COMMENT OS Artificial Sequence
 PN JP 2001046074-A/10
 PD 20-FEB-2001
 PF 09-AUG-1999 JP 1999225839
 PR HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIOHARU DOI
 PI C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N9/10,C12P7/62, PC
 PC C12N15/00,C12N5/00
 CC

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGAATCATGGCGACC 30

ORIGIN

RESULT 15
 AR399392
 LOCUS AR399392 42 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 10 from patent US 6620601.
 ACCESSION AR399392
 VERSION AR399392.1 GI:40141254
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 42)
 AUTHORS Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
 TITLE Methods for transformation of plants, transformed plants and processes for preparation of polyesters
 JOURNAL Patent: US 6620601-A 10 16-SEP-2003;
 FEATURES Location/Qualifiers
 source 1..42
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGAATCATGGCGACC 30

ORIGIN

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGAATCATGGCGACC 30

RESULT 16
 AX137508
 LOCUS AX137508 42 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 10 from Patent EP1076095.
 ACCESSION AX137508
 VERSION AX137508.1 GI:14273702
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.
 TITLE Methods for transformation of plants, transformed plants and processes for preparation of polyesters
 JOURNAL Patent: EP 1076095-A 10 14-FEB-2001;
 Riken (JP)
 FEATURES Location/Qualifiers
 source 1..42
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic DNA"

ORIGIN

Query Match 50.7%; Score 15.2; DB 6; Length 42;
 Best Local Similarity 71.4%; Pred. No. 6.6e+04;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTTCAGCC 29
 |||||
 Db 3 CGGATCCAGGGAGGAATCATGGCGACC 30

RESULT 17

BD240955
 LOCUS BD240955 29 bp DNA linear PAT 17-JUL-2003
 DEFINITION A novel human lysozyme gene, its encoded polypeptide and the method for preparing them.
 ACCESSION BD240955
 VERSION BD240955.1 GI:33050725
 KEYWORDS JP 2002523097-A/4.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 29)
 AUTHORS Yu,L., Fu,Q., Zhao,Y., Zhang,H. and Bi,A.
 TITLE A novel human lysozyme gene, its encoded polypeptide and the method for preparing them
 JOURNAL Patent: JP 2002523097-A 4 30-JUL-2002;
 COMMENT LONG YU
 OS Unidentified
 PN JP 2002523097-A/4
 PD 30-JUL-2002
 PF 30-AUG-1999 JP 2000567703
 PR 31-AUG-1998 CN 98 1 11044.4
 PI LONG YU, QIANG FU, YONG ZHAO, HONGLAI ZHANG, ANDING BI
 PC C12N15/09,A61K38/43,A61K39/395,A61P31/04,A61P35/00, PC
 C07K16/40,
 PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/36,C12P21/08//C12Q1/68,
 PC (C12N1/21,C12R1:19), (C12N5/10,C12R1:91), (C12N9/36,C12R1:19),
 PC (C12N9/36,C12R1:91), C12N15/00,C12N5/00,A61K37/48, (C12N5/00, PC
 C12R1:91)
 CC Primer
 FH Key
 FT source 1..29

COMMENT

```

FEATURES
  source
    FT
      Location/Qualifiers
        1..29
          /organism="Unidentified".
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"
ORIGIN
  Query Match
    Best Local Similarity 50.0%; Score 15; DB 6; Length 29;
    Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy
    1 CGGGATCCAGGTAGGCAGACTTG 23
    ||||| ||||| ||||| |||||
  Db
    3 CGGGATCCATGAAGGCATCCGTG 25
    ||||| ||||| ||||| |||||
RESULT 18
AR437642 AR437642 29 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 5 from patent US 6660512.
ACCESSION AR437642
VERSION AR437642.1 GI:40202794
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 29)
  Unclassified.
  AUTHORS
  YU,L., FU,Q., ZHAO,Y., ZHANG,H. and BI,A.
  TITLE
  Human lysozyme gene, it's encoded polypeptide and the method of
  preparing them
  JOURNAL
  Patent: US 6660512-A 5 09-DEC-2003;
  FEATURES
    source
      Location/Qualifiers
        1..29
          /organism="unknown"
          /mol_type="genomic DNA"
ORIGIN
  Query Match
    Best Local Similarity 50.0%; Score 15; DB 6; Length 29;
    Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy
    1 CGGGATCCAGGTAGGCAGACTTG 23
    ||||| ||||| ||||| |||||
  Db
    3 CGGGATCCATGAAGGCATCCGTG 25
    ||||| ||||| ||||| |||||
RESULT 19
AR173178 AR173178 25 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 20 from patent US 6303750.
ACCESSION AR173178
VERSION AR173178.1 GI:17912669
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 25)
  Unclassified.
  AUTHORS
  Friedman,S.M., Crow,M.K., Li,Y., Tumang,J.R. and Sun,G.-R.
  TITLE
  Conserved T-cell receptor sequences
  JOURNAL
  Patent: US 6303750-A 20 16-OCT-2001;
  FEATURES
    source
      Location/Qualifiers
        1..25
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match
    Best Local Similarity 49.3%; Score 14.8; DB 6; Length 25;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTCA 26
    ||||| ||||| ||||| |||||

```

```

Db
  4 AGGTCGACAGACTTGTCA 21
  ||||| ||||| ||||| |||||
RESULT 20
AR183091 AR183091 37 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 68 from patent US 6340461.
ACCESSION AR183091
VERSION AR183091.1 GI:20226684
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 37)
  Unclassified.
  Terman,D.Stephen.
  Superantigen based methods and compositions for treatment of
  diseases
  JOURNAL
  Patent: US 6340461-A 68 22-JAN-2002;
  FEATURES
    source
      Location/Qualifiers
        1..37
          /organism="unknown"
          /mol_type="unassigned DNA"
ORIGIN
  Query Match
    Best Local Similarity 49.3%; Score 14.8; DB 6; Length 37;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTCA 26
    ||||| ||||| ||||| |||||
  Db
    16 AGGCAGACAGACTTGTCA 33
    ||||| ||||| ||||| |||||
RESULT 21
AX956456 AX956456 24 bp DNA linear PAT 08-JAN-2004
LOCUS
DEFINITION Sequence 6 from Patent WO03097869.
ACCESSION AX956456
VERSION AX956456.1 GI:40784965
KEYWORDS
SOURCE
ORGANISM
Rosa sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE
  1
  Suesse,K.H.
  Microsatellite markers for genetic analyses and the differentiation
  of roses
  JOURNAL
  Patent: WO 03097869-A 6 27-NOV-2003;
  FEATURES
    source
      Location/Qualifiers
        1..24
          /organism="Rosa sp."
          /mol_type="unassigned DNA"
          /db_xref="taxon:36598"
ORIGIN
  Query Match
    Best Local Similarity 48.7%; Score 14.6; DB 6; Length 24;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  Qy
    9 AGGTAGGCAGACTTGTGACGC 29
    ||||| ||||| ||||| |||||
  Db
    2 AGGTAGGCAGAGAGTGACAGAC 22
    ||||| ||||| ||||| |||||
RESULT 22
AR137780 AR137780 31 bp DNA linear PAT 16-JUN-2001
LOCUS
DEFINITION Sequence 14 from patent US 6197558.
ACCESSION AR137780
VERSION AR137780.1 GI:14479289

```

```
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.

REFERENCE
AUTHORS      Unclassified.
TITLE        1 (bases 1 to 31)
JOURNAL      Fotheringham, I.G.
FEATURES     Transaminase biotransformation process
              Patent: US 6197558-A 14 06-MAR-2001;
              Location/Qualifiers
              1..31
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCGAGACTTGTTCAGCC 29
    |||||
Db 2 GCGGATCCATCATGCTGCTGCTGCAACCC 30

RESULT 23
BD192813
LOCUS      BD192813
DEFINITION Improved transaminase biotransformation process.
ACCESSION BD192813
VERSION    BD192813.1 GI:33002552
KEYWORDS   JP 2002514921-A/14.
SOURCE     Staphylococcus aureus
ORGANISM   Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE
AUTHORS    Fotheringham, I.G.
TITLE      Improved transaminase biotransformation process
JOURNAL    Patent: JP 2002514921-A 14 21-MAY-2002;
           NSC TECHNOLOGIES LLC
COMMENT    PN JP 2002514921-A/14
           PD 21-MAY-2002
           PF 19-MAY-1998 JP 1998550503
           PR 19-MAY-1997 US 08/858111
           PI IAN G FOTHERINGHAM
           PC C12P13/04, C12P7/26, C12P7/62, C12N15/63, C12N9/88, C12N9/10 CC
           Strandedness: Single;
           CC Topology: Linear;
           FH Key Location/Qualifiers.

FEATURES
SOURCE     1..31
           /organism="Staphylococcus aureus"
           /mol_type="genomic DNA"
           /db_xref="taxon:1280"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCGAGACTTGTTCAGCC 29
    |||||
Db 2 GCGGATCCATCATGCTGCTGCTGCAACCC 30

RESULT 24
AX955017
LOCUS      AX955017
DEFINITION Sequence 13 from Patent WO03093468.
ACCESSION  AX955017
VERSION     AX955017.1 GI:40784254
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM     Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Molday, R.S., Ahn, J. and Hauswirth, W.S.
TITLE        Expression system for large functional proteins
JOURNAL      Patent: WO 03093468-A 13 13-NOV-2003;
              University of British Columbia (CA)
FEATURES     Location/Qualifiers
              1..44
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
Query Match      48.7%; Score 14.6; DB 6; Length 44;
Best Local Similarity 81.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCGAGACTTGT 23
    |||||
Db 24 GAATCCAGAGACAGACTTGT 44

RESULT 25
AX033626
LOCUS      AX033626
DEFINITION Sequence 1 from Patent EP1029923.
ACCESSION  AX033626
VERSION     AX033626.1 GI:10280344
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM     other sequences; artificial sequences.

REFERENCE
AUTHORS      Method for conveying bnyvv resistance to sugar beet plants
TITLE        Patent: EP 1029923-A 1 23-AUG-2000;
JOURNAL      HAVE D J VAN DER BV (NL)
FEATURES     Location/Qualifiers
              1..27
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="primer P1"

ORIGIN
Query Match      48.0%; Score 14.4; DB 6; Length 27;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCGAGACTTGT 24
    |||||
Db 2 GCGGATCCACCATTGCGAGACTTGT 25

RESULT 26
AR071455
LOCUS      AR071455
DEFINITION Sequence 19 from patent US 5910628.
ACCESSION  AR071455
VERSION     AR071455.1 GI:7222343
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM     Unclassified.
              1 (bases 1 to 31)
              Miller, W.Allen. and Wang, S.
              Cap-independent translation sequences derived from barley yellow
              dwarf virus
              Patent: US 5910628-A 19 08-JUN-1999;
              Location/Qualifiers
              1..31
              /organism="unknown"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Miller, W.Allen. and Wang, S.
TITLE        Cap-independent translation sequences derived from barley yellow
JOURNAL      Patent: US 5910628-A 19 08-JUN-1999;
FEATURES     Location/Qualifiers
              1..31
              /organism="unknown"
```

```
ORIGIN
/mol_type="unassigned DNA"

Query Match      48.0%; Score 14.4; DB 6; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTC 25
||||| ||| ||| ||| |||
Db 8 CGGATCCTCTGGGAAACAGGCTTGAC 31

RESULT 27
LOCUS AR071444 33 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 8 from patent US 5910628.
ACCESSION AR071444
VERSION AR071444.1 GI:7222332
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 33)
Miller,W.Allen. and Wang,S.
Cap-independent translation sequences derived from barley yellow
dwarf virus
JOURNAL Patent: US 5910628-A 8 08-JUN-1999;
FEATURES
Location/Qualifiers
source
1..33
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match      48.0%; Score 14.4; DB 6; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCAGACTTGTC 25
||||| ||| ||| ||| |||
Db 9 CGGATCCTCTGGGAAACAGGCTTGAC 32

RESULT 28
LOCUS AR152460/c 40 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 28 from patent US 6235263.
ACCESSION AR152460
VERSION AR152460.1 GI:15119992
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 40)
Wong,A.K.C., Bartel,P.L., Teng,D.H.-P. and Tavtigian,S.V.
Carboxy-terminal BRCA1 interacting protein
JOURNAL Patent: US 6235263-A 28 22-MAY-2001;
FEATURES
Location/Qualifiers
source
1..40
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match      48.0%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CGATCCAGGTAGGCAGACTTGTC 26
||||| ||| ||| ||| |||
Db 36 GAATCCTGTTGGCAGAAATGGTCA 13

RESULT 29
LOCUS AX456419
DEFINITION Sequence 277 from Patent WO0216944.
ACCESSION AX456419
VERSION AX456419.1 GI:21715323
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Wood,K.V., Wood,M.G., Zhuang,Y. and Paguio,A.
Synthetic nucleic acid molecule compositions and methods of
preparation
Patent: WO 0216944-A 277 28-FEB-2002;
PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="An oligonucleotide"

ORIGIN

Query Match      48.0%; Score 14.4; DB 6; Length 40;
Best Local Similarity 93.8%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAG 18
||||| ||| ||| ||| |||
Db 23 GGCTCCAGGTAGGCAG 38

RESULT 30
LOCUS AR143578/c 44 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 34 from patent US 6204371.
ACCESSION AR143578
VERSION AR143578.1 GI:15104864
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 44)
Levinson,D.Adam.
Compositions and methods for the treatment and diagnosis of immune
disorders
JOURNAL Patent: US 6204371-A 34 20-MAR-2001;
FEATURES
Location/Qualifiers
source
1..44
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match      48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TCACAGGTAGGCAGACTTGTCAGCC 29
||||| ||| ||| ||| |||
Db 40 TGCAGGTGTGCAGACTTGGGATCC 17

RESULT 31
LOCUS AR168947/c 44 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 34 from patent US 6288218.
ACCESSION AR168947
VERSION AR168947.1 GI:17905145
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 44)
Levinson,D.Adam.
```

TITLE Compositions and methods for the treatment and diagnosis of immune disorders
JOURNAL Patent: US 6288218-A 34 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCACC 29
40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 32

LOCUS AR232695/c 44 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 34 from patent US 6455685.
ACCESSION AR232695
VERSION AR232695.1 GI:27274972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Levinson,D.A.
TITLE Compositions and methods for the treatment and diagnosis of immune disorders
JOURNAL Patent: US 6455685-A 34 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"
/mol_type="mRNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCACC 29
40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 33

LOCUS AR262637/c 44 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 27 from patent US 6323334.
ACCESSION AR262637
VERSION AR262637.1 GI:28074173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kingsbury,G.A. and Leiby,K.R.
TITLE Nucleic acid molecules encoding a 103 gene product and uses therefor
JOURNAL Patent: US 6323334-A 27 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCACC 29
40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 34
LOCUS AR316574/c 44 bp mRNA linear PAT 17-AUG-2003

DEFINITION Sequence 34 from patent US 6562343.
ACCESSION AR316574
VERSION AR316574.1 GI:33695435
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Levinson,D.A.
TITLE Compositions and methods for the treatment and diagnosis of immune disorders
JOURNAL Patent: US 6562343-A 34 13-MAY-2003;
FEATURES Location/Qualifiers
source 1..44
/organism="unknown"
/mol_type="mRNA"

ORIGIN

Query Match 48.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGCACC 29
40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 35
LOCUS BD188256/c 45 bp DNA linear PAT 17-JUL-2003

DEFINITION bHLH-PAS proteins, its gene and use thereof.
ACCESSION BD188256
VERSION BD188256.1 GI:32997995
KEYWORDS JP 2003000279-A/65.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 45)
AUTHORS Oe,N.
TITLE bHLH-PAS proteins, its gene and use thereof
JOURNAL Patent: JP 2003000279-A 65 07-JAN-2003;
COMMENT SUMITOMO CHEMICAL CO LTD
OS Artificial Sequence
PN JP 2003000279-A/65
PD 07-JAN-2003
PF 27-DEC-2001 JP 2001396288
PI NORIHISA OE
PC C12N15/09,A61K38/00,A61P25/28,C07K14/47,C07K16/18,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/PC 483,
PC G01N33/50,G01N33/53,G01N33/566//G01N27/447,G01N27/447,C12N15/00,
PC C12N5/00,A61K37/02,G01N27/26,G01N27/26
CC Designed oligonucleotide primer for PCR
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1..45
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN


```

DEFINITION Sequence 12 from patent US 6346389.
ACCESSION ARI84482
VERSION ARI84482.1 GI:20230447
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Altieri,D.C.
TITLE Method for selectively modulating the interactions between survivin
and tubulin
JOURNAL Patent: US 6346389-A 12 12-FEB-2002;
FEATURES
    Location/Qualifiers
        1..28
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match          47.3%; Score 14.2; DB 6; Length 28;
Best Local Similarity 70.4%; Pred. No. 2e+05;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy      2 CGGATCCAGGTAGGACACTTGTTCAGC 28
      |||||
Db      2 CGGATCCAGAGAGATGACTTTTAAAC 28
      |||||

Search completed: November 18, 2005, 17:42:49
Job time : 835.457 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 CGGATCCAGTAGCAGACTGTGTCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	AAQ91122 Beta-card
2	30	100.0	30	9	ACA63112 Human bet
3	30	100.0	30	13	ADR05298 Human bet
C 4	16.6	55.3	37	5	Aaf27237 Pseudomon
5	16.6	55.3	37	4	Aaf82378 Human C-r
6	16.2	54.0	26	6	ABK88923 Human agg
C 7	15.6	52.0	23	8	ABT32007 Rubql for
8	15.6	52.0	41	2	AAQ77830 Human CTL
C 9	15.6	52.0	45	2	AAV81531 Oligonuc1
C 10	15.6	52.0	45	3	AAV73048 Transglut
11	15.6	52.0	50	2	AAV81532 Oligonuc1
12	15.6	52.0	50	3	AAZ73049 Transglut
13	15.4	51.3	29	3	AAZ58442 Primer us
C 14	15.4	51.3	30	6	ABA96284 Human IRG
15	15.4	51.3	33	6	ABK87354 Human G p
16	15.2	50.7	33	2	AAQ45507 Sequence
17	15.2	50.7	42	4	Aaf84270 Poly-3-hy
18	15	50.0	29	3	AAA07726 Human lys
19	14.8	49.3	25	2	AAT04797 T cell re
C 20	14.8	49.3	25	12	ADP13952 Renal cel

21	14.8	49.3	26	2	AAQ15070	Aaql5070 T-cell re
22	14.8	49.3	26	2	AAT10374	Aat10374 T-cell re
C 23	14.8	49.3	31	8	ACD56891	ACd56891 HCV DNAY
C 24	14.8	49.3	31	12	ADI87346	Adi87346 HCV DNAY
25	14.8	49.3	37	2	AAV42608	Aav42608 PCR prime
26	14.6	48.7	24	12	ADH68394	Adh68394 Rosa sp r
27	14.6	48.7	31	2	AAx05623	Aax05623 E. coli K
28	14.6	48.7	44	10	ADE94330	Ade94330 Human ABC
C 29	14.4	48.0	25	9	ACI03125	ACi03125 Human m1c
30	14.4	48.0	27	3	AAa74492	Aaa74492 Beet near
31	14.4	48.0	31	2	AAx60078	Aax60078 3' untran
32	14.4	48.0	33	2	AAx60067	Aax60067 3' untran
33	14.4	48.0	38	6	ACN17176	ACn17176 WNV Inozy
C 34	14.4	48.0	40	2	AAx76467	Aax76467 Human BRC
35	14.4	48.0	40	6	ABL99294	AbI99294 Synthetic
C 36	14.4	48.0	44	2	AAT38282	Aat38282 Murine 10
C 37	14.4	48.0	44	3	AAa51915	Aaa51915 Reverse p
C 38	14.4	48.0	44	4	AAO03383	Aao03383 3' primer
C 39	14.4	48.0	44	4	AAc92152	Aac92152 Mouse 103
C 40	14.4	48.0	44	4	AAf23475	Aaf23475 3' oligon
C 41	14.4	48.0	44	4	AAI70278	Aai70278 Mouse 103
C 42	14.4	48.0	44	4	AAf82626	Aaf82626 Murine TH
C 43	14.4	48.0	44	6	ABs53332	AbS53332 Mouse 103
C 44	14.4	48.0	44	8	ABq77055	Abq77055 Murine 10
C 45	14.4	48.0	44	9	ADB37507	AdB37507 Mouse Th-

ALIGNMENTS

RESULT 1
AAQ91122
ID AAQ91122 standard; cDNA; 30 BP.

AC AAQ91122;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer B.

XX Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
KW diagnosis; primer; mutation; detection; ss.

OS Synthetic.

PN US5429923-A.

PD 04-JUL-1995.

PF 11-DEC-1992; 92US-00989160.

PR 11-DEC-1992; 92US-00989160.

PA (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GHEO-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

WP1; 1995-245715/32.

XX Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

Example 1; Col 10; 22pp; English.

AAQ91121-091130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. Cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGATCCAGGTAGGCAGACTTGTTCAGCCT 30

Db 1 GCGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 2

ACa63112
 ID ACa63112 standard; DNA; 30 BP.

XX ACa63112;

28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer B.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

XX US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

DR WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain cDNA containing an FHC-associated mutation

XX Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGATCCAGGTAGGCAGACTTGTTCAGCCT 30

Db 1 GCGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 3

ADRo5298
 ID ADRo5298 standard; DNA; 30 BP.

XX ADRo5298;

XX 21-OCT-2004 (first entry)

DE Human beta cardiac myosin heavy chain mutation detection primer B.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

PI Seidman C, Seidman J, Watkins H, Rosenzweig A;

DR WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
 PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 PT myosin heavy-chain DNA and detecting the mutation in the amplified
 PT product.

XX Claim 18; SEQ ID NO 2; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.
SQ Sequence 30 BP; 6 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 4

AAF27237/c
ID AAF27237 standard; DNA; 34 BP.

AC AAF27237;

DT 11-SEP-2003 (revised)
24-APR-2001 (first entry)

XX Pseudomonas aeruginosa strain PAO128 oligonucleotide.

DE Selective cloning; mismatch detection; mismatch binding protein; Muts;
KW mutant gene; strain PAO128; bacterial infection; ss.

XX Pseudomonas aeruginosa; strain PAO128.

OS JP2000308489-A.

PN 07-NOV-2000.

PD 28-APR-1999; 99JP-00121957.

PF 28-APR-1999; 99JP-00121957.

PR (DAUC) DAIICHI PHARM CO LTD.

XX WPI; 2001-127778/14.

XX Detection of minutely mutated DNA useful for detection and treatment of
XX Pseudomonas aeruginosa, and development of antibacterial agents comprises
XX cloning a structurally characterized DNA.

PS Example 6; Fig 6; 13pp; Japanese.

XX The invention relates to a method of cloning a structurally
CC characterised DNA or a flanking DNA containing part of the characterised

CC region by concentrating the DNA of interest using a substance which
CC specifically recognises the structurally characterised region or a
CC fragment thereof, and selectively cloning only the DNA of interest by
CC subtraction treatment. The invention especially relates to a method for
CC cloning or detecting a minutely mutated DNA by concentrating the mutated
CC DNA using a substance (such as a mismatch repair protein) which
CC specifically recognises mismatched DNA, and selectively cloning only the
CC mutant DNA. Such a method of detection may also be used in the diagnosis
CC of disease associated with DNA mutations. The method was exemplified by
CC the cloning and sequencing of DNA from the PAO128 strain of Pseudomonas
CC aeruginosa using an immobilised maltose binding protein (MBP)-Muts fusion
CC protein, and the corresponding DNA from Pseudomonas aeruginosa strain
CC PAO1 (which was designated as the wild-type). The Muts portion of the
CC fusion protein recognised mismatches in PAO1/PAO128 DNA duplexes. The
CC mutant (i.e., PAO128) DNA was thus concentrated, amplified via PCR, and
CC contaminating DNA removed by RDA. A Pseudomonas aeruginosa strain PAO128
CC library was constructed and its genome sequenced. Such a protocol may be
CC used for the detection of Pseudomonas aeruginosa infection, and in the
CC development of antibacterial agents. The present sequence represents a
CC fragment of an unidentified gene from Pseudomonas aeruginosa strain
CC PAO128. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 34 BP; 4 A; 11 C; 13 G; 6 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 5; Length 34;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 8 CAGGTAGGCAGACTTGTTCAGCCT 30

Db 27 CAGGCAGGCAGACTTGTTCAGCCT 5
||||| ||||| ||||| |||||

RESULT 5

AAF82378
ID AAF82378 standard; DNA; 37 BP.

XX AAF82378;

DT 25-JUN-2001 (first entry)

XX Human C-reactive protein 5' primer.

DE Human; C-reactive protein; CRP; chicken embryo lethal orphan virus; CELO;
KW recombinant avian egg; chicken adenovirus expression vector; ACEV;
KW recombinant protein production; vaccine; gene therapy; PCR primer; ss.

XX Homo sapiens.

OS WO200119968-A1.

PN 22-MAR-2001.

XX 15-SEP-2000; 2000WO-US025489.

PF 17-SEP-1999; 99US-0154393P.

PR (CHEM-) CHEMOGEN INC.

XX Grabko VI, Blyden ER;

XX WPI; 2001-328015/34.

XX Use of avian adenovirus for producing recombinant proteins by mixing
XX vector containing avian adenovirus DNA with purified adenovirus DNA,
XX introducing DNA mixture into embryonated avian egg, and harvesting
XX proteins.

PS Example 5; Page 22; 70pp; English.

XX The present sequence was used in the construction of recombinant human C-
CC reactive protein (CRP). It was used in an example illustrating an
CC invention relating to the use of avian adenovirus for producing

CC recombinant proteins in an avian egg. The method involves preparing a
 CC vector containing avian adenovirus DNA, preparing a mixture of vector DNA
 CC into purified adenovirus DNA or adenovirus particles, introducing mixture
 CC into embryonated avian egg or avian cell culture, incubating, and
 CC harvesting fluids from egg containing recombinant protein molecule
 CC encoded by vector DNA. The method is useful for producing recombinant
 CC proteins such as therapeutic proteins, immunostimulatory proteins, or
 CC tumour antigens in an avian egg. The eggs may be used as a vaccine to
 CC elicit an immunological response to the antigenic portion of the protein
 CC encoded by the DNA present in the chimeric gene of a prepared infectious
 CC adenovirus. The chicken adenovirus expression vector (AdCEV)/egg system
 CC is simple and economical and allows isolation of the protein in a
 CC biologically active form, free of endotoxins

XX
 SQ Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 4; Length 37;
 Best Local Similarity 82.6%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGACGACTTGTCTC 25
 ||||| | | | | | | | | |
 Db 6 GGATCCATGCACACAGACATGTC 28

RESULT 6
 ID ABK88923
 XX ABK88923 standard; DNA; 26 BP.
 AC ABK88923;
 DT 07-OCT-2002 (first entry)
 XX Human aggrecanase cDNA PCR primer #5.
 XX Human; aggrecanase; primer; computer aided drug design; osteoarthritis;
 KW aggrecan; genetic disorder; proteolytic activity; articular cartilage;
 KW osteoarthritic; antiarthritic; ss; PCR.
 XX Homo sapiens.
 XX WO200242439-A2.
 XX 30-MAY-2002.
 XX 25-OCT-2001; 2001WO-US049814.
 XX 27-OCT-2000; 2000US-0243916P.
 XX (GENE-) GENETICS INST LLC.
 XX Racie LA, Twine NC, Agostino MU, Wolfman NM, Morris EA;
 XX WPI; 2002-575238/61.

XX Novel purified aggrecanase polypeptide useful for developing inhibitors
 FT of aggrecanase for treating various aggrecanase-associated conditions
 PT such as osteoarthritis.

PS Example 1; Page 22; 49pp; English.

XX The invention relates to a purified aggrecanase polypeptide and the
 CC polynucleotide encoding it. The polypeptide is useful in a method for
 CC developing inhibitors of aggrecanase, where the method comprises three
 CC dimensional structural analysis or computer aided drug design. The
 CC sequences of the invention are useful for inhibiting or preventing the
 CC effects of aggrecanase, and for inhibiting the proteolytic activity of
 CC aggrecanase. The sequences and the inhibitors are useful for treating
 CC various aggrecanase-associated conditions such as osteoarthritis,
 CC conditions characterised by degradation of articular cartilage, or
 CC diseases characterised by degradation of aggrecan and/or an upregulation
 CC of aggrecanase, and also for detecting or diagnosing genetic disorders
 CC involving aggrecanase or disorders involving cellular, organ or tissue

CC disorders in which aggrecanase is irregularly transcribed or expressed.
 CC This sequence represents a PCR primer used to amplify human aggrecanase
 CC DNA
 XX
 SQ Sequence 26 BP; 7 A; 8 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 26;
 Best Local Similarity 85.7%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CAGGTAGGACGACTTGTGACG 28
 || | | | | | | | | | |
 Db 6 CATCTATGCAGACTTGTGACG 26

RESULT 7
 ABT32007/c
 ID ABT32007 standard; DNA; 23 BP.
 XX
 AC ABT32007;
 XX
 DT 08-MAY-2003 (first entry)
 XX RubQ1 forward PCR primer SEQ ID No 72.
 DE
 XX Plant growth regulant; phosphate uptake; plant; mycorrhizal fungus;
 KW phosphate deficiency; phosphate sufficiency; plant biotechnology;
 KW transport; translocation; photosynthetic plant; rice; PCR; primer; ss.
 XX Oryza sativa.
 XX WO2003000897-A2.
 XX 03-JAN-2003.

XX 24-JUN-2002; 2002WO-EP006967.

XX 22-JUN-2001; 2001US-0300112P.

XX 26-SEP-2001; 2001US-0325277P.

XX 21-NOV-2001; 2001US-0332064P.

XX 21-MAR-2002; 2002US-0361819P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Paszkowski U, Briggs S, Cooper B, Goff SA, Moughamer T;
 XX Glazebrook J, Katagiri F, Krebs J, Provart N, Ricke D, Zhu T;
 XX WPI; 2003-201428/19.

XX New isolated nucleic acids encoding polypeptides that mediate phosphate
 FT uptake into plant cells, useful in plant biotechnology, particularly in
 PT regulating transport and translocation of phosphorus in photosynthetic
 PT plants.

XX Example 5; Page 93; 235pp; English.

XX The invention relates to novel nucleic acid molecules comprising a
 CC nucleotide sequence encoding a polypeptide that mediates phosphate uptake
 CC into the a plant cell in the presence of a mycorrhizal fungus, but not
 CC under conditions of phosphate deficiency, phosphate sufficiency, or a
 CC nucleotide sequence encoding a polypeptide that mediates phosphate uptake
 CC into the plant cell in response to phosphate availability. The nucleic
 CC acids are useful in plant biotechnology, particularly in regulating the
 CC transport and translocation of phosphorus in plants, or in modifying the
 CC uptake or translocation of phosphorus in photosynthetic plants, e.g.
 CC maize, soybean, barley, alfalfa, sunflower, canola, tomato, banana,
 CC cotton, peanut, sorghum, tobacco, sugarbeet, wheat or rice. This
 CC polynucleotide sequence represents a PCR primer relating to the OsPHT
 CC phosphate transporter proteins of the invention

XX Sequence 23 BP; 4 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

XX Query Match 52.0%; Score 15.6; DB 8; Length 23;

```
Best Local Similarity 81.8%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTCTAGCC 29
   |||||
Db 23 CAATAGGCAGACTTGTGACC 2

RESULT 8
AAQ77830
ID AAQ77830 standard; DNA; 41 BP.
XX
AC AAQ77830;
XX
DT 25-MAR-2003 (revised)
DT 16-JUN-1995 (first entry)
XX
DE Human CTLA-1 transcriptional control region PCR primer.
XX
KW Human CTLA-1; granzyme B; transcription control region; cytomegalovirus;
KW HCMV; immediate early gene IE94 enhancer;
KW chloramphenicol acetyl transferase reporter construct; T cell expression;
KW T cell activation-induced expression; ss.
XX
OS Synthetic.
XX
PN WO9422489-A1.
XX
PD 13-OCT-1994.
XX
PF 04-APR-1994; 94WO-US003659.
XX
PR 06-APR-1993; 93US-00044539.
XX
PA (TARG-) TARGETED GENETICS CORP.
XX
PI Lupton SD, Allen JM, Feldhaus AL;
DR WPI; 1994-332835/41.
XX
XX Recombinant polynucleotide encoding stimulatory factor poly:peptide -
PT under control of region causing activation-induced expression in T
PT lymphocytes to reduce their dependence on helper cells.
XX
PS Example 15; Page 33; 79pp; English.
XX
CC The human CTLA-1 transcriptional control region was amplified directly
CC from human genomic DNA by PCR using oligonucleotides AAQ77829 and
CC AAQ77830. The amplified product was operatively linked to a reporter gene
CC encoding chloramphenicol acetyl transferase (CAT) in a HyTK plasmid. A
CC fragment spanning the HCMV IE94 enhancer was ligated upstream of the CTLA-
CC -1-CAT. The plasmid was electroporated into human Jurkat cells. The CTLA-
CC 1 transcriptional control region in combination with the CMV enhancer
CC mediates activation-induced expression in human T lymphocytes. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 41 BP; 9 A; 12 C; 13 G; 7 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 2; Length 41;
Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCAGACTTG 23
   |||||
Db 8 CGGATCCAGGAAGGTCGCTG 29

RESULT 9
AAV81531/C
ID AAV81531 standard; DNA; 45 BP.
XX
AC AAV81531;
XX

Best Local Similarity 81.8%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
   |||||
Db 42 ATCCAGGTAGGCAGACTTCA 21

RESULT 10
AAV73048/C
ID AAA73048 standard; DNA; 45 BP.
XX
AC AAA73048;
XX
DT 24-NOV-2000 (first entry)
XX
XX Transglutaminase related oligonucleotide sequence SEQ ID NO:24.
XX Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
XX ss.
XX Unidentified.
XX
PN WO200040706-A1.
XX
```

```
DT 01-APR-1999 (first entry)
XX Oligonucleotide used for codon optimisation of transglutaminase gene.
DE Transglutaminase; microbial; gelled food; jelly; yogurt; cheese;
XX cosmetic; meat quality; microcapsule production; high thermal stability;
KW carrier; immobilised enzyme; codon optimised; ss.
XX
OS Synthetic.
OS Streptomyces sp.
XX
XX EP889133-A2.
XX
XX PD 07-JAN-1999.
XX
XX PF 02-JUL-1998; 98EP-00112315.
XX
XX PR 04-JUL-1997; 97JP-00180010.
XX
XX PA (AJIN) AJINOMOTO CO INC.
XX
XX PI Yokoyama K, Nakamura N, Miwa T, Seguro K;
XX
XX WPI; 1999-062664/06.
XX
XX New microbial transglutaminase with N-terminal aspartic acid deleted -
PT allowing high level recombinant production without added methionine in E.
PT coli, useful in production of gelled foods, cosmetics etc.
XX
XX Example 1; Page 34; 56pp; English.
XX
CC AAV81521-60 were used for construction of a synthetic Streptovorticillium
CC sp. transglutaminase gene (see AAV81508). The synthetic gene is codon
CC altered for high expression in Escherichia coli. The specification
CC describes a new microbial transglutaminase that has the N-terminal
CC aspartic acid of transglutaminase deleted. Eliminating the N-terminal Asp
CC from microbial transglutaminase allows efficient removal of the terminal
CC Met residue added when the protein is expressed in E. coli. The E. coli
CC methionine aminopeptidase acts well on Met-Ser but only poorly on Met-
CC Asp, so problems of antigenicity associated with Met-terminated proteins
CC are avoided. Recombinant transglutaminase is used to produce gelled foods
CC (jellies, yogurt and cheeses) or cosmetics, to improve the quality of
CC meat, in the production of materials for microcapsules of high thermal
CC stability and as a carrier for immobilised enzymes
XX
SQ Sequence 45 BP; 14 A; 10 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 2; Length 45;
Best Local Similarity 81.8%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
   |||||
Db 42 ATCCAGGTAGGCAGACTTCA 21

RESULT 10
AAV73048/C
ID AAA73048 standard; DNA; 45 BP.
XX
AC AAA73048;
XX
DT 24-NOV-2000 (first entry)
XX
XX Transglutaminase related oligonucleotide sequence SEQ ID NO:24.
XX Transglutaminase; gelled food; jelly; yoghurt; gelled cosmetic; cheese;
XX ss.
XX Unidentified.
XX
PN WO200040706-A1.
XX
```


CC (such as recombinant transglutaminase) which can be used in the food
 CC industry for the production of gelled foods such as jellies, yoghurts and
 CC cheeses, and for the production of gelled cosmetics. The present sequence
 CC represents an oligonucleotide which is used in the exemplification from
 CC the present invention

XX SQ Sequence 50 BP; 12 A; 11 C; 11 G; 16 T; 0 U; 0 Other;

Query Match 52.0%; Score 15.6; DB 3; Length 50;

Best Local Similarity 81.8%; Pred. No. 4.4e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ATCCAGGTAGGCAGACTTGTCA 26

DB 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 13

AAZ58442

ID AAZ58442 standard; DNA; 29 BP.

XX AC AAZ58442;

XX DT 23-MAY-2000 (first entry)

XX DE Primer used in pCMVbipepER/CI-2A construction.

XX KW Chymotrypsin inhibitor; CI-2A; barley; plasmid pCMVbipep;

XX KW endoplasmic reticulum retention signal; CellScreen;

XX KW enzyme activity modulator; enzyme inhibitor; drug discovery;

XX KW peptide library; PCR primer; ss.

XX OS Unidentified.

XX PN WO200005406-A1.

XX PD 03-FEB-2000.

XX PF 16-JUL-1999; 99WO-DK000408.

XX PR 20-JUL-1998; 98DK-00000956.

XX PR 29-JUL-1998; 98US-0094868P.

XX PA (MEBI-) M & E BIOTECH AS.

XX PI Halkier T, Jespersen L, Jensen A;

XX DR WPI; 2000-182719/16.

XX PT Novel screen comprising a pool of vectors with randomly modified

XX PT nucleotide sequences, useful for identifying modulators of enzyme

XX PT activity useful for selecting antibiotic agents.

XX PS Example 1-c; Page 73; 136pp; English.

XX The present sequence is that of a primer used in a PCR amplification
 CC designed to add an endoplasmic reticulum retention signal in frame to the
 CC C-terminus of the chymotrypsin inhibitor 2A (CI-2A) in plasmid
 CC pCMVbipepER/CI-2A (see AAZ58442). The invention relates to improvements
 CC in CellScreen technology that encompass screening in prokaryotic as well
 CC as eukaryotic cells, and which can be used to identify and/or prepare
 CC peptides or RNAs capable of modulating the activity in vivo of target
 CC enzymes in eukaryotic cells. Previously unknown interactions between
 CC targets and ligands can be identified. Enzyme inhibitor structures such
 CC as CI-2A are used as scaffolds to display intracellularly potentially
 CC biologically active peptides or RNAs in a stable form. Preparation of a
 CC medicinal product is based on initial identification of targets or
 CC ligands using the methods of the invention

XX SQ Sequence 29 BP; 9 A; 6 C; 11 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 51.3%; Score 15.4; DB 3; Length 29;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 GGATCCAGGTAGGCAGACTTGTCA 27

DB 3 GGATCCATGAAGACAGAGTGGCCAG 27

RESULT 14

ABA96284/c

ID ABA96284 standard; DNA; 30 BP.

XX AC ABA96284;

XX DT 15-MAR-2002 (first entry)

XX DE Human IRG27 PCR primer SEQ ID NO 6.

XX KW Human; IRG27; carcinostatic; cytostatic; anti-viral; cancer; cytokine;
 XX KW cell growth; differentiation; p53; infection; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200187349-A1.

XX PD 22-NOV-2001.

XX PF 18-MAY-2001; 2001WO-JP004155.

XX PR 19-MAY-2000; 2000JP-00149097.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI Enjoji T, Tohdoh N, Imamura M;

XX DR WPI; 2002-114218/15.

XX KW Carcinostatic or anti-viral agents comprising a IRG27 polypeptide, useful
 XX KW for the treatment of cancer and viral infection.

XX PS Example 2; Page 94; 104pp; Japanese.

XX The invention relates to carcinostatic, cytostatic or anti-viral agents
 CC comprising an IRG27 polypeptide that is induced by a mutated or modified
 CC cancer controlling gene p53, a cytokine that controls cell growth and/or
 CC by differentiation and is increased in cancer tissue. The gene and IRG27
 CC are useful for treatment and prevention of cancer and viral infection.
 CC The present sequence is that of a PCR primer for amplifying the IRG27
 CC encoding polynucleotide

XX SQ Sequence 30 BP; 8 A; 5 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 6; Length 30;

Best Local Similarity 94.1%; Pred. No. 5.1e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 GGACAGCTTGTGCAGCCT 30

DB 22 GGCAAACTTGTGCAGCCT 6

RESULT 15

ABK87354

ID ABK87354 standard; DNA; 33 BP.

XX AC ABK87354;

XX DT 24-SEP-2002 (first entry)

XX DE Human G protein-coupled receptor IGS70 PCR primer IP15,490.

XX KW Human; ss; PCR; G protein-coupled receptor; GPCR; IGS70; CNS; primer;
 KW psychiatric disorder; central nervous system disorder; schizophrenia;
 KW Alzheimer's disease; multiple sclerosis; anxiety; cardiovascular disease;

KW heart failure; angina pectoris; myocardial infarction; kidney disease;
 KW renal failure; gastrointestinal disorder; irritable bowel syndrome; IBS;
 KW inflammatory bowel disease; ulcer; gastric ulcer; inflammation; cancer;
 KW asthma; infection; human immunodeficiency virus infection; HIV; diabetes;
 KW osteoporosis; allergy.

OS Homo sapiens.

XX WO200244212-A2.

XX PD 06-JUN-2002.

XX PF 23-NOV-2001; 2001WO-EP013706.

XX PR 30-NOV-2000; 2000EP-00204280.

XX PR 05-DEC-2000; 2000US-0251045P.

XX PA (SOLV) SOLVAY PHARM BV.

XX PI Deleersnijder W, Blockx H, De Moor L;

XX DR WPI; 2002-527703/56.

XX PT Novel G-protein coupled receptor IGS70 polypeptide useful for treating
 PT dysfunctions, disorders or disease related to lung, bone marrow, spinal
 PT cord immune system.

XX PS Example 1; Page 33; 58pp; English.

XX CC The invention relates to a G protein-coupled receptor (GPCR) IGS70
 CC polypeptide including sequences that are 98-99.6% identical. Also
 CC included are the polynucleotide encoding IGS70 (including sequences 98-
 CC 99.6% identical to the polynucleotide or the DNA insert contained in
 CC plasmid CBS 109818), a hybridisation probe derived from the
 CC polynucleotide, a DNA or RNA expression system producing IGS70, a host
 CC comprising the expression system, IGS70 receptor membrane preparation
 CC derived from the cell, an antibody immunospecific for IGS70, IGS70 is
 CC useful for diagnosing a disease or a susceptibility to disease in a
 CC subject related to expression or activity of the IGS70 polypeptide in a
 CC subject by determining the presence or absence of mutation in the
 CC nucleotide sequence encoding IGS70 in the genome of the subject in a
 CC sample derived from the subject. IGS70 is also useful identifying agonist
 CC or antagonist. The IGS70 protein, polynucleotide, antibody and identified
 CC an/agonists are useful for treating psychiatric and central nervous
 CC system (CNS) disorders such as schizophrenia, Alzheimer's disease,
 CC multiple sclerosis, anxiety, cardiovascular diseases such as heart
 CC failure, angina pectoris, myocardial infarction, kidney disease such as
 CC renal failure, gastrointestinal disorders such as irritable bowel
 CC syndrome (IBS), inflammatory bowel disease, ulcers such as gastric ulcer,
 CC inflammation, cancers, asthma, infection (such as bacterial, viral,
 CC fungal, protozoal) especially human immunodeficiency virus infection
 CC (HIV), diabetes, osteoporosis and allergies. The present sequence is a
 CC PCR primer used to isolate the cDNA encoding the human GPCR IGS70

XX SQ Sequence 33 BP; 8 A; 9 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 6; Length 33;
 Best Local Similarity 76.0%; Pred. No. 5.1e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGACACTTCTCAG 27

Db 3 GGATCCAGCTCTGAAAGCTTGTCTCAG 27

RESULT 16

AAQ45507

ID AAQ45507 standard; DNA; 33 BP.

XX AC AAQ45507;

XX DT 25-MAR-2003 (revised)

DT 30-NOV-1993 (first entry)

XX DE Sequence of a kappa constant region 3' primer.

XX KW Antibody; C-erbB-2; variable region; therapy; diagnosis; cancer; mammary;
 KW ovary; tumour; PCR; primer; ss.

XX OS Synthetic.

XX XX WO9312220-A1.

XX PD 24-JUN-1993.

XX PF 04-DEC-1992; 92WO-US010437.

XX PR 12-DEC-1991; 91US-00808462.

XX PA (BERL-) BERLEX LAB INC.

XX PI Shawver LK, Liu HC, Parkes DL, Mcbrogan MP, Brandis JW;

XX DR WPI; 1993-214162/26.

XX PT Recombinant and chimeric antibodies to C-ERBB-2 - used as therapeutic and
 PT diagnostic agents for tumours expressing C-ERBB-2.

XX PS Example; Page 69; 106pp; English.

XX CC The human heavy chain gamma-1 constant (C-gamma-1) gene and the human
 CC light chain kappa (C-kappa) gene were cloned from human IGG producing
 CC cell line ARH-77 (ATCC CRL 1621) using PCR. Each amplified C-gamma-1 and
 CC C-kappa gene fragment contd. several hundred base pair flanking sequences
 CC at both the 5' and 3' end. The kappa constant region was amplified from
 CC ARH-77 genomic DNA using PCR. The primers used are found in AAQ45506 (5'
 CC primer) and AAQ45507 (3' primer). The amplified DNA was verified to be
 CC the kappa constant region by Southern blot (AAQ45511 for probe) and
 CC sequence analysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 33 BP; 7 A; 10 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 2; Length 33;
 Best Local Similarity 71.4%; Pred. No. 6.3e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGACACTTCTCAGCT 30

Db 4 GGATCCTGACCGTAAGACCTGTCCACCT 31

RESULT 17

AAF84270

ID AAF84270 standard; DNA; 42 BP.

XX AC AAF84270;

XX DT 13-JUN-2001 (first entry)

XX DE Poly-3-hydroxybutyrate synthase gene, phbC, PCR primer rbs-CU.

XX KW Plant; polyester synthase; alkyl 3-hydroxyvalcanoic acid; PCR primer;
 KW phbC; poly-3-hydroxybutyrate synthase; plastid; ss.

XX OS Ralstonia eutropha.

XX XX EP1076095-A1.

XX PD 14-FEB-2001.

XX PF 08-AUG-2000; 2000EP-00117037.

XX PR 09-AUG-1999; 99JP-00225832.

XX PR 09-AUG-1999; 99JP-00225839.

XX PA (RIKE) RIKEN KK.

XX Yamaguchi I, Nakashita H, Yoshioka K, Doi Y;
XX WPI; 2001-292601/31.
XX Transforming plants for producing polyester, involves ligating an operon
PT containing a promoter and several genes of interest to a vector and
PT integrating the recombinant vector into a plasmid chromosome.
XX Example 1; Page 10; 37pp; English.
XX The present invention relates to methods for transformation of plants.
CC The methods comprise ligating an operon containing a promoter and 2-100
CC genes of interest, to a vector and integrating the resulting recombinant
CC vector into a plasmid chromosome. The methods are useful for transforming
CC a plant, belonging to any family such as Gramineae, Malvaceae,
CC Brassicaceae, Compositae, Pedaliaceae, Oleaceae, Myrtaceae, Rosaceae,
CC Theaceae, Leguminosae, Palmae, Sterculiaceae or Rubiaceae, in particular
CC Nicotiana tabacum of Solanaceae family, for producing polyester, which is
CC copolymer of lower alkyl 3-hydroxyalkanoic acid. In the present invention
CC polyester synthase genes were used in the method to generate a plant
CC which produces polyester. The present sequence is a PCR primer for the
CC the polyester synthase gene poly-3-hydroxybutyrate synthase (phbC;
CC AAF84262)
XX
XX Sequence 42 BP; 11 A; 10 C; 17 G; 4 T; 0 U; 0 Other;
SQ Query Match 50.7%; Score 15.2; DB 4; Length 42;
Best Local Similarity 71.4%; Pred. No. 6.5e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 CGGATCCAGGTAGGCGAGACTTGTCCAGCC 29
|||||
DB 3 CGGATCCAGGAGGCGATCATGGCGACC 30
|||||
RESULT 18
AAAA07726
ID AAA07726 standard; DNA; 29 BP.
XX
XX AAA07726;
AC
XX
XX 23-JUN-2000 (first entry)
XX Human lysozyme LYC4 cDNA amplifying primer.
DE
XX
XX Lysozyme; LYC4; glycosidic bond; food preservation; antibacterial;
KW tumour inhibition; stomach cancer; mammary cancer; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200012717-A1.
PN
XX
XX 09-MAR-2000.
PD
XX
XX 30-AUG-1999; 99WO-CN000133.
PF
XX
XX 31-AUG-1998; 98CN-00111044.
PR
XX
XX (YULL/) YU L.
PA
XX
XX Yu L, Fu Q, Zhao Y, Zhang H, Bi A;
PI
XX
XX WPI; 2000-237878/20.
DR
XX
XX Novel gene of human lysozyme family with human LYC4 protein activity,
PT antibacterial effect and function of inhibiting tumor growth, useful e.g.
PT in anti-bacterial and anti-cancer agents.
XX
XX Example 3; Page 10; 24pp; Chinese.
PS
XX
XX The invention provides a human lysozyme polypeptide LYC4. The LYC4
CC polypeptide can be expressed by standard recombinant methodology.

CC Lysozyme is useful in cleavage of glycosidic bonds in the cell walls of
CC bacteria, causing lysis. The LYC4 polypeptide can be used in preserving
CC the freshness of foods including meat and wine. It may also be used as an
CC antibacterial agent through its ability to cleave glycosidic bonds to
CC destroy bacterial cells. LYC4 is also a non-specific immune molecule,
CC inhibitor of tumour growth e.g. stomach cancer and mammary cancer.
CC Sequences AAA07726-27 represent PCR primers for amplifying LYC4 cDNA
XX
SQ Sequence 29 BP; 5 A; 7 C; 9 G; 8 T; 0 U; 0 Other;
Query Match 50.0%; Score 15; DB 3; Length 29;
Best Local Similarity 78.3%; Pred. No. 7.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GCGGATCCAGGTAGGCGAGACTTG 23
|||||
DB 3 GCGGATCCATGAGGCGATCCGTG 25
|||||
RESULT 19
AAT04797
ID AAT04797 standard; cDNA to mRNA; 25 BP.
XX
XX AAT04797;
AC
XX
XX 31-MAY-1996 (first entry)
DT
XX
XX T cell receptor CDR3 alpha constant region antisense PCR primer.
DE
XX
XX T cell; receptor; rheumatoid arthritis; CDR3; V-beta region; homologous;
KW synovial; immunotherapy; probe; diagnosis; PCR; primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9528481-A1.
PN
XX
XX 26-OCT-1995.
PD
XX
XX 14-APR-1995; 95WO-US004803.
PF
XX
XX 18-APR-1994; 94US-00229285.
PR
XX
XX (NYRU-) NEW YORK SOC RUPTURED & CRIPPLED MAINTAI.
PA
XX
XX Friedman SM, Crow MK, Li Y, Tumang JR, Sun G;
PI
XX
XX WPI; 1995-373796/48.
DR
XX
XX New conserved T cell receptor sequences in rheumatoid arthritis - used to
PT develop prods. for the diagnosis and therapy of rheumatoid arthritis.
XX
XX Example 9; Page 23; 47pp; English.
PS
XX
XX AAT04796 and AAT04797 are primers used to amplify T cell receptor (TCR)
CC DNA sequences from rheumatoid arthritis (RA) patients, for analysis of
CC the TCR alpha rearrangements. The amplified sequences are derived from
CC synovial tissue T cells and encode the alpha region of the CDR3 region of
CC the TCR. Both alpha and beta chain DNA can be used as probes in the
CC diagnosis of RA and can also be used for immunotherapy for RA, e.g. by
CC using them as blocking antigenic peptides, activation of immunoregulatory
CC cells, induction of an anti-TCR antibody or in monoclonal antibody
CC mediated detection of the pathogenic V gene expressing T cells
XX
SQ Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 25;
Best Local Similarity 88.9%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 AGGTAGGCGAGACTTGTC 26
|||||
DB 4 AGGTCCGACGACTTGTC 21
|||||

RESULT 20
ADP13952/C
ID ADP13952 standard; DNA; 25 BP.
XX
XX AC ADP13952;
XX
XX 26-AUG-2004 (first entry)
XX
XX Renal cell carcinoma differentially expressed gene probe #357.
XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
XX
XX WO2004048933-A2.
XX
XX 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burcynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 688; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed) (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 8 CAGGTAGGCAGACTTGTC 25
|||||
Db 25 CAGGAGGCAGACTCGTC 8
|||||

RESULT 21
AAQ15070
ID AAQ15070 standard; DNA; 26 BP.
XX
XX AC AAQ15070;
XX
XX 25-MAR-2003 (revised)
DT 19-FEB-1992 (first entry)
XX
XX T-cell receptor C-alpha primer.
DE
XX TCR; multiple sclerosis; MS; brain; amplification; primer; ss.
XX
XX Synthetic.
OS
XX WO9117268-A.
XX
XX 14-NOV-1991.
XX
XX 01-MAY-1990; 90US-00517245.
PF
XX 01-MAY-1990; 90US-00517245.
PR
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX Steinman L, Oksenberg J, Bernard C;
PI
XX WPI; 1991-353787/48.
XX
XX Method for diagnosing T-cell associated disease - comprises identifying
PT rearranged variable region of appropriate T-cell also T-cell compans. for
PT treating neo:proliferative conditions.
XX
XX Disclosure; Page 31; 53pp; English.
XX
XX TCR V-alpha and V-beta rearrangements were studied in 16 MS brains and in
CC 10 control brains. TCRValpha-Jalpha-Calpha and Vbeta-Dbeta-Jbeta-Cbeta
CC rearrangements were confirmed with Southern blotting and hybridisation of
CC the PCR product obtained by amplification using a Calpha or Cbeta primer
CC and a Valpha or a Vbeta specific primer. See AAQ15052-92 for Valpha,
CC Vbeta, Calpha and Cbeta primers. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 26 BP; 8 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 26;
Best Local Similarity 88.9%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 9 AGGTAGGCAGACTTGTC 26
|||||
Db 4 AGGTGACAGACTTGTC 21
|||||

RESULT 22
AAT10374
ID AAT10374 standard; cDNA; 26 BP.
XX
XX AAT10374;
XX
XX 02-APR-1996 (first entry)
XX
XX T-cell receptor primer C beta 3'.
XX
XX T cell receptor; beta chain; variable region; rheumatoid arthritis;
KW synovial joint fluid; PCR; amplification; primer; immunogen; vaccine;
KW immune disease; ss.
XX
XX Synthetic.
OS
XX WO9523164-A1.
XX
XX 31-AUG-1995.

XX PF 23-FEB-1995; 95WO-BF000670.
 XX PR 23-FEB-1994; 94EP-00200454.
 XX PA (ALKU) AKZO NOBEL NV.
 XX PI Van Der Maaden JM, Rijnders AMW, Graus JPM;
 XX DR WPI; 1995-311502/40.
 XX PT Peptide contained in the variable region of a T-cell receptor beta chain
 PT - specifically associated with immune disease, esp. rheumatoid arthritis.
 XX PS Example 2; Page 24; 55pp; English.
 CC The primers AAT10352-97 were used to PCR amplify the T cell receptor beta
 CC chain variable regions from T cell culture clones, isolated from the
 CC synovial joint fluid of 11 patients suffering from rheumatoid arthritis.
 CC The coding sequences were shown to contain the nucleotide sequence
 CC AAT07409. The encoded polypeptide can be used as an immunogenic cpd. for
 CC the detection of or predisposition to an immune disease, or for use as a
 CC vaccine for prevention or treatment of an immune disease
 XX SQ Sequence 26 BP; 9 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 49.3%; Score 14.8; DB 2; Length 26;
 Best Local Similarity 88.9%; Pred. No. 9.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 AGGTAGGCGACACTTGTCA 26
 DB |||||
 4 AGGCACACAGCACTTGTCA 21
 RESULT 23
 ACDS56891/c
 ID ACDS56891 standard; DNA; 31 BP.
 AC ACDS56891;
 XX DT 23-SEP-2003 (first entry)
 XX DE HCV DNazyme sequence #37.
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; ss.
 XX OS Hepatitis C virus.
 OS WO200281494-A1.
 XX PD 17-OCT-2002.
 XX PF 26-MAR-2002; 2002WO-US009187.
 XX PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.

(PAVC/) PAVCO P.
 PA (LEBP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX PS Claim 1; Page 234; 387pp; English.
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents one of the HCV DNazyme or
 CC minus strand DNazyme sequences disclosed in the present invention
 XX SQ Sequence 31 BP; 7 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 49.3%; Score 14.8; DB 8; Length 31;
 Best Local Similarity 73.1%; Pred. No. 9.4e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 2 CGGATCCAGGTAGCGACACTTGTGAC 27
 DB |||||
 27 CGGATCGTTGTAGCTAGCCTTGCCAG 2
 RESULT 24
 ADI87346/c
 ID ADI87346 standard; DNA; 31 BP.
 XX AC ADI87346;
 XX DT 03-JUN-2004 (first entry)
 XX DE HCV DNazyme sequence #37.
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
 KW HCV infection; type I interferon; DNazyme.
 OS Hepatitis C virus.
 OS Synthetic.
 XX US2003125270-A1.
 XX PD 03-JUL-2003.
 XX PF 18-DEC-2000; 2000US-00740332.
 XX PR 18-DEC-2000; 2000US-00740332.
 XX (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (ROBE/) ROBERTS E.
 PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.
 XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
 XX WPI; 2004-031273/03.
 DR Enzymatic nucleic acid molecules which specifically cleave RNA derived
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
 PT especially in combination with type I interferon therapy.
 XX Claim 2; SEQ ID NO 4834; 198pp; English.
 XX The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
 CC the binding arms of the enzymatic nucleic acid molecule comprises
 CC sequences complementary to any of the defined substrate sequences given
 CC in the specification. The nucleic acid molecule may be administered for
 CC the treatment of HCV infections, especially in combination with type I
 CC interferons. The present sequence represents a HCV DNazyme sequence.
 XX Sequence 31 BP; 7 A; 9 C; 9 G; 6 T; 0 U; 0 Other;
 SQ Query Match 49.3%; Score 14.8; DB 12; Length 31;
 Best Local Similarity 73.1%; Pred. No. 9.4e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 2 CGGATCCAGGTAGGACGACTTGTTCAG 27
 Db 27 CGGATCGTGTAGCTAGCGCTTGCCAG 2
 RESULT 25
 AAV42608
 ID AAV42608 standard; DNA; 37 BP.
 XX AAV42608;
 XX 07-OCT-1998 (first entry)
 XX PCR primer used to amplify TCR alpha chain cDNA.
 XX Superantigen; treatment; cancer; tumour-specific antigen;
 KW autoimmune disease related antigen; infection; bacterial; viral;
 KW eukaryotic; autoimmune disease; inhibit; pathological response;
 KW immune response; mouse; T cell receptor; TCR; PCR primer; ss.
 XX Synthetic.
 OS WO9826747-A2.
 XX 25-JUN-1998.
 XX 17-DEC-1997; 97WO-US023637.
 XX 17-DEC-1996; 96US-0033172P.
 PR 17-APR-1997; 97US-0044074P.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 1998-362497/31.
 XX Conjugates and polymers containing superantigen and therapeutic antigen -
 PT for treatment of cancer, infection, autoimmune disease and graft
 PT rejection, also treatment by administering lymphocytes treated in vitro
 PT by these antigens.
 XX Example 10; Page 88; 139pp; English.
 FS PCR primers AAV42608-11 were used to amplify the T cell receptor (TCR)
 CC alpha chain cDNA. The products were used to prepare effector T cells with
 CC tumour specificity. The specification describes a method for treatment

CC of cancer which comprises incubating lymphocytes with a tumour-specific
 CC antigen or autoimmune disease related antigen and a superantigen. The
 CC treated cells are then introduced into the patient. The superantigen and
 CC the tumour-specific antigen or autoimmune disease related antigen can be
 CC conjugated together. The products are used to treat cancer (carcinoma,
 CC melanoma, lymphoma etc.) infections (bacterial, viral or eukaryotic) and
 CC autoimmune disease (e.g. idiopathic thrombocytopenic purpura, rheumatoid
 CC arthritis, systemic lupus erythematosus, multiple sclerosis etc.). The
 CC antigens either induce an immune response or inhibit a pathological
 CC response
 XX Sequence 37 BP; 10 A; 8 C; 10 G; 9 T; 0 U; 0 Other;
 SQ Query Match 49.3%; Score 14.8; DB 2; Length 37;
 Best Local Similarity 88.9%; Pred. No. 9.7e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 9 AGGTAGGACGACTTGTTCAC 26
 Db 16 AGGACGACGACTTGTTCAC 33
 RESULT 26
 ADH68394
 ID ADH68394 standard; DNA; 24 BP.
 XX ADH68394;
 XX 25-MAR-2004 (first entry)
 XX Rosa sp reverse PCR primer for microsatellite marker RMS003.
 DE microsatellite marker; rose genome; PCR; hypervariable region;
 KW genetic mapping; relatedness analysis; hybrid identification; plant;
 KW breeding; primer; ss.
 XX Rosa sp.
 OS WO2003097869-A2.
 XX 27-NOV-2003.
 XX 16-MAY-2003; 2003WO-DE001572.
 XX 17-MAY-2002; 2002DE-01022632.
 PR (CONC-) CON CIPIO GMBH.
 XX Sues K;
 XX WPI; 2004-012541/01.
 XX New oligonucleotides from rose microsatellite markers, useful for genomic
 XX analysis, including identification of varieties and hybrids.
 XX Claim 1; Page 5; 52pp; German.
 XX This invention describes novel oligonucleotides derived from
 CC microsatellite markers and used for the amplification of the rose genome.
 CC The invention also describes a test kit for genetic analysis of cultured
 CC or wild forms of the genus Rosa sp. that contains at least one of the new
 CC oligonucleotide primers and preparing microsatellite markers of Rosa sp.
 CC by PCR amplification of hypervariable genomic regions, using at least one
 CC primer pair, to produce polymorphic fragments which are separated and
 CC amplified. The primer pairs flank the microsatellite locus being
 CC especially on high-resolution agarose or native or denatured,
 CC polyacrylamide gels, or by mass spectrometry. After separation, the
 CC amplicons are detected by staining (ethidium bromide or silver),
 CC radioactive labelling and autoradiography, automated sequencing using
 CC primers labelled with dyes or fluorophores or by mass spectrometry. A
 CC genomic library of 0.5-1.5 kb fragments from the rose variety
 CC 'Lichtblick' was constructed in pUC18 and used to transform Escherichia

CC coli and the cells tested against a high-density array of synthetic
 CC microsatellites. Inserts in plasmids that hybridised were sequenced and
 CC the identified sequences selected for ability to differentiate between a
 CC set of 30 rose varieties. The oligonucleotides are used for genetic
 CC analysis of cultivated and wild types of roses, particularly for genetic
 CC mapping and labelling of mono- or poly-genic traits, selection, analysis
 CC of relatedness, identification of varieties and evaluation of varietal
 CC purity, identification of hybrids and plant breeding. The
 CC oligonucleotides are useful in automated processes, do not require
 CC radioactive detection methods and can differentiate between almost all
 CC commercial rose varieties. ADH68375-ADH68674 represent the PCR primers
 CC used to amplify the rose microsatellite regions described in the method
 CC of the invention.

XX Sequence 24 BP; 10 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 48.7%; Score 14.6; DB 12; Length 24;
 Best Local Similarity 81.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACCC 29
 DB 2 AGGTAGGCAGAGTGACAGAC 22

RESULT 27
 AAX05623
 ID AAX05623 standard; DNA; 31 BP.

XX AC AAX05623;

XX DT 21-APR-1999 (first entry)

XX DE E. coli K12 ilva gene fragment generating primer.

XX KW Transaminase; enzyme; pyruvate; acetolactate synthase; keto acid;
 KW flavouring agent; sweetener; nutritional supplement; pharmaceutical;
 KW L-2-aminobutyrate; ilva gene; PCR primer; ss.

XX OS Synthetic.
 XX ES Escherichia coli.
 XX PN WO9853088-A1.

XX PD 26-NOV-1998.

XX PF 19-MAY-1998; 98WO-US010169.

XX PR 19-MAY-1997; 97US-00858111.

XX PA (MONS) MONSANTO CO.

XX PI Fotheringham IG;

XX WPI; 1999-070156/06.

XX PT Preparation of amino acid - which does not react with transaminase.

XX PS Example 2; Page 20; 57pp; English.

XX CC The invention relates to preparation of natural and unnatural amino acids
 CC that (a) reacting a first amino acid and a keto acid with transaminase
 CC enzyme to produce an amino acid and pyruvate, and (b) reacting pyruvate
 CC with acetolactate synthase enzyme to produce a compound that does not
 CC react with transaminase enzyme. The amino acids produced in these
 CC processes are useful as flavouring agents, sweeteners, nutritional
 CC supplements, synthetic intermediates in the preparation of
 CC pharmaceuticals. Acetolactate synthase enzyme eliminates the keto acid
 CC produced by the transaminase enzyme reaction, thus preventing the
 CC formation of an equilibrium of the reaction and driving the amino acid
 CC production to completion. The preparations are especially used to produce
 CC L-2-aminobutyrate. Sequences AAX05623-24 represent PCR primers used for
 CC generating the E. coli K12 ilva gene fragment. This is used in the

CC construction of an expression vector pIF347 comprising the ilva gene
 CC encoding threonine deaminase
 XX Sequence 31 BP; 6 A; 13 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 48.7%; Score 14.6; DB 2; Length 31;
 Best Local Similarity 69.0%; Pred. No. 1.2e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGCGATCCAGGTAGGCAGACTTGTGACCC 29
 DB 2 CGCGATCCATCATGCTGACTCGCAACCC 30

RESULT 28

ADE94330

ID ADE94330 standard; DNA; 44 BP.

XX AC ADE94330;

XX DT 12-FEB-2004 (first entry)

XX DE Human ABCA1 C-half PCR primer SEQ ID NO:13.

XX KW ATP-binding cassette subfamily; ABCA subfamily; ABC transporter;
 KW PCR primer; human; ss.

XX OS Synthetic.
 XX OS Homo sapiens.

XX PN WO2003093468-A2.

XX PD 13-NOV-2003.

XX PF 06-MAY-2003; 2003WO-CA000633.

XX PR 06-MAY-2002; 2002CA-02385110.

XX PR 27-JUN-2002; 2002US-0391644P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI Molday RS, Ahn J, Hauswirth WS;

XX WPI; 2003-903674/82.

XX PT New nucleic acid composition for expression of a functional member of the
 PT ATP-binding cassette (ABCA) subfamily of ABC transporters in a host cell,
 PT useful in treating a mammal in need of the member of the ABCA subfamily
 PT of ABC transporters.

XX PS Example 1; SEQ ID NO 13; 55pp; English.

XX CC The present invention describes a nucleic acid composition (1) for the
 CC expression of a functional member of the ATP-binding cassette (ABCA)
 CC subfamily of ABC transporters in a host cell comprising two or more
 CC different nucleic acid molecules, each of which encodes one or more
 CC domains of an ABC transporter, where the domains are functionally
 CC complementary. Also described: (1) a host cell comprising (1); (2) a
 CC method for expressing a functional member of the ABCA subfamily of ABC
 CC transporters in a host cell; (3) a system for expressing a functional
 CC member of the ABCA subfamily of ABC transporters in a host cell
 CC comprising 2 or more expression vectors; (4) a host cell comprising the
 CC the ABCA subfamily of ABC transporters; (6) a pharmaceutical composition
 CC comprising the nucleic acid or system; and (7) a kit for expressing a
 CC functional member of the ABCA subfamily of ABC transporters in a host
 CC cell. The nucleic acid composition (1) can be used for the expression of
 CC a functional member of the ABCA subfamily of ABC transporters in a host
 CC cell, which is useful in treating a mammal in need of functional member
 CC of the ABCA subfamily of ABC transporters. The present sequence
 CC represents a PCR primer used in the exemplification of the present
 CC invention.

```
SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 48.7%; Score 14.6; DB 10; Length 44;
Best Local Similarity 81.0%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGACAGACTTG 23
| ||||| ||||| |||||
Db 24 GAATCCAGAGAGACAGACTTG 44

RESULT 29
ACI03125/C
ID ACI03125 standard; DNA; 25 BP.
XX AC ACI03125;
XX DT 13-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 3116.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
XX PA (APFY-) APFYMATRIX INC.
XX PI Mittmann MP;
XX DR WPI; 2003-567953/53.
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 3116; 9pp; English.
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX CC Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 U; 0 Other;

SQ Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 48.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCA 17
| ||||| ||||| |||||
Db 20 CGGACCCAGGTAGGCA 5

RESULT 30
AAA74492
ID AAA74492 standard; DNA; 27 BP.
XX AC AAA74492;
XX DT 01-DEC-2000 (first entry)
XX DE Beet necrotic yellow vein virus PCR primer P1.
XX KW BNYVV-resistance; rhizomania; sugar beet; transgenic plant; PCR primer;
XX KW ss.
XX OS Beet necrotic yellow vein virus.
XX PN WO2000044915-A1.
XX PD 03-AUG-2000.
XX PF 26-JAN-2000; 2000WO-EP000609.
XX PR 27-JAN-1999; 99EP-00200236.
XX PA (SESE-) SES EURO NV SA.
XX PI Richards K, Jonard G, Guillely H, Van Dun CMP;
XX DR WPI; 2000-505981/45.
XX CC Conveying resistance to beet necrotic yellow vein virus (BNYVV) to sugar
XX CC beet (Beta vulgaris) comprises introducing a DNA fragment having a
XX CC nucleotide sequence which is homologous to the sequence of the genomic
XX CC RNA 1 of BNYVV.
XX PS Example 1; Page 12; 31pp; English.
XX CC Beet necrotic yellow vein virus (BNYVV) causes rhizomania disease in
XX CC sugar beet plants. The present sequence is a PCR primer for BNYVV. The
XX CC resulting PCR fragment was cloned and used to convey resistance to BNYVV
XX CC to a sugar beet plant, to result in production of a transgenic BNYVV-
XX CC resistant sugar beet plant
XX SQ Sequence 27 BP; 5 A; 9 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 3; Length 27;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGATCCAGGTAGGACAGACTTGT 24
| ||||| ||||| |||||
Db 2 GCGATCCACCATGGCAGACTTGT 25

RESULT 31
AAAX60078
ID AAAX60078 standard; RNA; 31 BP.
XX AC AAAX60078;
XX DT 17-OCT-2003 (revised)
XX DT 04-AUG-1999 (first entry)
XX DE 3' untranslated region sequence of a viral genome.
XX
```

KW Protein production; eukaryotic cell; uncapped mRNA;
KW barley yellow dwarf virus PAV serotype; BYDV-PAV; ss.

XX unidentified tobacco necrosis virus.

XX US5910628-A.

XX 08-JUN-1999.

XX 20-MAY-1997; 97US-00858623.

XX 20-MAY-1996; 96US-0017199P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

XX Wang S, Miller WA;

XX WPI; 1999-356844/30.

XX Cap-independent in eukaryotic cells.

XX Example 19; Fig 13; 49pp; English.

XX The specification describes a method for producing a protein in a
CC eukaryotic cell, from an uncapped mRNA using sequences derived from the
CC barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are
CC useful for increasing the production of a protein translated from an
CC uncapped eukaryotic mRNA. AAX60075-85 represent 3' untranslated regions
CC of viral genomes, and were used in the course of the invention. (Updated
CC on 17-OCT-2003 to standardise OS field)

XX Sequence 31 BP; 9 A; 7 C; 11 G; 0 T; 4 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 2; Length 31;

Best Local Similarity 62.5%; Pred. No. 1.4e+04;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCGAGACTTGTGTC 25

DB 8 CGGAUCCUGGGAACACAGGCUUGAC 31

RESULT 32

AAX60067

ID AAX60067 standard; RNA; 33 BP.

XX AAX60067;

XX 17-OCT-2003 (revised)

XX 04-AUG-1999 (first entry)

XX 3' untranslated region sequence of a viral genome.

XX Protein production; eukaryotic cell; uncapped mRNA;

XX barley yellow dwarf virus PAV serotype; BYDV-PAV; ss.

XX unidentified tobacco necrosis virus.

XX US5910628-A.

XX 08-JUN-1999.

XX 20-MAY-1997; 97US-00858623.

XX 20-MAY-1996; 96US-0017199P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

XX Wang S, Miller WA;

XX WPI; 1999-356844/30.

XX Cap-independent in eukaryotic cells.

XX Example 5; Fig 4; 49pp; English.

XX The specification describes a method for producing a protein in a
CC eukaryotic cell, from an uncapped mRNA using sequences derived from the
CC barley yellow dwarf virus PAV serotype (BYDV-PAV). The sequences are
CC useful for increasing the production of a protein translated from an
CC uncapped eukaryotic mRNA. AAX60064-74 represent 3' untranslated regions
CC of viral genomes, and were used in the course of the invention. (Updated
CC on 17-OCT-2003 to standardise OS field)

XX Sequence 33 BP; 9 A; 7 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 2; Length 33;

Best Local Similarity 62.5%; Pred. No. 1.4e+04;

Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGCGAGACTTGTGTC 25

DB 9 CGGAUCCUGGGAACACAGGCUUGAC 32

RESULT 33

ACN17176

ID ACN17176 standard; RNA; 38 BP.

XX ACN17176;

XX 22-APR-2004 (first entry)

XX WNV Inozyme SEQ ID NO 17179.

XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 17179; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX SQ Sequence 38 BP; 8 A; 12 C; 11 G; 0 T; 6 U; 1 Other;

Query Match 48.0%; Score 14.4; DB 6; Length 38;

XX Best Local Similarity 60.0%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 4 GATCCAGGTAGGCAGACTTGTGCAGC 28

Db 14 GAGGCCGUAGGCCGAANUGUCAGC 38

RESULT 34

AAAX76467/c

ID AAX76467 standard; DNA; 40 BP.

XX AC AAX76467;

XX DT 05-AUG-1999 (first entry)

XX DE Human BRCA1 interacting protein gene B112 PCR primer B112.2T.

XX KW Human; BRCA1 interacting protein; B112; CtIP; tumour suppressor; cancer;
XX KW therapy; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9927075-A1.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-US024831.

XX PR 21-NOV-1997; 97US-00975703.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Wong AKC, Bartel PL, Teng DHP, Tavtigian SV;

XX DR WPI; 1999-357827/30.

XX PT A carboxy-terminal BRCA1 interacting protein.

XX PS Example 4; Page 42; 93pp; English.

CC The present invention describes a human BRCA1 interacting protein,
CC designated B112. BRCA1 is a tumour suppressor protein. Methods and
CC compositions from the present invention are useful for diagnosis of,
CC determining predisposition to or lack of predisposition to, and treatment
CC of human cancer, such as breast or pancreatic cancer, as a result of a
CC mutation in CtIP or BRCA1. The methods and compositions can also be used
CC in rational drug design for cancer therapeutics. The present sequence
CC represents a PCR primer for B112 which is used in an example from the
CC present invention

XX SQ Sequence 40 BP; 15 A; 10 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 2; Length 40;

XX Best Local Similarity 75.0%; Pred. No. 1.5e+04;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 3 GGATCCAGGTAGGCAGACTTGTCA 26

Db 36 GAATCCTGTTGGCAGAAATGTCA 13

RESULT 35

ABL99294

ID ABL99294 standard; DNA; 40 BP.

XX AC

ABL99294;

XX DT 27-JUN-2002 (first entry)

XX DE Synthetic Renilla luciferase preparation oligo SEQ ID NO:277.

XX KW Luciferase; synthetic nucleic acid; transcriptional characteristic;
XX KW transcription; codon usage; PCR; primer; ss.

XX OS Renilla sp.

XX OS Synthetic.

XX PN WO200216944-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026566.

XX PR 24-AUG-2000; 2000US-00645706.

XX PA (PROM-) PROMEGA CORP.

XX PI Wood KV, Wood MG, Zhuang Y, Paguio A;

XX DR WPI; 2002-304140/34.

XX PT Preparing a synthetic nucleic acid molecule with reduced inappropriate
XX PT transcriptional characteristics when expressed in a cell, for e.g making
XX PT fusion proteins, by altering a wild type or another synthetic nucleic
XX PT acid sequence.

XX PS Example 1; Fig 10; 294pp; English.

XX CC The present invention relates to the preparation of synthetic nucleic
XX CC acid molecules which have altered transcriptional regulatory sequences
XX CC compared to the wild-type. These sequences are then transcribed with less
XX CC frequency compared to the wild-type. In particular, the invention relates
XX CC to altered luciferase sequences. This can be used to detect weak promoter
XX CC activity, to express fusion proteins, to detect and/or measure levels of
XX CC gene expression, subcellular localisation or targeting, in life science
XX CC research, agrogenetics, gene therapy, developmental science and
XX CC pharmaceutical development. The present sequence is an oligonucleotide
XX CC described in the exemplification of the invention

XX SQ Sequence 40 BP; 7 A; 14 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 6; Length 40;

XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GGATCCAGGTAGGCAGC 18

Db 23 GGCTCCAGGTAGGCAGC 38

RESULT 36

AAT38282/c

ID AAT38282 standard; DNA; 44 BP.

XX AC AAT38282;

XX DT 29-DEC-1996 (first entry)

XX DE Murine 103 gene 3' primer for construction of transgenic clone.

XX KW T helper cell; TH cell; T-cell; T-lymphocyte; 103 gene;

XX KW differential expression; immune disorder; multiple sclerosis; asthma;
XX KW lepromatous leprosy; diagnosis; therapy; primer; PCR;

XX KW polymerase chain reaction; transgenic mouse; ss.

XX OS Synthetic.


```

PN WO9627603-A1.
XX
XX 12-SEP-1996.
XX
XX 01-MAR-1996; 96WO-US002798.
XX
XX 03-MAR-1995; 95US-00398633.
XX
XX 07-JUN-1995; 95US-00487748.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Levinson DA;
XX
XX WPI; 1996-433404/43.
XX
XX Genes and their products differentially expressed in T helper cells -
XX useful in diagnosis and treatment of immune disorders, e.g. multiple
XX sclerosis, asthma, lepromatous leprosy, etc.
XX
XX Example 11, Page 167; 218pp; English.
XX
XX A 5' primer (AAT38281) and 3' primer (AAT38282) contg. 5' SpeI and 3'
XX BamHI sites were used to amplify the murine 103 gene (see also AAT38272)
XX that is differentially expressed in T helper TH2 cells. Murine TH2-type
XX cell line D10G4 cDNA was used as template. The PCR product was used to
XX replace the IL-10 gene in plasmid pCil-10. The final construct, pCD2-103L
XX -GH, contained the human CD2 enhancer and Pvu promoter and the murine 103
XX gene coding sequence. It was used to produce transgenic mice that
XX expressed the 103 gene product (see also AAT38283-84). Such mice can be
XX used as models of TH2 cell subpopulation-related disorders
XX
XX Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 48.0%; Score 14.4; DB 2; Length 44;
XX Best Local Similarity 75.0%; Pred. No. 1.5e+04;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 6 TCCAGGTAGGCAGACTTGTGAGCC 29
XX | ||||| ||||| ||||| |||||
XX Db 40 TGCAGGTGTGCAGACTTGGGATCC 17
XX
XX RESULT 37
XX AAA51915/C
XX ID AAA51915 standard; DNA; 44 BP.
XX
XX AC AAA51915;
XX
XX DT 31-OCT-2000 (first entry)
XX
XX DE Reverse primer to construct a murine 103 gene transgenic clone.
XX
XX KW T helper cell; differential expression; 200 gene; immunomodulator;
XX anti-inflammatory; anti-arthritis; antibacterial; immunosuppressive;
XX thymomimetic; anti-thyroid; anti-asthmatic; anti-allergic; antiviral;
XX protozoacide; lymphocyte; modulator; gene therapy; primer; ss.
XX
XX OS Mus sp.
XX
XX PN US6084083-A.
XX
XX PD 04-JUL-2000.
XX
XX PF 28-MAR-1997; 97US-00829525.
XX
XX PR 03-MAR-1995; 95US-00398633.
XX
XX PR 07-JUN-1995; 95US-00487748.
XX
XX PR 01-MAR-1996; 96US-00609583.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Levinson DA;
XX
XX
XX WPI; 2000-464385/40.
XX
XX New isolated human 200 gene products or polypeptides, useful for treating
XX and diagnosing immune disorders, especially T helper lymphocyte-related
XX disorders.
XX
XX Example; Col 91; 107pp; English.
XX
XX Genes which are differentially expressed within and among T helper (TH)
XX cells and TH cell subpopulations, e.g. TH0, TH1 and TH2 subpopulations,
XX can be used diagnostically or as targets for therapeutic intervention.
XX The polypeptides are useful for treating and diagnosing of immune
XX disorders, especially T lymphocyte-related disorders. These disorders
XX include chronic inflammatory diseases and disorders (e.g. Crohn's
XX disease, reactive arthritis, Lyme disease, Hashimoto's thyroiditis or
XX Grave's disease), or atopic conditions (e.g. asthma and allergy,
XX including allergic rhinitis or food allergies). Also included are certain
XX pathogen susceptibilities (e.g. leishmaniasis), and viral (e.g. HIV) or
XX bacterial (e.g. tuberculosis or lepromatous leprosy) infections
XX
XX Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 48.0%; Score 14.4; DB 3; Length 44;
XX Best Local Similarity 75.0%; Pred. No. 1.5e+04;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 6 TCCAGGTAGGCAGACTTGTGAGCC 29
XX | ||||| ||||| ||||| |||||
XX Db 40 TGCAGGTGTGCAGACTTGGGATCC 17
XX
XX RESULT 38
XX AAD03383/C
XX ID AAD03383 standard; DNA; 44 BP.
XX
XX AC AAD03383;
XX
XX DT 13-JUN-2001 (first entry)
XX
XX DE 3' primer, to amplify long form of murine 103 gene.
XX
XX KW 103 gene; immune disorder; T helper lymphocyte 2 related disorder; TH2;
XX ST2; T1; Fit-1; therapy; asthma; allergy; IgE; IL-4; antiviral;
XX immunoglobulin E mediated condition; interleukin-4 mediated condition;
XX Crohn's disease; arthritis; insulin-dependent diabetes; antihelminthic;
XX multiple sclerosis; Hashimoto's thyroiditis; Grave's disease;
XX contact dermatitis; psoriasis; allergic rhinitis; conjunctivitis;
XX glomerular nephritis; systemic lupus erythematosus; eosinophilia;
XX neuroprotective; ophthalmological; antibacterial; immunosuppressive;
XX sarcoidosis; scleroderma; murine; PCR primer; ss.
XX
XX OS Mus musculus.
XX
XX PN WO200121641-A1.
XX
XX PD 29-MAR-2001.
XX
XX PF 25-SEP-2000; 2000WO-US026555.
XX
XX PR 24-SEP-1999; 99US-0155862P.
XX
XX PR 28-APR-2000; 2000US-00560639.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Leiby KR, Kingsbury GA;
XX
XX WPI; 2001-211462/21.
XX
XX New 103 gene products and immunospecific antibodies, useful for the
XX diagnosis and treatment of T helper lymphocyte 2 (like) related immune
XX disorders e.g. asthma, allergy, immunoglobulin E and interleukin-4
XX mediated conditions.
XX

```

PS Example; Page 112; 197pp; English.

CC The invention relates to methods and compositions for treatment and

CC diagnosis of immune disorders, especially T lymphocyte-related disorders.

CC The methods and compositions of the present invention particularly

CC relates to detection and/or modulation of expression and/or activity of

CC 103 gene. This gene is alternatively referred as ST2, T1 and Fit-1 and is

CC differentially expressed in T helper lymphocyte 2 (TH2) cells. Antibodies

CC specific for 103 gene are useful for the treatment and prevention of

CC immune disorders in humans, preferably TH2 related disorders, such as

CC asthma, allergy, immunoglobulin E (IgE) mediated conditions and

CC interleukin-4 (IL-4) mediated conditions. Modulators of 103 gene such as

CC antibodies, ribozymes, antisense oligonucleotides and peptides are useful

CC for the treatment and diagnosis of immune disorders such as Crohn's

CC disease, arthritis, insulin-dependent diabetes, multiple sclerosis,

CC Hashimoto's thyroiditis, Grave's disease, graft rejection, contact

CC dermatitis, psoriasis, allergic rhinitis, conjunctivitis, graft- versus-

CC host disease, glomerular nephritis, sarcoidosis, eosinophilia, systemic

CC lupus erythematosus, scleroderma and helminthic (e.g leishmaniasis),

CC viral and bacterial infections (e.g. tuberculosis and lepromatous

CC leprosy). The present sequence is 3' primer used to amplify long form of

CC murine 103 gene

XX

SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 4; Length 44;

Best Local Similarity 75.0%; Pred. No. 1.5e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 6 TCCAGGTAGGCAGACTTGTTCAGCC 29

Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 39

AAC92152/c

ID AAC92152 standard; DNA; 44 BP.

XX AAC92152;

AC AAC92152;

XX

DT 20-MAR-2001 (first entry)

XX

DE Mouse 103 gene PCR primer SEQ ID NO:34.

XX

XX Treatment; diagnosis; immune disorder; mast cell related disorder;

KW T-helper lymphocyte-related disorder; ischaemic disorder; identification;

KW vasodilator; cardiac; antianginal; angina pectoris;

KW ischaemic renal disease; myocardial ischaemia; myocardial infarction;

KW cortical infarction; ischaemic injury; kidney transplant; PCR primer; ss.

XX

OS Mus musculus.

XX

XX WO200073498-A1.

XX

XX 07-DEC-2000.

XX

XX 31-MAY-2000; 2000WO-US014986.

XX

XX 02-JUN-1999; 99US-00324986.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Levinson DA, Lloyd CM, McCarthy SA;

XX

XX WPI; 2001-016510/02.

XX

XX Ameliorating a symptom of an ischemic disorder or injury in a mammal e.g.

PT ischemic renal disease or myocardial ischemia, by administering a 200

PT gene product (S1), a nucleic acid encoding (S1) or an antibody directed

PT against (S1).

XX

XX Example 6; Page 190; 309pp; English.

XX

CC The present invention describes a method for ameliorating a symptom of an

CC ischaemic disorder or injury in a mammal. The method comprises

CC administering a 200 gene product, a nucleic acid encoding (S1) or an

CC antibody directed against (S1). The method is useful for treating a

CC symptom of an ischaemic disorder such as ischaemic renal disease or

CC myocardial ischaemia (such as angina pectoris), myocardial or cortical

CC infarction. The method is also useful for treating a symptom of an

CC ischaemic injury occurring due to transplantation of a kidney. The

CC present sequence represents a PCR primer which is used in the

CC exemplification of the present invention

XX

SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 48.0%; Score 14.4; DB 4; Length 44;

Best Local Similarity 75.0%; Pred. No. 1.5e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 6 TCCAGGTAGGCAGACTTGTTCAGCC 29

Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 40

AAF23475/c

ID AAF23475 standard; DNA; 44 BP.

XX AAF23475;

AC AAF23475;

XX

DT 21-MAR-2001 (first entry)

XX

XX 3' oligonucleotide used in construction of 103 gene clone.

XX

KW Cysteine protease; immune disorder; T lymphocyte; Crohn's; arthritis;

KW diabetes; multiple sclerosis; viral infection; bacterial; HIV; ds.

XX

XX Unidentified.

XX

XX US6156887-A.

XX

XX 05-DEC-2000.

XX

XX 03-OCT-1997; 97US-00939729.

XX

XX 03-MAR-1995; 95US-00398633.

PR 07-JUN-1995; 95US-00487748.

PR 01-MAR-1996; 96US-00609583.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Levinson DA;

XX

XX WPI; 2001-101473/11.

XX

XX Novel polypeptide exhibiting cysteine protease activity, useful for

PT treating and diagnosing immune disorders, especially T lymphocyte-related

PT disorders, e.g. Crohn's disease, multiple sclerosis, graft versus host

PT disease or allergies.

XX

XX Example; Col 93; 107pp; English.

XX

XX The present invention relates to a novel cysteine protease. The protein

CC of the invention is useful for treating and diagnosing immune disorders,

CC especially T lymphocyte-related disorders. In particular, the polypeptide

CC is useful for treating or diagnosing T helper (TH) cell or TH cell

CC subpopulation-related disorders. These disorders include Crohn's disease,

CC reactive arthritis, Lyme disease, insulin-dependent diabetes, organ-

CC specific autoimmunity, multiple sclerosis, Hashimoto's thyroiditis,

CC Grave's disease, contact dermatitis, psoriasis, graft rejection, graft

CC versus host disease, sarcoidosis, atopic (e.g. asthma or allergy),

CC eosinophilia, conjunctivitis, glomerular nephritis, or helminthic (e.g.

CC leishmaniasis), viral (e.g. HIV (human immunodeficiency virus)) or

CC bacterial (e.g. tuberculosis or lepromatous leprosy) infections

XX

SQ Sequence 44 BP; 9 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
 Query Match 48.0%; Score 14.4; DB 4; Length 44;
 Best Local Similarity 75.0%; Pred. No. 1.5e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 6 TCCAGGTAGGCAGACTTGTGACGCC 29
 Db 40 TGCAGGTGTGCAGACTTGGGATCC 17

Search completed: November 18, 2005, 11:52:20
 Job time : 209.578 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1434.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-2
Perfect score: 30
Sequence: 1 GCGATCCAGGTAGGCAGACTTGTCAGCCT 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700.residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssi:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	53.3	45	9	CL212784
2	15.2	50.7	45	8	AZ331000
3	14.8	49.3	39	1	AJ428912
4	14.6	48.7	25	9	AG264147
5	14.6	48.7	31	9	EX662359
6	14.6	48.7	46	9	CG784706
7	14.4	48.0	34	1	AA996291
8	14.4	48.0	38	9	CL522268
9	14.4	48.0	46	1	AA836932
10	14.4	48.0	50	1	AU103386
11	14	46.7	49	1	A1312023
12	13.8	46.0	29	8	AZ441837
13	13.8	46.0	31	9	TA31H09P
14	13.8	46.0	40	4	BG431777
15	13.8	46.0	43	8	CC325528
16	13.6	45.3	32	8	AZ303920
17	13.6	45.3	43	9	AL953049
18	13.6	45.3	50	1	AU103363
19	13.4	44.7	33	8	AZ352257
20	13.4	44.7	39	9	CL302526
21	13.4	44.7	50	8	AZ920008
22	13.2	44.0	45	8	BZ764481
23	13.2	44.0	48	5	BUS82005
24	13.2	44.0	50	1	AU104377

C	25	13.2	44.0	50	1	AU107676
	26	13.2	44.0	50	9	CR127702
	27	13	43.3	36	9	DR43H15T
	28	13	43.3	39	8	CC057135
C	29	13	43.3	45	8	BH857661
	30	13	43.3	46	1	AA932841
C	31	13	43.3	49	1	AI185949
	32	13	43.3	50	1	AU107828
	33	13	43.3	50	1	AU107829
C	34	13	43.3	50	8	BZ586756
	35	12.8	42.7	27	1	AU260098
	36	12.8	42.7	28	9	AJ622435
C	37	12.8	42.7	37	4	BI080927
	38	12.8	42.7	43	7	H40051
C	39	12.8	42.7	49	9	EX948677
	40	12.8	42.7	50	1	AU102393
C	41	12.8	42.7	50	1	AU104419
	42	12.8	42.7	50	2	AW507256
C	43	12.8	42.7	50	2	AW507292
	44	12.8	42.7	50	9	EX893038
C	45	12.6	42.0	24	8	AZ437757

ALIGNMENTS

RESULT 1
LOCUS CL212784
DEFINITION CL212784 G050F11 GGTCC Gene Trap Library GV07C05 Mus musculus cDNA clone
ACCESSION G050F11, mRNA sequence.
VERSION CL212784.2 GI:49489438
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 45)
AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE 22810117
PUBMED 12904583
COMMENT On Jun 30, 2004 this sequence version replaced gi:40729685.
Contact: GGTCC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G050F11', ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 16659
Class: Gene trap.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G050F11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129SvEvTac] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN

Query Match 53.3%; Score 16; DB 9; Length 45;

AUTHORS TITLE JOURNAL

Sato, S.
Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)

FEATURES

Location/Qualifiers
1..25
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjT59109 sfi"
/clone_lib="genomic TAC library"
/note="VECTOR: pYLTA7-synonym: Lotus japonicus"

ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCGATCCAGGTAGGACGACT 21
|||||
DB 5 GCGATCCAGGTAGGACGACT 25

RESULT 5 BX662359/c

LOCUS BX662359 31 bp DNA linear GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-688E05-023078,
genomic survey sequence.

ACCESSION BX662359.1 GI:37618781

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS Li, X., Rosso, M.G., Strizhov, N., Viehovever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829
PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, X., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147
PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, X., Rosso, M.G., Viehovever, P., Dekker, K.A. and
Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 31)

AUTHORS Rosso, M.G., Li, X., Strizhov, N. and Weishaar, B.

TITLE Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T13b4. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the

FEATURES source

MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers
1..31

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-688E05-023078"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ517514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.4e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACGACTTTCAGCCT 30
|||||

DB 31 CGGAACCATAAACCAGATTTATCAGCGT 3

RESULT 6

CG784706

LOCUS CG784706

DEFINITION RRR527 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
mRNA sequence.

ACCESSION CG784706

VERSION CG784706.1 GI:38157266

KEYWORDS GSS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 46)

REFERENCE BayGenomics.

AUTHORS http://baygenomics.ucsf.edu/

TITLE http://baygenomics.ucsf.edu/

JOURNAL Unpublished (2001)

COMMENT Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=

CELL.LINES&KEY=RRR527

Class: Gene Trap.

Location/Qualifiers

1..46

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 ola"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"

/note="Vector: pGT0Lxf"

ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 46;
Best Local Similarity 69.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;


```
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="CAS11861"  
/clone_lib="Sugano Homo sapiens cDNA library"
```

Query Match 48.0%; Score 14.4; DB 1; Length 50;
Best Local Similarity 93.8%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 1; Indels

RESULT 11
AT312023/0

AI312023 49 bp mRNA linear EST 03-FEB-1999
Q778D08.x1 Soares fetal_lung_NBHL19W Homo sapiens cDNA clone
IMAGE:1929111 3' similar to TR:Q60980 Q60980 BASIC KRUPPEL-LIKE
FACTOR 1; mRNA sequence.

Query Match 48.0%; Score 14.4; DB 1; Length 46;
Best Local Similarity 75.0%; Pred. No. 1.8e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Contact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov

FEATURES
SOURCE

```
1. 49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:192911"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicil
/clone_lib="Soares fetal
```

ORIGIN

Query Match 46.7%; Score 14; DB 1; Length 49;
Best Local Similarity 77.3%;
Pred. No. 2.7e+05;
Matches 17; Conservative 0; Mismatches 5; Indels

Db
45 ATGTCGCCATACTTGTTAGCCT 24

```
1. .50
/organism="Homo sapiens"
```

```

RESULT 12
AZ441837/c
LOCUS          AZ441837          29 bp    DNA          linear          GSS 03-OCT-2000
DEFINITION     clone UUGC1M0234007 F, genomic survey sequence.
ACCESSION      AZ441837
VERSION        AZ441837.1  GI:10565850
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL
COMMENT        Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112 USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0234 row: 0 column: 07
               Seq primer: CGTTGTAACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 29.
               Location/Qualifiers
FEATURES               source
   1..29
       /organism="Mus musculus"
       /mol_type="genomic DNA"
       /strain="CS7BL/6J"
       /db_xref="taxon:10090"
       /clone="UUGC1M0234007"
       /sex="Male"
       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
       /clone_lib="Mouse 10kb plasmid UUGC1M library"
       /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus CS7BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid Ri. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
ORIGIN
Query Match          46.0%; Score 13.8; DB 8; Length 29;
Best Local Similarity 72.0%; Pred. No. 3e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACGACTTGTCA 26
   ||||| ||| ||||| |||||
DB 26 CTGATTCAGACATTCAGAGTTGTCA 2

```

```

RESULT 13
TA21H09P
LOCUS          TA21H09P          31 bp    DNA          linear          GSS 13-DEC-2000
DEFINITION     T. brucei sheared genomic DNA clone 21h09, forward sequence,
               genomic survey sequence.
ACCESSION      AL454798
VERSION        AL454798.1  GI:11844296
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
REFERENCE
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
               Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
               Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
JOURNAL
COMMENT        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
               Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/Projects/T_brucei/.
               Location/Qualifiers
FEATURES               source
   1..31
       /organism="Trypanosoma brucei"
       /mol_type="genomic DNA"
       /strain="TREU927"
       /db_xref="taxon:5691"
       /clone="21h09"
ORIGIN
Query Match          46.0%; Score 13.8; DB 9; Length 31;
Best Local Similarity 72.0%; Pred. No. 3.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGACGACTTGTTCAGCCT 30
   ||||| ||| ||||| |||||
DB 1 TACTGGAAGCGAGACTTGTCAACAT 25

RESULT 14
BG431777/c
LOCUS          BG431777          40 bp    mRNA          linear          EST 14-MAR-2001
DEFINITION     60249583F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613012 5',
               mRNA sequence.
ACCESSION      BG431777
VERSION        BG431777.1  GI:13338283
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 40)
JOURNAL        NIH-MGC http://mgc.nci.nih.gov/.
               National Institutes of Health, Mammalian Gene Collection (MGC)
               Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-re@mail.nih.gov
               Tissue Procurement: CLONTECH Laboratories, Inc.
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
               DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM1362 row: f column: 21

High quality sequence stop: 40.

FEATURES

Location/Qualifiers

1..40

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4613012"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctgggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 Kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 46.0%; Score 13.8; DB 4; Length 40;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

2 CGGATCCAGGTAGGCAGATTGTCA 26

DB

34 CGCATCCGGGTAGGCACCATCCA 10

RESULT 15

CC325528/c

LOCUS

DEFINITION CC325528 TEA007 BayGenomics Gene Trap Library pGTILxf Mus musculus cDNA, mRNA sequence. 43 bp mRNA linear GSS 14-MAY-2003

ACCESSION

CC325528

VERSION

CC325528.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 43)

BayGenomics.

TITLE

<http://baygenomics.ucsf.edu/>

JOURNAL

Unpublished (2001)

CONTACT

Bay Area Functional Genomics Consortium (BayGenomics)

Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from BayGenomics. Annotation

information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=TEA007

Class: Gene trap.

Location/Qualifiers

1..43

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 ola"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic stem cell"

/clone_lib="BayGenomics Gene Trap Library pGTILxf"

/note="Vector: pGTILxf"

ORIGIN

Query Match 46.0%; Score 13.8; DB 8; Length 43;

Best Local Similarity 88.2%; Pred. No. 3.2e+05;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

6 TCCAGGTAGGCAGACTT 22

DB

39 TCCCGTATGCAGACTT 23

RESULT 16

AZ303920/c

LOCUS

DEFINITION AZ303920 32 bp DNA linear GSS 29-SEP-2000

clone UUGC1M0003F19 R, genomic survey sequence.

ACCESSION

AZ303920

VERSION

AZ303920.1

KEYWORDS

GSS

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 32)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Muscle whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0003 row: F column: 19

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0003F19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi4732114|gbAF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 45.3%; Score 13.6; DB 8; Length 32;

Best Local Similarity 80.0%; Pred. No. 3.7e+05; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTT 22
|||||
Db 30 GGACCCAGGTGAGAGACTT 11

RESULT 17
AL953049/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-348B03-016247,
DEFINITION Genomic survey sequence.

ACCESSION AL953049
VERSION AL953049.1 GI:24409671

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.

AUTHORS GABI-Kat SimpleSearch: a flanking sequence tag (EST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE 2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

AUTHORS Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147

PUBMED 14756321

REFERENCE 3 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and

AUTHORS Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA

JOURNAL mutagenized Arabidopsis thaliana lines

PUBMED Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE 4 Li, Y., Rosso, M.G., Li, Y. and Weissshaar, B.

AUTHORS Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer

JOURNAL Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
F23H6. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. .43

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-348B03-016247"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 45.3%; Score 13.6; DB 9; Length 43;

Best Local Similarity 67.9%; Pred. No. 3.9e+05;

Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGC 28

Db 34 GAGCAATCAGATACGCAGCCCTGTTCATC 7

RESULT 18

AUI03363

LOCUS

DEFINITION

AUI03363

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

source

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HBMA0059"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 45.3%; Score 13.6; DB 1; Length 50;

Best Local Similarity 80.0%; Pred. No. 4e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTTC 25

Db 18 TCCACACAGGCAGACTTGAC 37

RESULT 19

AZ352257/c

LOCUS

DEFINITION

AZ352257

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0030 row: G column: 11
 Seq primer: CACACAGGACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 33.

FEATURES

source
 1. .33
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0090G11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number: Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 33;
 Best Local Similarity 73.9%; Pred. No. 4.6e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TCCAGGTAGGCAGACTTGTGACG 28
 ||||| ||||| ||||| |||||
 Db 28 TCCAGGGAGACAGATCTCGACG 6

RESULT 20
 CL302526
 LOCUS G061A09 GGTG Gene Trap Library GV07C05 Mus musculus cDNA clone
 DEFINITION G061A09, mRNA sequence.
 ACCESSION CL302526
 VERSION CL302526.2 GI:49489458
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 39)
 Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,

TITLE

JOURNAL MEDLINE
 PUBMED
 COMMENT

Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
 A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 22810117
 12904583
 On Jun 30, 2004 this sequence version replaced gi:42743355.
 Contact: GGTC
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de
 U3CEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=G061A09'. ES cell line harboring insertion mutation of target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm 1' Inhouse Sequence Identifier: 18060
 Class: Gene Trap.

FEATURES

source
 1. .39
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="G061A09"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
 /clone_lib="GGTC Gene Trap Library GV07C05"
 /note="Vector: U3CEO"

ORIGIN

Query Match 44.7%; Score 13.4; DB 9; Length 39;
 Best Local Similarity 65.4%; Pred. No. 4.7e+05;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 5 ATCCAGGTAGGCAGACTTGTGACGCT 30
 ||||| ||||| ||||| |||||
 Db 13 ATCCAGGATGTCAGANNGTGAGGCT 38

RESULT 21
 AZ920008/c
 LOCUS AZ920008
 DEFINITION 1006017F11.y1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.
 ACCESSION AZ920008
 VERSION AZ920008.1 GI:13390291
 KEYWORDS GSS.
 SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 50)

REFERENCE

AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1006017 row: 37
 Class: transposon-tagged.
 Location/Qualifiers
 1. .50
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"

/tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1006 - RescueMu Grid G"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 50;
 Best Local Similarity 73.9%; Pred. No. 4.8e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CCAGGTAGGCAGACTTGTCCAGC 29
 ||||| ||||| ||||| ||||| |||||
 Db 47 CCAGCCACCAGCCTTGTCCGCC 25

RESULT 22

BZ764481

LOCUS

DEFINITION SALK_124922.26.85.x Arabidopsis thaliana DNA linear GSS 13-MAR-2003
 Arabidopsis thaliana genomic clone SALK_124922.26.85.x, genomic survey sequence.

ACCESSION BZ764481

VERSION BZ764481.1 GI:28937034

KEYWORDS

GSS

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.

REFERENCE

1 (bases 1 to 45)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel.: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckergsalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 5' end of

At2g20721 and 300 bases of the 3' end of At2g20723.

Class: TDNA tagged.

Location/Qualifiers

1..45

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_124922.26.85.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 45;
 Best Local Similarity 69.2%; Pred. No. 5.8e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCCAGCCT 30

||| ||||| ||||| ||||| |||||

Db 1 AACAAATGAGCAGAAATTGAATCCT 26

RESULT 23

BZ582005/c

LOCUS

DEFINITION BZ582005 48 bp mRNA linear EST 18-SEP-2002
 Oryctolagus cuniculus adult subtractive hybridization library

ACCESSION BZ582005

VERSION BZ582005.1 GI:23186905

KEYWORDS

EST.

SOURCE

Oryctolagus cuniculus (rabbit)

ORGANISM

Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 48)

Zhang,B., Wang,Z. and Zhu,P.

Cloning and identification of injury-related gene(s) in the process

of fetal rabbit skin healing

Unpublished (2002)

Contact: Zhang Bo

Department 4

Research Institute of surgery

Changjiangzhu 10, Chongqing, P.R.China., 400042

Tel: 86-23-68757444

Fax: 86-23-68819750

Email: john.power1201@hotmail.com.

Location/Qualifiers

1..48

/organism="Oryctolagus cuniculus"

/mol_type="mRNA"

/db_xref="taxon:9986"

/sex="female"

/tissue_type="skin"

/dev_stage="adult"

/lab_host="E.coli HB101"

/clone_lib="Oryctolagus cuniculus adult subtractive

hybridization library"

/note="Vector: pUCm-T; inserts-subtractive hybridization

and PCR products"

Query Match 44.0%; Score 13.2; DB 5; Length 48;

Best Local Similarity 69.2%; Pred. No. 5.8e+05;

Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GGATCCAGGTAGGCAGACTTGTCCAGC 28

||||| ||||| ||||| ||||| |||||

Db 42 GGATCCAGATCTCCAGTCTTTTCGAGC 17

RESULT 24

AUI04377

LOCUS

DEFINITION AUI04377 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP21718, mRNA sequence.

ACCESSION AUI04377

VERSION AUI04377.1 GI:13553898

KEYWORDS EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

JOURNAL
MEDLINE
PUBMED
COMMENT

FEATURES
source

Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP21718"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGATCCAGTAGGACAGACTTGTTCAGC 28
|||||
DB 11 GGAGCCAGGTCGTATAGCGCCAGC 36

RESULT 25
AU107676/c

LOCUS AU107676 50 bp mRNA linear EST 28-JAN-2004
DEFINITION HEP21286, Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU107676
ACCESSION HEP21286, mRNA sequence.
VERSION AU107676.1 GI:13557197
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL
MEDLINE
PUBMED

21270072

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source

Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP21286"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACAGACTTGTTCAG 27
|||||
DB 32 CGCAACCGGTAGTCGCGCTTCTCAG 7

RESULT 26
CR127702

LOCUS CR127702 50 bp DNA linear GSS 06-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP408a08, genomic survey sequence.
ACCESSION CR127702
VERSION CR127702.1 GI:49875154
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 50)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR

TITLE

JOURNAL

FEATURES

Location/Qualifiers
1. .50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP408a08"
/clone_lib="MHP"

ORIGIN

Query Match 44.0%; Score 13.2; DB 9; Length 50;
Best Local Similarity 69.2%; Pred. No. 5.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGGATCCAGGTAGGACAGACTTGTTCAG 27
|||||
DB 5 CGGATCAAGAAACAGACTTCAAAG 30

RESULT 27
DR43H15T

LOCUS DR43H15T 36 bp DNA linear GSS 22-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-43H15, genomic survey sequence.
ACCESSION AL981997
VERSION AL981997.1 GI:25184424
KEYWORDS GSS.

SOURCE

ORGANISM

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 36)

AUTHORS

TITLE

JOURNAL

COMMENT

Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphray@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 43H15. 43H15 is part of the Daniokey BAC Library created by R. Plasterk and N.V. KeyGene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

Location/Qualifiers
1. .36

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"

```

/clone="DKEY-43H15"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"

ORIGIN
Query Match      43.3%; Score 13; DB 9; Length 36;
Best Local Similarity 76.2%; Pred. No. 6.8e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTCA 26
Db 14 TGCAGGCATGCAAGCTTGTC 34

RESULT 28
CC057135
LOCUS
DEFINITION
SALK 111730.14.10.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_111730.14.10.n, genomic
survey sequence.
GSS.
CC057135.1 GI:29476919
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 39)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of AC5948010.
Class: TDNA tagged.
Location/Qualifiers
1..39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="SALK 111730.14.10.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      43.3%; Score 13; DB 8; Length 39;
Best Local Similarity 76.2%; Pred. No. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACT 21
Db 18 GCCAATACAGGAGGAGGAGT 38

RESULT 29
BH857661/c
LOCUS
DEFINITION
SALK 016405.53.70.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_016405.53.70.x, genomic
survey sequence.
GSS.
BH857661.1 GI:21708482
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g10190.
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK 016405.53.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      43.3%; Score 13; DB 8; Length 45;
Best Local Similarity 76.2%; Pred. No. 7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGAGCC 29
Db 31 AAGTAGACATACCTTATTAGCC 11

RESULT 30
AA932841
LOCUS
DEFINITION
AA932841.1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570260 3'
similar to SW:ASH1_HUMAN P50553 ACHAETE-SCUTE HOMOLOG 1. ;, mRNA
sequence.
AA932841
AA932841.1 GI:3086806
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

```


Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation by: Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1206 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

```
1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1570260"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
```

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

```
Query Match 43.3%; Score 13; DB 1; Length 46;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 5 ATCCAGGTAGGCAGACTTGTC 25
Db 23 ATCCATCTTGGCAGACTCTTC 43
```

RESULT 31

A1185949/c

LOCUS

DEFINITION

IMAGE:1740390 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ; mRNA sequence.

ACCESSION

A1185949

VERSION

A1185949.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

A1185949

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 360 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

```
1. .49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

```
/clone="IMAGE:1740390"
/dev stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NDH19W"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDH19W."
```

ORIGIN

```
Query Match 43.3%; Score 13; DB 1; Length 49;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 7 CCAGTAGGCAGACTTGTCAG 27
Db 39 CCAAGAGGCAGCTGTTGTAAG 19
```

RESULT 32

A1185949

LOCUS

DEFINITION

A1185949

ACCESSION

A1185949.1

VERSION

A1185949.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

A1185949

AUTHORS

Department of Virology

TITLE

Institute of Medical Science, University of Tokyo

JOURNAL

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

MEDLINE

Email: yuzuki@ims.u-tokyo.ac.jp

PUBMED

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

COMMENT

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 145-156 (1997)

Location/Qualifiers

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAE00112"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

```
Query Match 43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 1 GCGGATCCAGTAGGCAGACT 21
Db 23 GCGGATCGGGAAGCCGACT 43
```

```

RESULT 33
AUI07829
LOCUS
DEFINITION
AUI07829 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV61043, mRNA sequence.
ACCESSION
AUI07829
VERSION
AUI07829.1 GI:13557351
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Teunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isoqai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.,
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
21270072
MEDLINE
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="ZRV61043"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GCGGATCCAGGTAGGCGAGACT 21
|||||
Db 26 GCGGATCGGGNAGCGGACT 46
|||||

RESULT 34
BZ586756/c
LOCUS
DEFINITION
BZ586756 50 bp DNA linear GSS 17-DEC-2002
genomic survey sequence.
ACCESSION
BZ586756
VERSION
BZ586756.1 GI:27221817
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 50)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

```

```

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590.1.20.1 column: 7
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..50
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3590 - RescueMu Grid M"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."
ORIGIN
Query Match 43.3%; Score 13; DB 8; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.1e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 7 CCAGGTAGGCGAGACTTGTCTAG 27
|||||
Db 22 CCAGCGACGCACAGTTGTCTAG 2
|||||

RESULT 35
AUI260098
LOCUS
DEFINITION
AUI260098 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0016170 3', mRNA sequence.
ACCESSION
AUI260098
VERSION
AUI260098.1 GI:20327257
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@is.nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES
source
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="BED0016170"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
ORIGIN
Query Match 42.7%; Score 12.8; DB 1; Length 27;

```

Best Local Similarity 70.8%; Pred. No. 8e+05; 7; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GATCCAGGTAGGCAGACTTGTCTAG 27
Db 1 GATCCAAGAAAGCCTTATTAG 24

RESULT 36
AJ622435 28 bp DNA linear GSS 28-JAN-2004
LOCUS Drosophila melanogaster flanking sequence of RS P element insertion
DEFINITION P[RS5]5-HA-2412, clone library P[RS5], genomic survey sequence.
ACCESSION AJ622435
VERSION AJ622435.1 GI:41366647
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
AUTHORS Ryder, E.J., Ashburner, M., Bagunya, J., Blows, P., Bucheton, A.,
Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N.,
Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P.,
Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A.,
Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and
Russell, S.

TITLE Mapping of RS P element insertions in Drosophila melanogaster for
the DrosDel second generation deficiency kit

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 28)

AUTHORS Ryder, E.J.

JOURNAL Direct Submission

COMMENT Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
The insertion point of the P element is before base 1 of the
sequence. Further information about this P element insertion line
can be found at <http://www.flyseq.org.uk> and
<http://www.drosdel.org.uk>.

FEATURES Location/Qualifiers

1..28
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/chromosome="2L"
/clone="P[RS5]5-HA-2412"
/clone_lib="P[RS5]"
/note="read=5' end"

misc_feature 1..28
/note="P element insertion in the 3' to 5' orientation"

ORIGIN

Query Match 42.7%; Score 12.8; DB 9; Length 28;
Best Local Similarity 87.5%; Pred. No. 8e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GCAGACTTGTCCGCT 30
Db 3 GCAGACTTGTCCGACT 18

RESULT 37
BI080927/c 37 bp mRNA linear EST 20-JUN-2001
LOCUS 60287838F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010561 5',
DEFINITION mRNA sequence.
ACCESSION BI080927
VERSION BI080927.1 GI:14499257
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 37)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing By: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM1058 row: k column: 10
High quality sequence stop: 37.

FEATURES Location/Qualifiers

1..37
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5010561"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 42.7%; Score 12.8; DB 4; Length 37;
Best Local Similarity 70.8%; Pred. No. 8.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTCTAGCC 29
Db 25 TCCAGGTCTCCGCCATGTCAGCC 2

RESULT 38

H40051/c

LOCUS

DEFINITION Y144d10.r1 Soares breast 3NDH8st Homo sapiens cDNA clone
IMAGE:161107 5' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;
mRNA sequence.

ACCESSION H40051

VERSION H40051.1 GI:916103

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 43)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 910

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 910 Std Error: 0.00

Seq primer: M13Rev

High quality sequence stop: 1.

FEATURES

```

source
  1. .43
    /location/Qualifiers
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="GDB:575217"
    /db_xref="GDB:9806"
    /clone="IMAGE:161107"
    /sex="Female"
    /dev_stage="adult"
    /lab_host="DH10B (ampicillin resistant)"
    /clone_lib="Soares breast 3NBH8et"
    /note="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

```

ORIGIN

```

Query Match      42.7%; Score 12.8; DB 7; Length 43;
Best Local Similarity 87.5%; Pred. No. 8.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 7 CCAGGTAGGCAGACTT 22
    |||||
Db 41 CCGATAGGCCAACTT 26

```

RESULT 39

```

BX948677/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-792A06-025017,
genomic survey sequence.

```

```

ACCESSION
BX948677.1 GI:42598363

```

```

VERSION
BX948677.1

```

```

KEYWORDS
GSS.

```

```

SOURCE
Arabidopsis thaliana (thale cress)

```

ORGANISM

```

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```

REFERENCE

```

1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana

```

JOURNAL

```

MEDLINE
Bioinformatics 19 (11), 1441-1442 (2003)

```

PUBMED

```

22755829
12874060

```

REFERENCE

```

2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics

```

JOURNAL

```

MEDLINE
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

```

PUBMED

```

23117147
14756321

```

REFERENCE

```

3
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

```

TITLE

JOURNAL

```

PUBMED
14682050

```

REFERENCE

```

4 (bases 1 to 49)
Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

```

AUTHORS

```

Direct Submission

```

TITLE

```

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T20F20. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

```

FEATURES

```

source

```

```

  1. .49
    /location/Qualifiers
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /strain="Columbia 0"
    /db_xref="taxon:3702"
    /clone="GK-792A06-025017"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /ecotype="Col-0"
    /note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

```

ORIGIN

```

Query Match      42.7%; Score 12.8; DB 9; Length 49;
Best Local Similarity 70.8%; Pred. No. 8.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 3 GGATCCAGGTAGGCAGACTTGTCA 26
    |||||
Db 31 GGTACAGATATGCATGTTGTCA 8

```

RESULT 40

```

AU102393/c
LOCUS
DEFINITION
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF4942, mRNA sequence.

```

```

ACCESSION
AU102393
VERSION
AU102393.1 GI:13551913
EST.
SOURCE
Homo sapiens (human)

```

ORGANISM

```

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

```

REFERENCE

```

1
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929

```

TITLE

```

JOURNAL
MEDLINE
11375929

```

PUBMED

```

11375929

```

COMMENT

```

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

```

FEATURES

```

Location/Qualifiers

```

source 1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLP4942"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match : 42.7%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 8.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GATCCAGGTAGGCAGACTTGTTCAG 27
||| ||| ||| ||| ||| ||| |||
Db 33 GAACCTGGAAGGCAGAGGCTTCAG 10

Search completed: November 18, 2005, 21:12:37
Job time : 1437.98 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 GCGGATCCAGGTAGGACAGACTTGTGCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-2
2	16	53.3	25	4	US-09-396-196G-80578
3	15.6	52.0	41	2	US-08-244-548-14
4	15.6	52.0	41	4	US-09-213-993-14
5	15.6	52.0	45	3	US-09-103-063-26
6	15.6	52.0	45	4	US-09-448-310-26
7	15.6	52.0	45	4	US-09-884-948-26
8	15.6	52.0	45	4	US-09-892-864A-25
9	15.6	52.0	50	3	US-09-109-063-27
10	15.6	52.0	50	4	US-09-448-310-27
11	15.6	52.0	50	4	US-09-884-948-27
12	15.6	52.0	50	4	US-09-892-864A-26
13	15.2	50.7	42	4	US-09-635-132-10
14	15	50.0	29	4	US-09-786-025A-5
15	14.8	49.3	25	3	US-08-963-121C-20
16	14.8	49.3	25	3	US-09-543-513-20
17	14.8	49.3	25	4	US-09-396-196G-6441
18	14.8	49.3	25	5	PCT-US95-04803-21
19	14.8	49.3	37	3	US-08-992-877-68
20	14.6	48.7	25	4	US-09-396-196G-15342
21	14.6	48.7	25	4	US-09-396-196G-18196
22	14.6	48.7	31	3	US-08-858-111-14
23	14.4	48.0	31	2	US-08-858-623A-19
24	14.4	48.0	33	2	US-08-858-623A-8
25	14.4	48.0	40	3	US-08-975-703-28
26	14.4	48.0	40	3	US-09-515-884-28
27	14.4	48.0	44	3	US-08-829-525-34

C 28	14.4	48.0	44	3	US-08-609-583A-34	Sequence 34, Appl
C 29	14.4	48.0	44	3	US-08-937-399-34	Sequence 34, Appl
C 30	14.4	48.0	44	3	US-09-560-639-27	Sequence 27, Appl
C 31	14.4	48.0	44	3	US-09-310-367-34	Sequence 34, Appl
C 32	14.4	48.0	44	3	US-09-032-337-34	Sequence 34, Appl
C 33	14.4	48.0	44	4	US-09-464-231-34	Sequence 34, Appl
C 34	14.2	47.3	25	4	US-09-396-196G-107784	Sequence 107784,
C 35	14.2	47.3	28	3	US-09-283-144-12	Sequence 12, Appl
C 36	14.2	47.3	30	1	US-08-123-702-42	Sequence 42, Appl
C 37	14.2	47.3	39	3	US-08-936-632B-41	Sequence 41, Appl
C 38	14.2	47.3	39	3	US-08-582-333A-92	Sequence 92, Appl
C 39	14.2	47.3	47	4	US-09-671-317-767	Sequence 767, App
C 40	14	46.7	23	3	US-09-209-668-22	Sequence 22, Appl
C 41	14	46.7	25	4	US-09-396-196G-4728	Sequence 4728, Ap
C 42	14	46.7	25	4	US-09-396-196G-59663	Sequence 59663, A
C 43	14	46.7	25	4	US-09-396-196G-80579	Sequence 80579, A
C 44	14	46.7	31	3	US-08-973-965-11	Sequence 11, Appl
C 45	14	46.7	33	4	US-09-530-095B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-989-160-2
; Sequence 2, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-07-989-160-2

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGATCCAGGTAGGACAGACTTGTGCAGCCT 30
|||||

Db 1 GCGGATCCAGGTAGGCAGACTTGTGCAGCCT 30

RESULT 2

US-09-396-196G-80578/G

Query Match 53.3%; Score 16; DB 4; Length 25;

Best Local Similarity 79.2%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

US-09-396-196G-80578

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 80578

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-80578

Query Match 53.3%; Score 16; DB 4; Length 25;

Best Local Similarity 79.2%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 24 GTGGATCCAGTCAGCCAGACGCT 1

RESULT 3

US-08-244-548-14

Query Match 52.0%; Score 15.6; DB 2; Length 41;

Best Local Similarity 81.8%; Pred. No. 9.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

US-08-244-548-14

GENERAL INFORMATION:

APPLICANT: LUPTON, STEPHEN D.

APPLICANT: ALLEN, JAMES M.

TITLE OF INVENTION: HYBRID GENES FOR USE IN THE PRODUCTION

OF TH-INDEPENDENT CYTOTOXIC T CELLS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/213,993

FILING DATE: 16-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/244,548

FILING DATE: 6-JUN-1994

APPLICATION NUMBER: PCT/US94/03659

FILING DATE: 4-APR-1994

APPLICATION NUMBER: US 08/044,539

FILING DATE: 6-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: POLIZZI, CATHERINE M.

REGISTRATION NUMBER: 40,130

REFERENCE/DOCKET NUMBER: 22627-20005.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5651

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-213-993-14

Query Match 52.0%; Score 15.6; DB 4; Length 41;

Best Local Similarity 81.8%; Pred. No. 9.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 8 CGGATCCAGGAGGCTGCCCTG 29


```
RESULT 5
US-09-109-063-26/c
; Sequence 26, Application US/09109063
; Patent No. 6013498
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/109,063
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: JP 180010/1997
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-26
Query Match      52.0%; Score 15.6; DB 3; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TCA 21
|||||

RESULT 6
US-09-448-310-26/c
; Sequence 26, Application US/09448310
; Patent No. 6538122
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/448,310
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-448-310-26
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TCA 21
|||||

RESULT 7
US-09-884-948-26/c
; Sequence 26, Application US/09884948
; Patent No. 6821763
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-26
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TCA 21
|||||

RESULT 8
US-09-892-864A-25/c
; Sequence 25, Application US/09892864A
; Patent No. 6833258
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUUTAMINASE
; FILE REFERENCE: 209524USOCNT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-25
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TCA 21
|||||

RESULT 9
US-09-109-063-27
; Sequence 27, Application US/09109063
; Patent No. 6013498
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-27
Query Match      52.0%; Score 15.6; DB 4; Length 45;
Best Local Similarity 81.8%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 ATCCAGGTAGGCAGACTTGTC A 26
Db      42 ATCCAGGTAAGCAGATTCA TCA 21
|||||
```

```
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/109,063
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: JP 180010/1997
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-109-063-27

Query Match          52.0%; Score 15.6; DB 3; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCA 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 10
US-09-448-310-27
; Sequence 27, Application US/09448310
; Patent No. 6538122
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/448,310
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-448-310-27

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCA 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 11
US-09-884-948-27
; Sequence 27, Application US/09884948
; Patent No. 6821763
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
```

```
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-27

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCA 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 12
US-09-892-864A-26
; Sequence 26, Application US/09892864A
; Patent No. 6833258
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-26

Query Match          52.0%; Score 15.6; DB 4; Length 50;
Best Local Similarity 81.8%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTTGTCA 26
Db 13 ATCCAGGTAAGCAGATTTCATCA 34

RESULT 13
US-09-635-132-10
; Sequence 10, Application US/09635132
; Patent No. 6620601
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, ISAMU
; APPLICANT: NAKASHITA, HIDEO
; APPLICANT: YOSHIOKA, KEIKO
; APPLICANT: DOI, YOSHIHARU
; TITLE OF INVENTION: METHODS FOR TRANSFORMATION OF PLANTS, TRANSFORMED
; FILE REFERENCE: 081356/0148
; CURRENT APPLICATION NUMBER: US/09/635,132
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: JP 11-225832
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: JP 11-225839
; PRIOR FILING DATE: 1999-08-09
```

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-635-132-10

Query Match 50.7%; Score 15.2; DB 4; Length 42;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGCGAGACTTGTCCAGCC 29
|||||
Db 3 CGGATCCAGGAGGGAATCATGGCGACC 30
|||||

RESULT 14
US-09-786-025A-5
; Sequence 5, Application US/09786025A
; Patent No. 6660512

; GENERAL INFORMATION:
; APPLICANT: Yu, Long
; APPLICANT: Fu, Qiang
; APPLICANT: Zhao, Yong
; APPLICANT: Bi, Anding
; TITLE OF INVENTION: A NOVEL HUMAN LYSOZYME GENE, ITS ENCODED
; FILE REFERENCE: A34052-PCT-USA
; CURRENT APPLICATION NUMBER: US/09/786,025A
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: CN98111044.4
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer

US-09-786-025A-5
Query Match 50.0%; Score 15; DB 4; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGATCCAGGTAGGCGAGACTTGT 23
|||||
Db 3 GCGGATCCATGAGGCGATCCGCTG 25
|||||

RESULT 15
US-08-963-121C-20
; Sequence 20, Application US/08963121C
; Patent No. 6084087
; GENERAL INFORMATION:
; APPLICANT: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,121C
; FILING DATE: October 28, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/427,009
; FILING DATE: April, 24, 1995
; APPLICATION NUMBER: 08/229,285
; FILING DATE: April 18, 1994
; APPLICATION NUMBER: 07/766,751, Patent No. 6084087 5,480,895
; FILING DATE: September 27, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/17499-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
US-08-963-121C-20

Query Match 49.3%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AGGTAGGCGAGACTTGTCA 26
|||||
Db 4 AGGTCGACAGACTTGTCA 21
|||||

RESULT 16
US-09-543-513-20
; Sequence 20, Application US/09543513
; Patent No. 6303750
; GENERAL INFORMATION:
; APPLICANT: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,513

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/963,121
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/17499-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ANTI-SENSE: YES
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
;
US-09-543-513-20
Query Match 49.3%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTC A 26
Db 4 AGGTCGACAGACTTGTC A 21

RESULT 17
US-09-396-196G-6441/c
; Sequence 6441, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6441
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
;
US-09-396-196G-6441
Query Match 49.3%; Score 14.8; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ATCCAGGTAGGCAGACTT 22
Db 18 ATCCAGGCAGGCAGCCTT 1

RESULT 18
PCT-US95-04803-21
; Sequence 21, Application PC/TUS9504803
; GENERAL INFORMATION:
; APPLICANT: New York Society For the ruptured and
```

```
;
; APPLICANT: Crippled Maintaining The Hospital for
; APPLICANT: Special Surgery
; APPLICANT: INVENTORS: Friedman, Steven M
; APPLICANT: Crow, Mary K
; APPLICANT: Yi, Y.
; APPLICANT: Tumang, Joseph
; APPLICANT: Sun, Guang-Rong
; TITLE OF INVENTION: Conserved T-Cell Receptor Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04803
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 5983/09449
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: TCra 3'antisense
;
PCT-US95-04803-21
Query Match 49.3%; Score 14.8; DB 5; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 AGGTAGGCAGACTTGTC A 26
Db 4 AGGTCGACAGACTTGTC A 21

RESULT 19
US-08-992-877-68
; Sequence 68, Application US/08992877
; Patent No. 6340461
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: SUPERANTIGEN USED METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF INFECTIOUS DISEASE
; FILE REFERENCE: superantigen
; CURRENT APPLICATION NUMBER: US/08/992,877
; CURRENT FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/044,074
; PRIOR FILING DATE: 1997-04-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 37
```

Query Match 48.7%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;

RESULT 23
US-08-858-623A-19
; Sequence 19, Application US/08858623A
; Patent No. 5910628
; GENERAL INFORMATION:
; APPLICANT: Miller, W.A., and Wang, S.
; TITLE OF INVENTION: Cap-Independent Translation Sequences
; TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America

```
;
;
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,623A
; FILING DATE: May 20, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,199
; FILING DATE: May 20, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: genomic RNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Tobacco Necrosis Virus Strain A
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; OTHER INFORMATION: GenBank Accession No. 5910628 X58455
; PUBLICATION INFORMATION:
; US-08-858-623A-19

Query Match 48.0%; Score 14.4; DB 2; Length 31;
Best Local Similarity 62.5%; Pred. No. 3.1e+03;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGACGACTTGTC 25
Db 8 CGGAUCCUGGAGAAACAGGCUUGAC 31

RESULT 24
US-08-858-623A-8
; Sequence 8, Application US/08858623A
; Patent No. 5910628
; GENERAL INFORMATION:
; APPLICANT: Miller, W.A., and Wang, S.
; TITLE OF INVENTION: Cap-Independent Translation Sequences
; TITLE OF INVENTION: Derived From Barley Yellow Dwarf Virus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,623A
; FILING DATE: May 20, 1997

;
;
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,623A
; FILING DATE: May 20, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,199
; FILING DATE: May 20, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: genomic RNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Tobacco Necrosis Virus Strain A
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; OTHER INFORMATION: GenBank Accession No. 5910628 X58455
; PUBLICATION INFORMATION:
; US-08-858-623A-19

Query Match 48.0%; Score 14.4; DB 2; Length 31;
Best Local Similarity 62.5%; Pred. No. 3.1e+03;
Matches 15; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGATCCAGGTAGGACGACTTGTC 25
Db 8 CGGAUCCUGGAGAAACAGGCUUGAC 31

RESULT 25
US-08-975-703-28/c
; Sequence 28, Application US/08975703
; Patent No. 6030832
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Bartel, Paul L.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Tavtigian, Sean V.
; TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,703
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2318-0174
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
US-08-975-703-28

Query Match

Best Local Similarity 48.0%; Score 14.4; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTCA 26
DB 36 GAATCCTGTTGGCAGAAATGGTCA 13

RESULT 26

US-09-515-884-28/c
Sequence 28, Application US/09515884
Patent No. 6235263
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
Bartel, Paul L.
Teng, David H.-P.
Tavtiglian, Sean V.

TITLE OF INVENTION: A Carboxy-Terminal BRCA1 Interacting Protein
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East Tower
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975,703

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.

REGISTRATION NUMBER: 38,609

REFERENCE/DOCKET NUMBER: 2318-0174

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-515-884-28

Query Match

48.0%; Score 14.4; DB 3; Length 40;

Best Local Similarity 75.0%; Pred. No. 3.2e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTTGTCA 26
DB 36 GAATCCTGTTGGCAGAAATGGTCA 13

RESULT 27

US-08-829-525-34/c
Sequence 34, Application US/08829525
Patent No. 6084083
GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,525

FILING DATE: 28-MAR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/609,583

FILING DATE: 01-MAR-1996

APPLICATION NUMBER: US 08/487,748

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/398,633

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-081

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-829-525-34

Query Match

48.0%; Score 14.4; DB 3; Length 44;

Best Local Similarity 75.0%; Pred. No. 3.3e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGAGCC 29
DB 40 TGCAGGTGTCAGACTTGGATCC 17

RESULT 28

US-08-609-583A-34/c

Sequence 34, Application US/08609583A

Patent No. 6204371

GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

```
;
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-609-583A-34

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 29
US-08-937-399-34/c
; Sequence 34, Application US/08937399
; Patent No. 6288218
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,399
; FILING DATE:
```

```
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-937-399-34

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 30
US-09-560-639-27/c
; Sequence 27, Application US/09560639
; Patent No. 6323334
; GENERAL INFORMATION:
; APPLICANT: Kingsbury, G.
; APPLICANT: Leiby, K.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 7853-158
; CURRENT APPLICATION NUMBER: US/09/560,639
; CURRENT FILING DATE: 2000-04-28
; EARLIER APPLICATION NUMBER: 60/155,862
; EARLIER FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3' oligonucleotide
; US-09-560-639-27

Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
Db 40 TGCAGGTGTCAGACTTGGGATCC 17

RESULT 31
US-09-310-367-34/c
; Sequence 34, Application US/09310367
; Patent No. 641417
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
```


;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036/2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/310,367
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/829,525
;; FILING DATE: 28-MAR-1997
;; APPLICATION NUMBER: US/08/609,583
;; FILING DATE: 01-MAR-1996
;; APPLICATION NUMBER: US/08/487,748
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US/08/398,633
;; FILING DATE: 03-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-081
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 44 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-09-310-367-34
Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
DB 40 TGCAGGTGTGCAGACTTGGGATCC 17
RESULT 32
US-09-032-337-34/c
; Sequence 34, Application US/09032337
; Patent No. 6455685
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032,337
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/609,583
;; FILING DATE: 01-MAR-1996
;; APPLICATION NUMBER: US/08/487,748
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US/08/398,633
;; FILING DATE: 03-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-790-9090
;; TELEFAX: 212-869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 44 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-09-032-337-34
Query Match 48.0%; Score 14.4; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 TCCAGGTAGGCAGACTTGTGACCC 29
DB 40 TGCAGGTGTGCAGACTTGGGATCC 17
RESULT 33
US-09-464-231-34/c
; Sequence 34, Application US/09464231
; Patent No. 6562343
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US/08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.

Query Match 47.3%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 3.8e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0

ov 4 GATCCAGGTAGGCAGACTTTGTACGCT 30

Db
4 GG TGG AGG TAG GTAA CTT GAC TGC AT 30

```

RESULT 37
US-08-936-632B-41
; Sequence 41, Application US/08936632B
; Patent No. 6159705
; GENERAL INFORMATION:
; APPLICANT: Truehart, Joshua
; APPLICANT: Paul, Jeremy I.
; APPLICANT: Fuernkranz, Hans
; APPLICANT: Nathans, Debra
; APPLICANT: Holmes, Scott
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: IDENTIFYING RECEPTOR EFFECTORS
; NUMBER OF SEQUENCES: 47

```

```

;
;
; NUMBER OF SEQUENCES: 47
; TYPE OF INVENTION: IDENTIFYING RECEIVER EFFECTORS
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

```

/ 02100
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/936,632B
/
/ FILING DATE: 24-SEP-1997
/

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/718,910
FILING DATE: 24 SEPTEMBER 1996
APPLICATION NUMBER: US 08/851,469
FILING DATE: 05 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: DeCONTI, GIULIO A., JR.

REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: CPI-031CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs

```

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
;

```

Query Match 47.3%; Score 14.2; DB 4; Length 47;
Best Local Similarity 76.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGACAGACTT 25
|||||:|||||
Db 30 ATCCAARTAGCCAAATTGTC 10

RESULT 40
US-09-209-668-22
; Sequence 22, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-209-668-22

Query Match 46.7%; Score 14; DB 3; Length 23;
Best Local Similarity 77.3%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGACACTT 22
|||||||
Db 2 GCGGATCCGCTACTCAGAGTT 23

Search completed: November 18, 2005, 11:21:57
Job time : 58.289 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 403.232 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-2

Perfect score: 30

Sequence: 1 GCGGATCCAGGTAGGACACTTGTTCAGCCT 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/1/pubpna/PT_NEW_PUB.seq:
3:	/cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/1/pubpna/PTUS_PUBCOMB.seq:
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
14:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
17:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
18:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
19:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
20:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
21:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
22:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
23:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
24:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
25:	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
26:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
27:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
28:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	8	US-08-469-172-2
2	30	100.0	30	20	US-10-788-779-2
3	18.4	61.3	25	26	US-11-036-317-64086
4	16.8	56.0	25	22	US-10-719-900-107278
5	16.8	56.0	25	26	US-11-036-317-28585

c	6	16.8	56.0	25	26	US-11-036-317-411291	Sequence 411291,
	7	16.8	56.0	25	26	US-11-036-317-635455	Sequence 635455,
	8	16.8	56.0	37	26	US-11-004-843-25	Sequence 25, Appl
	9	16.6	55.3	25	26	US-11-036-317-621574	Sequence 621574,
	10	16.6	55.3	25	26	US-11-036-317-772379	Sequence 772379,
	11	16.6	55.3	25	26	US-11-036-317-839968	Sequence 839968,
	12	16.2	54.0	25	22	US-10-719-900-160368	Sequence 160368,
	13	16.2	54.0	25	22	US-10-956-157-127072	Sequence 127072,
	14	16.2	54.0	25	24	US-10-719-956-427846	Sequence 427846,
	15	16	53.3	25	22	US-10-719-900-851373	Sequence 851373,
	16	16	53.3	25	22	US-10-719-900-906412	Sequence 906412,
	17	16	53.3	25	22	US-10-809-189-80578	Sequence 80578, A
	18	16	53.3	25	24	US-10-719-956-83060	Sequence 83060, A
	19	16	53.3	25	24	US-10-719-956-167727	Sequence 167727,
	20	15.8	52.7	25	22	US-10-719-900-190832	Sequence 190832,
	21	15.8	52.7	25	22	US-10-719-900-243203	Sequence 243203,
	22	15.8	52.7	25	26	US-11-036-317-475065	Sequence 475065,
	23	15.6	52.0	23	22	US-10-481-113-72	Sequence 72, Appl
	24	15.6	52.0	25	22	US-10-719-900-156288	Sequence 156288,
	25	15.6	52.0	25	24	US-10-719-956-172680	Sequence 172680,
	26	15.6	52.0	25	24	US-10-719-956-634810	Sequence 634810,
	27	15.6	52.0	25	26	US-11-036-317-50978	Sequence 50978, A
	28	15.6	52.0	25	26	US-11-036-317-588184	Sequence 588184,
	29	15.6	52.0	25	26	US-11-036-317-791168	Sequence 791168,
	30	15.6	52.0	25	26	US-11-060-756-254016	Sequence 254016,
	31	15.6	52.0	45	9	US-09-892-864A-25	Sequence 25, Appl
	32	15.6	52.0	45	9	US-09-996-561-26	Sequence 26, Appl
	33	15.6	52.0	45	9	US-09-884-948-26	Sequence 26, Appl
	34	15.6	52.0	45	9	US-09-892-864A-26	Sequence 26, Appl
	35	15.6	52.0	50	9	US-09-996-561-27	Sequence 27, Appl
	36	15.6	52.0	50	9	US-09-884-948-27	Sequence 27, Appl
	37	15.4	51.3	25	22	US-10-719-900-258355	Sequence 258355,
	38	15.4	51.3	25	24	US-10-719-956-303122	Sequence 303122,
	39	15.4	51.3	25	24	US-10-719-956-463637	Sequence 463637,
	40	15.4	51.3	25	24	US-10-719-956-606347	Sequence 606347,
	41	15.4	51.3	25	22	US-10-719-900-107277	Sequence 107277,
	42	15.2	50.7	25	22	US-10-719-900-539634	Sequence 539634,
	43	15.2	50.7	25	22	US-10-719-900-580775	Sequence 580775,
	44	15.2	50.7	25	22	US-10-719-900-217141	Sequence 217141,
	45	15.2	50.7	25	26	US-11-036-317-217141	Sequence 217141,

ALIGNMENTS

RESULT 1
US-08-469-172-2
; Sequence 2, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-2

Query Match      100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 2
US-10-788-779-2
; Sequence 2, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-10-788-779-2

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-10-788-779-2

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-788-779-2

Query Match      100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30
Db 1 GCGGATCCAGGTAGGCAGACTTGTTCAGCCT 30

RESULT 3
US-11-036-317-64086/c
; Sequence 64086, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64086
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-64086

Query Match      61.3%; Score 18.4; DB 26; Length 25;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTTCAGC 28
Db 21 AGGTAGGCAGACTTGTTCAGC 2

RESULT 4
US-10-719-900-107278
; Sequence 107278, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 107278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-107278

Query Match      56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACTT 22
Db 5 GGTTCATGTAGGCAGACTT 24
```

```
RESULT 5
US-11-036-317-28585
; Sequence 28585, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-28585

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GTAGGCAGACTTGTGCAGCCT 30
Db 1 GAAGGCAGCCTTGTGCAGCCT 20

RESULT 6
US-11-036-317-411291/c
; Sequence 411291, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-411291

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GTAGGCAGACTTGTGCAGCCT 30
Db 1 GAAGGCAGCCTTGTGCAGCCT 20

RESULT 7
US-11-036-317-635455
; Sequence 635455, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-635455

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTCT 24
Db 21 AGCCAGGTAGCCAGACTTCT 2

RESULT 8
US-11-004-843-25
; Sequence 25, Application US/11004843
; Publication No. US20050239173A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, INC.
; TITLE OF INVENTION: PRODUCTION OF AMINO SUGARS
; FILE REFERENCE: 023829/0393
; CURRENT APPLICATION NUMBER: US/11/004,843
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 11/004,843
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 60/527,309
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-004-843-25

Query Match          56.0%; Score 16.8; DB 26; Length 37;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTGCAGC 28
Db 2 GCGGATCCAGAATGTGCATACAGTCAGC 29

RESULT 9
US-11-036-317-621574
; Sequence 621574, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 621574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-621574

Query Match          55.3%; Score 16.6; DB 26; Length 25;
```

```
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-635455

Query Match          56.0%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GTAGGCAGACTTGTGCAGCCT 30
Db 1 GAAGGCAGCCTTGTGCAGCCT 20

RESULT 8
US-11-004-843-25
; Sequence 25, Application US/11004843
; Publication No. US20050239173A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, INC.
; TITLE OF INVENTION: PRODUCTION OF AMINO SUGARS
; FILE REFERENCE: 023829/0393
; CURRENT APPLICATION NUMBER: US/11/004,843
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 11/004,843
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 60/527,309
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 25
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-004-843-25

Query Match          56.0%; Score 16.8; DB 26; Length 37;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGTGCAGC 28
Db 2 GCGGATCCAGAATGTGCATACAGTCAGC 29

RESULT 9
US-11-036-317-621574
; Sequence 621574, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 621574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-621574

Query Match          55.3%; Score 16.6; DB 26; Length 25;
```

Best Local Similarity 82.6%; Pred. No. 2.7e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 4;

QY 6 TCCAGGTAGGCAGACTTGTGCAG 28
||||| | | | | | | | | |
Db 3 TCCAGGATGTCAGATTGTGCAG 25

RESULT 10

US-11-036-317-772379
; Sequence 772379, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 772379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-772379

Query Match 55.3%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.7e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 4;

QY 6 TCCAGGTAGGCAGACTTGTGCAG 28
||||| | | | | | | | | |
Db 1 TCCAGGATGTCAGATTGTGCAG 23

RESULT 11

US-11-036-317-839968
; Sequence 839968, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 839968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-839968

Query Match 55.3%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.7e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 4;

QY 6 TCCAGGTAGGCAGACTTGTGCAG 28
||||| | | | | | | | | |
Db 2 TCCAGGATGTCAGATTGTGCAG 24

RESULT 12

US-10-719-900-160368/c
; Sequence 160368, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 160368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-160368

Query Match 54.0%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 7 CCAGGTAGGCAGACTTGTGCAG 27
||||| | | | | | | | | |
Db 25 CCAGGGCTGCAGACTTGTGCAG 5

RESULT 13

US-10-956-157-127072/c
; Sequence 127072, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127072
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-127072

Query Match 54.0%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 2 CCGATCCAGGTAGGCAGACTT 22
||||| | | | | | | | | |
Db 24 CCGATCCAAATAGGCTGACTT 4

RESULT 14

US-10-719-956-427846
; Sequence 427846, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 427846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-427846


```
Query Match          54.0%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0; Indels 3;

QY 9 AGCTAGGCAGACTTGTGACCC 29
Db 3 AGCTGTGCAGACTTGTGACCC 23

RESULT 15
US-10-719-900-851373/c
; Sequence 851373, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 851373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-851373

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 3 GCATCCAGGTAGGCAGACTTGCA 26
Db 24 GGAACAGGAGTGCACACTTCTCA 1

RESULT 16
US-10-719-900-906412
; Sequence 906412, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 906412
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-906412

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCAGACTTGTGACGCT 30
Db 4 GCAGACTTGTGACGCT 19

RESULT 17
US-10-809-189-80578/c
; Sequence 80578, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
```

```
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-80578

Query Match          53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 1 GCGGATCCAGGTAGGCAGACTTGT 24
Db 24 GTGGATCCAGTCAGCCAGACGTGT 1

RESULT 18
US-10-719-956-83060
; Sequence 83060, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 83060
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-83060

Query Match          53.3%; Score 16; DB 24; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGACGCT 30
Db 2 CCAGGGATGCAGAAATTCAGTCT 25

RESULT 19
US-10-719-956-167727/c
; Sequence 167727, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 167727
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-167727

Query Match      53.3%; Score 16; DB 24; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGCAGCT 30
   ||||| ||| ||| ||| ||
Db 24 CCAGGTAGGCAGCTTAGTCAAACT 1

RESULT 20
US-10-719-900-190832
; Sequence 190832, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 190832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-190832

Query Match      52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATCCAGGTAGGCAGACT 21
   ||||| ||| ||| |||
Db 2 GGATCCAGGCAGCCAGACT 20

RESULT 21
US-10-719-900-243203/c
; Sequence 243203, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 243203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-243203

Query Match      52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 TAGGCAGACTTGTGCAGCT 30
   ||||| ||| ||| |||
Db 24 TAGACAGACTTGGCAGCT 6

RESULT 22
US-11-036-317-475065
; Sequence 475065, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 475065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-475065

Query Match      52.7%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGGATCCAGGTAGGCACA 19
   ||| ||||| ||||| ||
Db 3 GCGCATCCAGGTAGGCACA 21

RESULT 23
US-10-481-113-72/c
; Sequence 72, Application US/10481113
; Publication No. US20050032156A1
; GENERAL INFORMATION:
; APPLICANT: Sessions, Allen
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen P.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PHOSPHATE TRANSPORTER GENE
; FILE REFERENCE: Case 60145USPT
; CURRENT APPLICATION NUMBER: US/10/481,113
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/332,064
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/361,819
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/06968
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 72
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-481-113-72

Query Match      52.0%; Score 15.6; DB 22; Length 23;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTGCAGCC 29
   ||| ||||| ||||| |||
Db 23 CAATAGGCAGACTTGTGACC 2
```

```
RESULT 24
US-10-719-900-156289/c
; Sequence 156289, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 156288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-156288

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACGCT 30
||||| ||||| ||||| ||||| |||||
Db 24 AGGTGGGAGTCTCGTCAACCT 3

RESULT 25
US-10-719-956-172680/c
; Sequence 172680, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 172680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-172680

Query Match          52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGACGCT 30
||||| ||||| ||||| ||||| |||||
Db 24 AAGTGGGAGACTTGACACTCT 3

RESULT 26
US-10-719-956-634810/c
; Sequence 634810, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 634810
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-634810

Query Match          52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CAGGTAGGCAGACTTGTGACGC 29
||||| ||||| ||||| ||||| |||||
Db 23 CAGGTAAGAAGAGTTGTGAGCC 2

RESULT 27
US-11-036-317-90978
; Sequence 90978, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90978
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-90978

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGACG 28
||||| ||||| ||||| ||||| |||||
Db 1 CCAGGATGTCAGATTGTGACG 22

RESULT 28
US-11-036-317-588184
; Sequence 588184, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 588184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-588184

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCAGGTAGGCAGACTTGTGACG 28
||||| ||||| ||||| ||||| |||||
Db 1 CCAGGATGTCAGATTGTGACG 22
```

```
RESULT 29
US-11-036-317-791168
; Sequence 791168, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 791168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-791168

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  TCCAGGTAGGCAGACTTGTGCAG 27
          |||||  |||||  |||||  |||||
Db      4  TCCAGGTAGGCAGACTTGTGCAG 25

RESULT 30
US-11-036-317-791169
; Sequence 791169, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 791169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-791169

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  TCCAGGTAGGCAGACTTGTGCAG 27
          |||||  |||||  |||||  |||||
Db      4  TCCAGGTAGGCAGACTTGTGCAG 25

RESULT 31
US-11-060-756-254016/c
; Sequence 254016, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
```

```
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-254016

Query Match          52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      9  AGGTAGGCAGACTTGTGCAGCCT 30
          |||||  |||||  |||||  |||||
Db     24  AGGGAGGTAGACTCGTTAGCCT 3

RESULT 32
US-09-892-864A-25/c
; Sequence 25, Application US/09892864A
; Patent No. US20020090675A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ENO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-25

Query Match          52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5  ATCCAGGTAGGCAGACTTGTCA 26
          |||||  |||||  |||||  |||||
Db     42  ATCCAGGTAGGCAGACTTCA 21

RESULT 33
US-09-996-561-26/c
; Sequence 26, Application US/09996561
; Patent No. US20020151703A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/996,561
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/449,310
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
```

; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-996-561-26

Query Match 52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTC A 26
|||||
Db 42 ATCCAGGTAAGCAGATTCATCA 21

RESULT 34
US-09-884-948-26/c
; Sequence 26, Application US/09884948
; Patent No. US20020173021A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-26

Query Match 52.0%; Score 15.6; DB 9; Length 45;
Best Local Similarity 81.8%; Pred. No. 7.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTC A 26
|||||
Db 42 ATCCAGGTAAGCAGATTCATCA 21

RESULT 35
US-09-892-864A-26
; Sequence 26, Application US/09892864A
; Patent No. US20020090675A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, Keiichi
; APPLICANT: ONO, Kunio
; APPLICANT: EJIMA, Daisuke
; TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
; FILE REFERENCE: 209524USOCONT
; CURRENT APPLICATION NUMBER: US/09/892,864A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP99/07250
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: JP 10-373131
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic DNA
US-09-892-864A-26

Query Match 52.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTC A 26
|||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 36
US-09-996-561-27
; Sequence 27, Application US/09996561
; Patent No. US20020151703A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/996,561
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/448,310
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/109,063
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-996-561-27

Query Match 52.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTC A 26
|||||
Db 13 ATCCAGGTAAGCAGATTCATCA 34

RESULT 37
US-09-884-948-27
; Sequence 27, Application US/09884948
; Patent No. US20020173021A1
; GENERAL INFORMATION:
; APPLICANT: YOKOYAMA, KEIICHI
; APPLICANT: NAKAMURA, NAMI
; APPLICANT: MIWA, TETSUYA
; APPLICANT: SEGURO, KATSUYA
; TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
; FILE REFERENCE: 0010-0937-0
; CURRENT APPLICATION NUMBER: US/09/884,948
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/448,310
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-884-948-27

Query Match 52.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 7.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTCA 26
|||||
Db 13 ATCCAGGTAAGCAGACTTCATCA 34

RESULT 38

US-10-719-900-258355
; Sequence 258355, Application US/10719900
; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-258355

Query Match 51.3%; Score 15.4; DB 22; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ATCCAGGTAGGCAGACTTGTGACGC 29
|||||
Db 1 ATCCAGGACGGCAGAGTTTCTGCC 25

RESULT 39

US-10-719-956-303122
; Sequence 303122, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 303122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-303122

Query Match 51.3%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGC 25
|||||
Db 3 AGGAAGGCAGACTTGTGC 19

RESULT 40

US-10-719-956-463637/c
; Sequence 463637, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 463637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-463637

Query Match 51.3%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 9.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 AGGTAGGCAGACTTGTGC 25
|||||
Db 23 AGGAAGGCAGACTTGTGC 7

Search completed: November 18, 2005, 15:41:03
Job time : 404.232 secs

Result No.	Query No.	Score	Query %		Length	DB	ID	Description
			Match					
	1	24	100.0		24	6	IL2896	IL2896 Sequence 3
	2	16	66.7		40	10	F272557S01	AF272557 Rattus n
C	3	15.8	65.8		41	6	AX515479	AX515479 Sequence
C	4	15.8	65.8		41	6	AX521027	AX521027 Sequence
C	5	15	62.5		25	6	CQ864052	CQ864052 Sequence
C	6	14.8	61.7		47	6	AR284760	AR284760 Sequence
C	7	14.6	60.8		30	6	AX316342	AX316342 Sequence
C	8	14.6	60.8		30	6	AX431254	AX431254 Sequence
C	9	14.6	60.8		30	6	AF671506	AF671506 Sequence
	10	14.6	60.8		40	6	AX456311	AX456311 Sequence
	11	14.6	60.8		47	6	AR291259	AR291259 Sequence
	12	14.4	60.0		17	6	BD254805	BD254805 Regulation
	13	14.4	60.0		20	6	BD250383	BD250383 Enzyme. 7
	14	14.4	60.0		20	6	AX038772	AX038772 Sequence
	15	14.4	60.0		50	6	CQ003936	CQ003936 Sequence
C	16	14.4	60.0		50	6	CQ008720	CQ008720 Sequence
	17	14	58.3		24	6	A84037	A84037 Sequence 24
	18	14	58.3		24	6	BD072714	BD072714 Gene conv
C	19	14	58.3		25	6	AX651215	AX651215 Sequence

```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 40)
Choudhuri,S., Ogura,K. and Klaassen,C.D.
Cloning of the full-length coding sequence of rat liver-specific
organic anion transporter-1 (rlst-1) and a splice variant and
partial characterization of the rat lst-1 gene
Biochem. Biophys. Res. Commun. 274 (1), 79-86 (2000)
20365831
MEDLINE
10903899
PUBMED
REFERENCE
2 (bases 1 to 40)
Choudhuri,S., Ogura,K. and Klaassen,C.D.
Direct Submission
TITLE
JOURNAL
Submitted (26-MAY-2000) Pharmacology, University of Kansas Medical
Center, 3901 Rainbow Blvd., Kansas City, KS 66160, USA
3 (bases 1 to 40)
Choudhuri,S., Ogura,K. and Klaassen,C.D.
Direct Submission
TITLE
JOURNAL
Submitted (15-FEB-2001) Pharmacology, University of Kansas Medical
Center, 3901 Rainbow Blvd., Kansas City, KS 66160, USA
REMARK
Sequence update by submitter
COMMENT
On Feb 15, 2001 this sequence version replaced gi:9624341.
FEATURES
source
1..40
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1..40
/gene="rlst-1"
/number=1
exon
ORIGIN
Query Match 66.7%; Score 16; DB 10; Length 40;
Best Local Similarity 79.2%; Pred. No. 5.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGCCACCTGCTCTGGAGGCCT 24
||||| | | | | | | | | |
Db 9 ATGCCACCTGCTCTAGAGCCT 32
||||| | | | | | | | | |
RESULT 3
AX515479/c
LOCUS
AX515479 41 bp DNA linear PAT 05-OCT-2002
DEFINITION
Sequence 1677 from Patent WO02052044.
ACCESSION
AX515479
VERSION
AX515479.1 GI:23562599
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
Detection of genetic polymorphisms
TITLE
JOURNAL
Patent: WO 02052044-A 1677 04-JUL-2002;
Riken (JP)
FEATURES
source
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 41;
Best Local Similarity 81.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CCAACCTGCTCTGGAGGCCT 24
||||| | | | | | | | | |
Db 25 CCAAYCCTACTCTGTGGGCCT 5
||||| | | | | | | | | |

```

```

RESULT 4
AX521027/c
LOCUS
AX521027 41 bp DNA linear PAT 05-OCT-2002
DEFINITION
Sequence 7225 from Patent WO02052044.
ACCESSION
AX521027
VERSION
AX521027.1 GI:23571753
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
Detection of genetic polymorphisms
TITLE
JOURNAL
Patent: WO 02052044-A 7225 04-JUL-2002;
Riken (JP)
FEATURES
source
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 41;
Best Local Similarity 81.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CCAACCTGCTCTGGAGGCCT 24
||||| | | | | | | | | |
Db 25 CCAAYCCTACTCTGTGGGCCT 5
||||| | | | | | | | | |
RESULT 5
CQ864052/c
LOCUS
CQ864052 25 bp DNA linear PAT 10-SEP-2004
DEFINITION
Sequence 2685 from Patent WO2004072265.
ACCESSION
CQ864052
VERSION
CQ864052.1 GI:51985041
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Burczynski,M., Twine,N., Dorner,A.J. and Trepicchio,W.L.
METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /1
TITLE
JOURNAL
Patent: WO 2004072265-A 2685 26-AUG-2004;
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 62.5%; Score 15; DB 6; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TGCCACCTGCTCTGGAGGCCT 24
||||| | | | | | | | | |
Db 25 TGTCCACCTGCTCTGGGTACCT 3
||||| | | | | | | | | |
RESULT 6
AR284760
LOCUS
AR284760 47 bp DNA linear PAT 10-APR-2003
DEFINITION
Sequence 812 from patent US 6528260.
ACCESSION
AR284760
VERSION
AR284760.1 GI:29721664
KEYWORDS

```


SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.
TITLE Biallelic markers related to genes involved in drug metabolism
JOURNAL Patent: US 6528260-A 812 04-MAR-2003;
FEATURES Location/Qualifiers
1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 61.7%; Score 14.8; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCCAACCTCTCTGGAG 20
Db 8 ATGCCAAGCTGATCTRGAG 27

RESULT 7
AX316342/c
LOCUS AX316342 30 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 30 from Patent WO0190188.
ACCESSION AX316342
VERSION AX316342.1 GI:17899515
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Eyckerman, S., van Ostade, X., Vandekerckhove, J., Verhee, A. and Tavernier, J.
TITLE Receptor-based interaction trap
JOURNAL Patent: WO 0190188-A 30 29-NOV-2001;
FEATURES Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="reverse primer: MBU-O-678; mCIS primer"

ORIGIN

Query Match 60.8%; Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCCCAACCTCTCTGGAGC 22
Db 21 TTCCAACTCTGATCTAGGC 1

RESULT 8
AX431254/c
LOCUS AX431254 30 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 18 from Patent WO0240543.
ACCESSION AX431254
VERSION AX431254.1 GI:21656136
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Tavernier, J., Eyckerman, S. and Zabeau, L.
TITLE Functional fragment of the lectine receptor
JOURNAL Patent: WO 0240543-A 18 23-MAY-2002;
FEATURES Location/Qualifiers
1..30
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer for murine CIS amplification"

ORIGIN

Query Match 60.8%; Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCCCAACCTCTCTGGAGC 22
Db 21 TTCCAACTCTGATCTAGGC 1

RESULT 9
AX671506/c
LOCUS AX671506 30 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 18 from Patent WO03004643.
ACCESSION AX671506
VERSION AX671506.1 GI:29329856
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Eyckerman, S., Tavernier, J. and Vandekerckhove, J.
TITLE Reversed mammalian protein-protein interaction trap
JOURNAL Patent: WO 03004643-A 18 16-JAN-2003;
FEATURES Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer; MBU-O-678; mCIS primer"

ORIGIN

Query Match 60.8%; Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCCCAACCTCTCTGGAGC 22
Db 21 TTCCAACTCTGATCTAGGC 1

RESULT 10
AX456311
LOCUS AX456311 40 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 169 from Patent WO0216944.
ACCESSION AX456311
VERSION AX456311.1 GI:21715225
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wood, K.V., Wood, M.G., Zhuang, Y. and Paguio, A.
TITLE Synthetic nucleic acid molecule compositions and methods of preparation
JOURNAL Patent: WO 0216944-A 169 28-FEB-2002;
FEATURES Location/Qualifiers
1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="An oligonucleotide"

ORIGIN

Query Match 60.8%; Score 14.6; DB 6; Length 40;
Best Local Similarity 81.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	3	GCCAACCTGCTCTGGAGGCC	23
Dn	16	GGCATTCTGTATCTGGAGGCC	36
RESULT 11			
LOCUS	AR291259	47 bp	DNA
DEFINITION	Sequence 2994 from patent US 6537751.		linear
ACCESSION	AR291259		
VERSION	AR291259.1	GI:31678543	
KEYWORDS	Unknown.		
SOURCE	ORGANISM	Unknown.	
REFERENCE	1	(bases 1 to 47)	
AUTHORS	Cohen,D., Chumakov,I. and Blumenfeld,M.		
TITLE	Biallelic markers for use in constructing a high density		
JOURNAL	disequilibrium map of the human genome		
FEATURES	Patent: US 6537751-A 2994 25-MAR-2003;		
source	Location/Qualifiers		
	1..47		
	/organism="unknown"		
ORIGIN	/mol_type="genomic DNA"		
Query Match	60.8%;	Score 14.6;	DB 6;
Best Local Similarity	73.9%;	Pred.No. 2.7e+04;	
Matches	17; Conservative	1; Mismatches	5; Indels 0; Gaps 0;
Qy	1	ATGCCAACCCTGCTCTGGAGGCC	23
Dn	11	ATGCCAAGGCTGCYCTTGATCCC	33
RESULT 12			
LOCUS	BD254805	17 bp	DNA
DEFINITION	Regulation of repressor genes using nucleic acid molecules.		linear
ACCESSION	BD254805		
VERSION	BD254805.1	GI:33064575	
KEYWORDS	JP 2002541795-A/2598.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.		
TITLE	Regulation of repressor genes using nucleic acid molecules		
JOURNAL	Patent: JP 2002541795-A 2598 10-DEC-2002;		
COMMENT	RIBOZYME PHARMACEUTICALS INC		
	OS Eukaryote		
	PN JP 2002541795-A/2598		
	PD 10-DEC-2002		
	PF 11-APR-2000 JP 2000611654		
	PR 12-APR-1999 US 60/129390		
	PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC		
	C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC		
	C12P21/02,		
	PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC		
	C12R1:91),		
	PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,		
	PC A61K37/02,		
	PC (C12N5/00,C12R1:91)		
	CC Regulation of repressor genes using nucleic acid molecules FH		
	Key Location/Qualifiers		
	FT source		
	1..17		
	/organism='Eukaryote'.		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="unidentified"		
	/mol_type="genomic DNA"		

source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 5 ACCCTGCTCTGGAGG 20

RESULT 15
LOCUS CQ003936 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 2576 from Patent WO0147944.
ACCESSION CQ003936
VERSION CQ003936.1 GI:41010568
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 2576 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26"
Accession number c943985274"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 50;
Best Local Similarity 93.8%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCACCCCTGCTCTG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 22 TGCCAGCCCTGCTCTG 37

RESULT 16
LOCUS CQ008720/c 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 7360 from Patent WO0147944.
ACCESSION CQ008720
VERSION CQ008720.1 GI:41015434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 7360 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"

misc_feature 25..26
/db_xref="taxon:9606"
/note="Nucleotide deleted between bases 25 and 26"
Accession number c943966585"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 3.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 39 ATGCTGACCTTGGCGCTGGAGGCTT 16

RESULT 17
LOCUS A84037 24 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 24 from Patent WO9846772.
ACCESSION A84037
VERSION A84037.1 GI:6733178
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Bovenberg, R.A. and Seltens, G.C.
TITLE GENE CONVERSION AS A TOOL FOR THE CONSTRUCTION OF RECOMBINANT
INDUSTRIAL FILAMENTOUS FUNGI
JOURNAL Patent: WO 9846772-A 24 22-OCT-1998;
BOVENBERG ROELOF ARY LANS (NL); GIST BROCADES BV (NL)
FEATURES
source
1..24
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 58.3%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GCCAACCCCTGCTCTGGAGGCCT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCCTACTCTGTTCTGGAGAGCT 22

RESULT 18
LOCUS BD072714 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Gene conversion as a tool for the construction of recombinant industrial organisms.
ACCESSION BD072714
VERSION BD072714.1 GI:22618317
KEYWORDS JP 2001518798-A/24.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 24)
AUTHORS Seltens, G.C.M., Swinkels, B.W. and Bovenberg, R.A.L.
TITLE Gene conversion as a tool for the construction of recombinant industrial organisms
JOURNAL Patent: JP 2001518798-A 24 16-OCT-2001;
DSM NV
COMMENT OS Unidentified
PN JP 2001518798-A/24
PD 16-OCT-2001
PF 09-APR-1998 JP 1998543456
PR 11-APR-1997 EP 97201091.2
PI GERARDUS CORNELIS MARIA SELTEN, BART WILLEM SWINKELS, PI
ROELOF ARY LANS BOVENBERG
PC C12N15/80, C12N15/65, C12N15/52, C12N1/15
CC Strandedness: Single;

```

CC Topology: Linear;
CC /desc = 'oligonucleotide';
FH Key Location/Qualifiers
FT source 1..24
   Location/Qualifiers
   1..24
   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCCAACCCCTGCTCGGAGGCT 24
   ||| ||| ||| ||| ||| ||| |||
Db 1 GCCTACTCTGTTCTGGAGAGCT 22

RESULT 19
AX651215/c
LOCUS AX651215 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3055 from Patent EP1273660.
ACCESSION AX651215
VERSION AX651215.1 GI:29154033
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 3055 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCGGAGGC 22
   ||| ||| ||| ||| ||| ||| |||
Db 25 ACGCAACTCTGATCTGAAGCC 4

RESULT 20
AX651216/c
LOCUS AX651216 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3056 from Patent EP1273660.
ACCESSION AX651216
VERSION AX651216.1 GI:29154034
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 3056 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCGGAGGC 22
   ||| ||| ||| ||| ||| ||| |||
Db 25 ACGCAACTCTGATCTGAAGCC 4

RESULT 21
CQ840251/c
LOCUS CQ840251 36 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 18 from Patent WO2004056863.
ACCESSION CQ840251
VERSION CQ840251.1 GI:50838027
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fagan,R.J., Phelps,C.B., Rodrigues,T.M., Power,C. and de Tiani,M.
TITLE Splice variant of human placental growth hormone
JOURNAL Patent: WO 2004056863-A 18 08-JUL-2004;
ARES TRADING S.A. (CH)
FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 36;
Best Local Similarity 77.3%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCGGAGGC 22
   ||| ||| ||| ||| ||| ||| |||
Db 34 ATCCAAACGCTGATGTGGAGGC 13

RESULT 22
CQ857597
LOCUS CQ857597 40 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 7 from Patent WO2004070060.
ACCESSION CQ857597
VERSION CQ857597.1 GI:51951747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cimadevilla,J.C. and Villahermosa,J.M.
TITLE Nucleic acid probes for the detection of small exons and methods of
designing the same
JOURNAL Patent: WO 2004070060-A 7 19-AUG-2004;
GENOMICA S.A.U. (ES)
FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCGGAGGC 22
   ||| ||| ||| ||| ||| ||| |||
Db 34 ATCCAAACGCTGATGTGGAGGC 13

RESULT 23
CQ857597
LOCUS CQ857597 40 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 7 from Patent WO2004070060.
ACCESSION CQ857597
VERSION CQ857597.1 GI:51951747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cimadevilla,J.C. and Villahermosa,J.M.
TITLE Nucleic acid probes for the detection of small exons and methods of
designing the same
JOURNAL Patent: WO 2004070060-A 7 19-AUG-2004;
GENOMICA S.A.U. (ES)
FEATURES
source
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCGGAGGC 22
   ||| ||| ||| ||| ||| ||| |||
Db 34 ATCCAAACGCTGATGTGGAGGC 13

```

[illegible]

LOCUS BD170870 34 bp DNA linear PAT 17-JAN-2003
 DEFINITION Human apoptosis-associated gene and human apoptosis-associated protein produced by the gene.
 ACCESSION BD170870
 VERSION BD170870.1 GI:27876682
 KEYWORDS WO 02057444-A/25.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 34)
 AUTHORS Kondo,S. and Akiyama,N.
 TITLE Human apoptosis-associated gene and human apoptosis-associated protein produced by the gene
 JOURNAL SHINAE KONDO,NOBUTAKE AKIYAMA
 COMMENT PATENT: WO 02057444-A 25 25-JUL-2002;
 OS Artificial Sequence
 PN WO 02057444-A/25
 PD 25-JUL-2002
 PF 22-JAN-2002 WO 2002JP000413
 PR 22-JAN-2001 JP 01P 013217,11-MAY-2001 JP 01P 141490 PI
 SHINAE KONDO,NOBUTAKE AKIYAMA
 PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,A61K38/00,A61K48/00, PC A61P35/00,A61P43/00,G01N33/15,G01N33/50/C12P21/08 CC
 Description of Artificial Sequence: Synthesized CC
 oligonucleotide
 FH Key Location/Qualifiers
 FT source 1..34
 FT /organism='Artificial Sequence'.
 FEATURES source
 1..34
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 ORIGIN
 Query Match 56.7%; Score 13.6; DB 6; Length 34;
 Best Local Similarity 80.0%; Pred. No. 8.9e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 CCAACCTGCTCTGGAGGCC 23
 Db 32 CCAGCCCTGGTGGAGGCC 13
 RESULT 33
 LOCUS BD095049 36 bp DNA linear PAT 27-AUG-2002
 DEFINITION Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it.
 ACCESSION BD095049
 VERSION BD095049.1 GI:22640637
 KEYWORDS JP 2001352977-A/2.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Watarai,H. and Yamaguchi,Y.
 TITLE Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it
 JOURNAL Patent: JP 2001352977-A 2 25-DEC-2001;
 KRIN BREWERY CO LTD
 COMMENT OS Artificial Sequence
 PN JP 2001352977-A/2
 PD 25-DEC-2001
 PF 12-JUN-2000 JP 2000176187
 PI HIROSHI WATARAI,YASUNORI YAMAGUCHI
 PC C12N15/02,C07K16/18,C12N15/09,C12P21/08,C12Q1/02,G01N33/53, PC G01N33/53,
 CC Description of Artificial Sequence: a sense primer specific for 5'-leader
 CC sequence of Siglec-9 gene

LOCUS BD172240 50 bp DNA linear PAT 18-FEB-2003
 DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.
 ACCESSION BD172240
 VERSION BD172240.1 GI:28413538
 KEYWORDS JP 200223786-A/13.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: JP 200223786-A 13 13-AUG-2002;
 GENENTECH INC
 COMMENT OS Artificial Sequence
 PN JP 200223786-A/13
 PD 13-AUG-2002
 PF 18-DEC-2001 JP 2001385135
 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR
 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR
 27-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR
 28-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR
 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
 29-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR
 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR
 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR
 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR
 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR
 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR
 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
 WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JUAN ZHENG,
 PI JEAN YUAN
 PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10,
 CC Description of Artificial Sequence: a sense primer specific for 5'-leader
 CC sequence of Siglec-9 gene

```
(C12P21/02,C12R1:645),C12N15/00,C12N5/00
CC Description of Artificial Sequence: Synthetic FH Key
FT Location/Qualifiers
FT source 1..50
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3
RESULT 35
BD172559/c
LOCUS BD172559 50 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION BD172559
VERSION BD172559.1 GI:28413861
KEYWORDS JP 2002238586-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
PATENT: JP 2002238586-A 13 27-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002238586-A/13
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR
28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/066120,21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
C12N5/10,
```

```
PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),
PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC
(C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,C12N5/00, PC
(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic FH Key
FT Location/Qualifiers
FT source 1..50
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3
RESULT 36
BD172878/c
LOCUS BD172878 50 bp DNA linear PAT 18-FEB-2003
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION BD172878
VERSION BD172878.1 GI:28414184
KEYWORDS JP 2002238587-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
PATENT: JP 2002238587-A 13 27-AUG-2002;
COMMENT OS Artificial Sequence
PN JP 2002238587-A/13
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR
18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR
28-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR
29-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/066120,21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
```


JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC
C12P21/02, C12P21/08, C12P21/02, C12R1/91, (C12P21/02, C12R1:19), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00, C12N15/00 CC
Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers
FT source 1.50
/organism='Artificial Sequence'.
FT Location/Qualifiers
1.50
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGCCAACCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGGAG 3

RESULT 37
BD173197/c
LOCUS
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.
ACCESSION BD173197
VERSION BD173197.1 GI:28414506
KEYWORDS JP 2002238588-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL
COMMENT Patent: JP 2002238588-A 13 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238588-A/13
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063127 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
27-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063435 PR
31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
07-NOV-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers
FT source 1.50
/organism='Artificial Sequence'.
FT Location/Qualifiers
1.50
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGCCAACCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGGAG 3

RESULT 38
BD175231/c
LOCUS
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.
ACCESSION BD175231
VERSION BD175231.1 GI:29120927
KEYWORDS JP 2002253280-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL
COMMENT Patent: JP 2002253280-A 13 10-SEP-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002253280-A/13
PD 10-SEP-2002
PF 18-DEC-2001 JP 2001385319
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063127 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
27-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063435 PR
31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
07-NOV-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770;24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453;25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN

PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
A61P25/00,
PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,
PC C07K19/00,
PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,
PC A61P43/00,
PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,
PC C12R1:91),
PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC
Description of Artificial Sequence: Synthetic FH Key

Location/Qualifiers
FT source 1..50
/organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20

Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 39
LOCUS AR410609/c
DEFINITION AR410609
Sequence 16 from patent US 6635468.
ACCESSION AR410609
VERSION AR410609.1 GI:40162109

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
Unclassified.
AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 16 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20

Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 40
LOCUS AR438973/c
DEFINITION AR438973
Sequence 16 from patent US 6664376.
ACCESSION AR438973

VERSION AR438973.1 GI:42664822

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
Unclassified.

AUTHORS Ashkenazi,A., Botstein,D., Desnovers,L., Eaton,D.L., Ferrara,N.,
Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J.,
Kljavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: US 6664376-A 16 16-DEC-2003;

FEATURES Location/Qualifiers
source 1..50
/organism="unknown"

ORIGIN /mol_type="genomic DNA"

Query Match 56.7%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20

Db 22 ATGCCACAGCTGCTGTGGAG 3

Search completed: November 18, 2005, 17:42:51
Job time : 667.986 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTCTCTGGAGGCCT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	2	AAQ91123
2	24	100.0	24	9	ACA63113
3	24	100.0	24	13	ADR05299
4	16.8	70.0	50	12	ADP10021
5	16.2	67.5	41	6	AB250443
6	16.2	67.5	41	6	AB244893
7	15.6	65.0	45	12	ADM97503
8	15.6	65.0	45	12	ADM97521
9	15.6	65.0	45	12	ADM97483
10	15	62.5	25	13	ADR55334
11	14.6	60.8	30	6	ABL60842
12	14.6	60.8	30	6	ABL16712
13	14.6	60.8	30	8	ABL52021
14	14.6	60.8	40	6	ABL99201
15	14.4	60.0	17	3	AAF02607
16	14.4	60.0	20	3	AAc62092
17	14.4	60.0	50	4	AAI29368
18	14.4	60.0	50	4	AAI34152
19	14.2	59.2	20	12	ADG86318
20	14.2	59.2	20	12	ADG86349

C 21	14.2	59.2	25	12	ADP17501
22	14	58.3	24	2	AAV68288
C 23	14	58.3	25	10	ADC06568
C 24	14	58.3	25	10	ADC08569
C 25	14	58.3	35	2	AAQ70259
C 26	14	58.3	36	12	ADP71324
27	14	58.3	40	13	ADQ99501
28	14	58.3	40	13	ADQ99500
29	14	58.3	42	6	AB249539
30	14	58.3	42	6	AB245912
C 31	13.8	57.5	20	9	ACH66436
32	13.8	57.5	20	10	ABZ84928
33	13.8	57.5	20	11	ABD21158
34	13.8	57.5	20	12	ADO31281
C 35	13.8	57.5	25	2	AAx05223
36	13.8	57.5	33	6	ABs55668
C 37	13.8	57.5	41	6	ABK11966
C 38	13.8	57.5	41	6	ABK11967
39	13.8	57.5	50	4	AAI73671
C 40	13.6	56.7	20	12	ADP22838
41	13.6	56.7	20	12	ADP22760
42	13.6	56.7	22	2	AAI35560
43	13.6	56.7	22	3	AAA39224
C 44	13.6	56.7	22	6	ABK88718
45	13.6	56.7	24	2	AAV82832

ALIGNMENTS

RESULT 1

AAQ91123

ID AAQ91123 standard; cDNA; 24 BP.

XX

AC AAQ91123;

XX

DT 19-FEB-1996 (first entry)

XX

DE Beta-cardiac myosin heavy chain PCR primer A'.

XX

MY Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

KW diagnosis; primer; mutation; detection; ss.

OS Synthetic.

XX

XX

PN USS429923-A.

XX

XX

PD 04-JUL-1995.

XX

PF 11-DEC-1992; 92US-00989160.

XX

PR 11-DEC-1992; 92US-00989160.

XX

PA (HARD) HARVARD COLLEGE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX

PI Ab250443 Human cyt

XX

PI Ab250443 Human cyt

XX

DR Adm97503 CD1d-IgG-

XX

DR Adm97521 CD1d-IgG-

XX

PT Adm97483 CD1d-IgG-

XX

PT Adm97483 Drug ther

XX

XX ABL60842 Murine CI

XX

PS ABL16712 CIS prime

XX

XX AAL52021 Recombina

XX

CC ABL99201 Green/red

CC

CC AAF02607 Hammerhea

CC

CC AAc62092 Reverse p

CC

CC AAI29368 Human SNP

CC

CC AAI34152 Human SNP

CC

CC ADG86318 Human SMR

CC

CC ADG86349 Human SMR

CC

AAQ91121-091130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 XX
 SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 Db 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 RESULT 2
 ACA63113
 ID ACA63113 standard; DNA; 24 BP.
 XX AC
 XX ACA63113;
 XX
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain PCR primer A'.
 XX
 KW Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 KW phenylketonuria; cystic fibrosis.
 XX
 OS Homo sapiens.
 XX
 XX US2003054343-A1.
 XX
 XX 20-MAR-2003.
 XX
 XX
 PF 06-JUN-1995; 95US-00469172.
 XX
 PR 11-DEC-1992; 92US-00989160.
 XX
 XX (SEID/) SEIDMAN C.
 PA (SEID/) SEIDMAN J.
 PA (WATK/) WATKINS H.
 PA (ROSE/) ROSENZWEIG A.
 XX
 XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX WPI; 2003-512374/48.
 XX
 DR
 XX
 PT Detecting a presence or absence of a mutation associated with
 PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 PT hemophilia, by detecting a mutation in an amplified product of a beta
 PT cardiac myosin heavy-chain DNA.
 XX
 XX Example 1; Page 5; 22pp; English.
 XX
 PS The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation
 XX
 SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 9; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 Db 1 ATGCCAACCCCTGCTCTGGAGGCCT 24
 RESULT 3
 ADR05299
 ID ADR05299 standard; DNA; 24 BP.
 XX AC
 XX ADR05299;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human beta cardiac myosin heavy chain mutation detection primer A'.
 XX
 KW Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 KW familial hypertrophic cardiomyopathy;
 KW sporadic hypertrophic cardiomyopathy.
 XX
 OS Homo sapiens.
 XX
 XX US2004152121-A1.
 XX
 XX 05-AUG-2004.
 XX
 XX 27-FEB-2004; 2004US-00788779.
 XX
 XX 11-DEC-1992; 92US-00989160.
 PR 06-JUN-1995; 95US-00469172.
 XX
 XX (SEID/) SEIDMAN C.
 PA (SEID/) SEIDMAN J.
 PA (WATK/) WATKINS H.
 PA (ROSE/) ROSENZWEIG A.
 XX
 XX Seidman C, Seidman J, Watkins H, Rosenzweig A;
 XX WPI; 2004-592586/57.
 XX
 DR
 XX
 PT Detecting mutations associated with hypertrophic cardiomyopathy to
 PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 PT myosin heavy-chain DNA and detecting the mutation in the amplified
 PT product.
 XX
 XX Claim 18; SEQ ID NO 3; 22pp; English.
 XX
 PS The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.
SQ . Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCAACCTGCTCTGGAGGCT 24
DB 1 ATGCCAACCTGCTCTGGAGGCT 24

RESULT 4
ADP10021/c
ID ADP10021 standard; DNA; 50 BP.
XX
AC ADP10021;
XX
DT 12-AUG-2004 (first entry)
XX
DE 50-mer oligonucleotide marker probe of the invention #30.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
FN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
WPI; 2004-400724/37.
XX
DR Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX

PS Claim 2; SEQ ID NO 30; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC 50 mer oligonucleotide marker for diagnosis and monitoring of allograft
CC rejection and other disorders.
XX
SQ Sequence 50 BP; 9 A; 13 C; 18 G; 10 T; 0 U; 0 Other;
Query Match 70.0%; Score 16.8; DB 12; Length 50;
Best Local Similarity 90.0%; Pred. No. 9.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCAACCCCTGCTCTGGAGGCC 23
DB 37 CCACCCCTCTCTGGAGGCC 18
RESULT 5
ABZ50443/c
ID ABZ50443 standard; DNA; 41 BP.
XX
AC ABZ50443;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human cytochrome P450 CYP4F3 gene polymorphic site, #7225.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-JP011592.
XX
PR 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00258662.
XX
PA (RIKE) RIKEN KK.
XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX
WPI; 2002-583571/62.
XX
DR Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
PS Claim 23; Page 213; 2785pp; English.
XX

CC Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

SQ Sequence 41 BP; 12 A; 6 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 41;
 Best Local Similarity 85.7%; Pred. No. 1.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCCT 24

DB 25 CCAACCTACTCTGTGGCCT 5

RESULT 6

ID AB244893/C

AC AB244893 standard; DNA; 41 BP.

XX DT 26-JUN-2003 (first entry)

XX DE Human cytochrome P450 CYP4F3 gene polymorphic site, #1677.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;

KW polymorphic site; drug evaluation; drug screening; genotyping;

KW genetic profiling; therapeutic customisation; adverse reaction;

KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT variation replace(21,A)

FT /*tag= a

FT /standard_name= "Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.

XX PD 04-JUL-2002.

XX PF 27-DEC-2001; 2001WO-P011592.

XX

PR 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.

XX PI Nakamura Y, Sekine A, Iida A, Saito S;

XX DR WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the
 XX effectiveness or side effect of a drug or treatment protocol, comprises
 XX detecting at least one polymorphism in the drug metabolizing enzyme
 XX nucleic acid.

XX Claim 23; Page 92; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

SQ Sequence 41 BP; 12 A; 6 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 41;

Best Local Similarity 85.7%; Pred. No. 1.8e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCCT 24

DB 25 CCAACCTACTCTGTGGCCT 5

RESULT 7

ID ADM97503/C

XX ID ADM97503 standard; DNA; 45 BP.

XX AC ADM97503;

XX DT 01-JUL-2004 (first entry)

XX DE CDId-IgG-B2M complex F(ab'2) fragment PCR primer SEQ ID NO: 26.

XX KW CDId complex; cytostatic; antiinflammatory; cancer; autoimmune disease;

KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

XX Unidentified.

XX WO2004029206-A2.

XX 08-APR-2004.

XX 26-SEP-2003; 2003WO-US030238.

XX 27-SEP-2002; 2002EP-00405838.

XX (VACC-) VACCINEX INC.

PA (ROBE/) ROBERT B.

PA (DOND/) DONDA A.

PA (CESS/) CESSON V.

PA (MACH/) MACH J.

PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;

XX WPI; 2004-316095/29.

XX New compound comprising CD1d complexes and an antibody specific for a
 PT cell surface marker, useful for preventing or treating tumors and
 PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
 PT diabetes or psoriasis.

XX Example 10; Page 85; 152pp; English.

XX The present invention relates to a compound comprising one or more CD1d
 CC complexes and an antibody or its fragment specific for a cell surface
 CC marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
 CC molecule, and are linked to the antibody or its fragment. The composition
 CC and methods are useful for preventing or treating tumors and
 CC autoimmune/inflammatory or infectious diseases, such as multiple
 CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
 CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
 CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
 CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
 CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
 CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
 CC sequence is a PCR primer used in the exemplification of the invention.

XX Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 12; Length 45;

Best Local Similarity 81.8%; Pred. No. 3.3e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCGAGGC 22

Db 40 ATGCCAACCCGTCGCCAGGAGGC 19

RESULT 8

ADM97521/c

ID ADM97521 standard; DNA; 45 BP.

XX ADM97521;

XX 01-JUL-2004 (first entry)

XX CD1d-IgG complex F(ab'2) fragment PCR primer SEQ ID NO: 44.

XX CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
 KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

OS Unidentified.

XX WO2004029206-A2.

XX 08-APR-2004.

XX 26-SEP-2003; 2003WO-US030238.

XX 27-SEP-2002; 2002EP-00405838.

XX (VACC-) VACCINEX INC.

PA (ROBE/) ROBERT B.

PA (DOND/) DONDA A.

PA (CESS/) CESSON V.

PA (MACH/) MACH J.

PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;

XX WPI; 2004-316095/29.

XX New compound comprising CD1d complexes and an antibody specific for a
 PT cell surface marker, useful for preventing or treating tumors and
 PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
 PT diabetes or psoriasis.

XX Example 15; Page 95; 152pp; English.

XX The present invention relates to a compound comprising one or more CD1d
 CC complexes and an antibody or its fragment specific for a cell surface
 CC marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
 CC molecule, and are linked to the antibody or its fragment. The composition
 CC and methods are useful for preventing or treating tumors and
 CC autoimmune/inflammatory or infectious diseases, such as multiple
 CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
 CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
 CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
 CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
 CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
 CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
 CC sequence is a PCR primer used in the exemplification of the invention.

XX Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 12; Length 45;

Best Local Similarity 81.8%; Pred. No. 3.3e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCGAGGC 22

Db 40 ATGCCAACCCGTCGCCAGGAGGC 19

RESULT 9

ADM97483/c

ID ADM97483 standard; DNA; 45 BP.

XX ADM97483;

XX 01-JUL-2004 (first entry)

XX CD1d-IgG-avidin complex F(ab'2) fragment PCR primer SEQ ID NO: 6.

XX CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
 KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
 KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
 KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
 KW beta2-microglobulin; ss; primer; PCR.

OS Unidentified.

XX WO2004029206-A2.

XX 08-APR-2004.

```

XX PF 26-SEP-2003; 2003WO-US030238.
XX PR 27-SEP-2002; 2002EP-00405838.
XX PA (VACC-) VACCINEX INC.
XX PA (ROBE/) ROBERT B.
XX PA (DOND/) DONDA A.
XX PA (CESS/) CESSON V.
XX PA (MACH/) MACH J.
XX
XX PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;
XX WPI; 2004-316095/29.
XX
XX New compound comprising CD1d complexes and an antibody specific for a
XX cell surface marker, useful for preventing or treating tumors and
XX autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
XX diabetes or psoriasis.
XX
XX Example 4; Page 74; 152pp; English.
XX
XX The present invention relates to a compound comprising one or more CD1d
XX complexes and an antibody or its fragment specific for a cell surface
XX marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
XX molecule, and are linked to the antibody or its fragment. The composition
XX and methods are useful for preventing or treating tumors and
XX autoimmune/inflammatory or infectious diseases, such as multiple
XX sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
XX uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
XX Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
XX arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
XX sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
XX cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
XX sequence is a PCR primer used in the exemplification of the invention.
XX
XX Sequence 45 BP; 5 A; 15 C; 17 G; 8 T; 0 U; 0 Other;
SQ
Query Match 65.0%; Score 15.6; DB 12; Length 45;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 ATGCCAACCCCTGCTGGAGGC 22
DB 40 ATGCCAACCCGTGCCAGGAGC 19
XX
XX RESULT 10
XX ADR55334/c
XX ID ADR55334 standard; DNA; 25 BP.
XX AC
XX ADR55334;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Drug therapy altered expressed gene #2685.
XX
XX drug activity monitoring; expression profile; gene expression;
XX peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
XX CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
XX mTOR; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO2004072265-A2.
XX
XX PD 26-AUG-2004.
XX
XX PF 11-FEB-2004; 2004WO-US004118.
XX
XX PR 11-FEB-2003; 2003US-0446133P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PR 23-JAN-2004; 2004US-0538246P.
XX
XX
XX (AMHP ) WYETH.
XX PA (BURC/) BURCZYNSKI M.
XX PA (TWIN/) TWINE N.
XX PA (DORN/) DORNER A J.
XX PA (TREP/) TREPICCHIO W L.
XX
XX PI Burczynski M, Twine N, Dornier AJ, Trepicchio WL;
XX WPI; 2004-642301/62.
XX
XX Monitoring drug activities in vivo comprises comparing an expression
XX profile of a gene in a peripheral blood sample of a patient before and
XX after drug therapy.
XX
XX Disclosure; SEQ ID NO 2685; 136pp; English.
XX
XX The invention relates to a method of monitoring drug activities in vivo
XX by comparing an expression profile of at least one gene in a peripheral
XX blood sample of a patient to a reference expression profile of the at
XX least one gene, where the at least one gene is differentially expressed
XX in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
XX blood disease and are subjected to a drug therapy as compared to PBMCs
XX isolated from the patient before the drug therapy, and where the patient
XX has the non-blood disease and is being treated by the drug therapy. The
XX method, kit, and nucleic acid array are useful for monitoring drug
XX activities in vivo. The drug is especially CCI-779, an ester analogue of
XX the immunosuppressant rapamycin which is a potent inhibitor of the
XX mammalian target of rapamycin (mTOR). This sequence represents a gene
XX expressed in PBMC altered by the drug therapy. (Note: this sequence does
XX no form part of the printed specification but was obtained in electronic
XX format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
XX
XX Sequence 25 BP; 7 A; 7 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 62.5%; Score 15; DB 13; Length 25;
Best Local Similarity 78.3%; Pred. No. 6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 2 TGCCAACCCCTGCTGGAGGCCT 24
DB 25 TGTCCACCCCTGCTGGGTACCT 3
XX
XX RESULT 11
XX ABL60842/c
XX ID ABL60842 standard; DNA; 30 BP.
XX AC ABL60842;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Murine CIS DNA fragment amplifying reverse primer.
XX
XX KW Leptin; receptor; cytokine signalling 3; SOCS3; CIS; Vav; anabolic;
XX cytokine-inducible SH2-containing protein; anorectic; vulnary;
XX cyostatic; PCR; primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO200240543-A1.
XX
XX PD 23-MAY-2002.
XX
XX PF 29-OCT-2001; 2001WO-EP012569.
XX
XX PR 14-NOV-2000; 2000EP-00204001.
XX PR 15-NOV-2000; 2000US-0248970P.
XX
XX (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Eyckerman S, Tavernier J, Zabeau L;
XX

```


DR WPI; 2002-500206/53.
XX
PT New functional fragment of leptin receptor, involved in suppressor of
PT cytokine signaling 3, cytokine-inducible SH2-containing protein and/or
PT Vav signaling, useful for modulating ligand induced signaling.
XX
PS Example; Page 9; 35pp; English.
XX
CC The invention relates to functional fragments of a leptin receptor,
CC involved in suppressor of cytokine signalling 3 (SOCS3), cytokine-
CC inducible SH2-containing protein (CIS) and/or Vav signalling. The leptin
CC receptor functional fragments are useful for modulating ligand (e.g.
CC leptin) induced signalling, and to screen compounds that interfere with
CC the binding of the functional fragment with a signalling molecule e.g.
CC Vav, SOCS3 or CIS. Modulators of leptin may be useful in food intake
CC disorders and regulation of weight, angiogenesis, wound healing and
CC susceptibility to digestive cancers. The present sequence represents a
CC PCR primer for amplifying the murine CIS DNA fragment
XX
SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGCCAACCTCTCTCTGGAGGC 22
Db 21 TTCCAACCTCTGATCTAGAGGC 1
RESULT 12
ID ABK16712/c
XX
AC ABK16712;
XX
DT 26-MAR-2002 (first entry)
XX
DE CIS primer MBU-O-678.
XX
KW Recombinant transmembrane receptor; PCR primer; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200190188-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-BP005916.
XX
PR 22-MAY-2000; 2000EP-00201771.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Eyckerman S, Van Ostade X, Vandekerckhove J, Verhee A;
PI Tavernier J;
XX
XX WPI; 2002-097646/13.
XX
PT New recombinant transmembrane receptor, useful for detecting compound-
PT compound binding, comprises extracellular ligand binding domain and
PT cytoplasmic domain containing heterologous bait polypeptide..
XX
PS Example 9; Page 41; 74pp; English.
XX
CC The invention describes a novel recombinant transmembrane receptor
CC comprising an extracellular ligand binding domain and a cytoplasmic
CC domain that contains a heterologous bait polypeptide. The receptor is
CC activated by binding of a ligand to the ligand binding domain and by
CC binding of a prey polypeptide to the heterologous bait peptide. The
CC receptor or the prey polypeptide is useful for detection of compound-
CC compound binding, where the binding is modification state dependent and

CC the modification is phosphorylation, acetylation, acylation, methylation,
CC ubiquitination or glycosylation. The binding is mediated by three or
CC more partners, where one or more of the partners is not or not completely
CC of proteinaceous nature. This sequence is one of 47 PCR primers (see
CC ABK16683-ABK16729) associated with the construction of the recombinant
CC transmembrane receptor, described in the method of the invention
XX
SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGCCAACCTCTCTCTGGAGGC 22
Db 21 TTCCAACCTCTGATCTAGAGGC 1
RESULT 13
ID AAL52021/c
XX
AC AAL52021 standard; DNA; 30 BP.
XX
DT 10-MAY-2003 (first entry)
XX
DE Recombinant receptor-related construction PCR primer #18.
XX
KW PCR; primer; ss; recombinant receptor; ligand binding domain;
KW heterologous bait polypeptide; protein-protein interaction; screening.
XX
OS Unidentified.
XX
PN WO2003004643-A2.
XX
PD 16-JAN-2003.
XX
PF 02-JUL-2002; 2002WO-EP007419.
XX
PR 03-JUL-2001; 2001EP-00202569.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Eyckerman S, Tavernier J, Vandekerckhove J;
XX
XX WPI; 2003-210363/20.
XX
PT New recombinant receptor comprising a ligand binding domain and a domain
PT that comprises a heterologous bait polypeptide, useful for screening
PT compounds that disrupt compound-compound binding.
XX
PS Example 3; Page 25; 45pp; English.
XX
CC The invention comprises a recombinant receptor which contains a ligand
CC binding domain and a heterologous bait polypeptide. The activation of the
CC receptor is inhibited by the binding of a prey polypeptide to the
CC heterologous bait polypeptide. The recombinant receptor is useful for
CC screening compounds that disrupt compound-compound binding - especially
CC protein-protein interactions that are essential to any biological
CC process. The present DNA sequence represents a PCR primer that is used in
CC the exemplification of the invention
XX
SQ Sequence 30 BP; 7 A; 5 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 8; Length 30;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 TGCCAACCTCTCTCTGGAGGC 22
Db 21 TTCCAACCTCTGATCTAGAGGC 1

```

RESULT 14
ABL9201
ID ABL99201 standard; DNA; 40 BP.
XX AC
XX ABL99201;
XX DT
XX 28-JUN-2002 (first entry)
XX DE
XX Green/red click beetle luciferase preparing oligo SEQ ID NO:169.
XX KW
XX Luciferase; synthetic nucleic acid; transcriptional characteristic;
XX KW transcription; codon usage; PCR; primer; ss.
XX OS
XX Coleoptera.
XX OS Synthetic.
XX XX
XX PN WO200216944-A2.
XX XX
XX PD 28-FEB-2002.
XX PF
XX 24-AUG-2001; 2001WO-US026566.
XX PR
XX 24-AUG-2000; 2000US-00645706.
XX PA (PROM-) PROMEGA CORP.
XX XX
XX PI Wood KV, Wood MG, Zhuang Y, Paguio A;
XX XX WPI; 2002-304140/34.
XX XX
XX PT Preparing a synthetic nucleic acid molecule with reduced inappropriate
XX PT transcriptional characteristics when expressed in a cell, for e.g making
XX PT fusion proteins, by altering a wild type or another synthetic nucleic
XX PT acid sequence.
XX PS
XX Example 1; Fig 6; 294pp; English.
XX CC
XX The present invention relates to the preparation of synthetic nucleic
XX CC acid molecules which have altered transcriptional regulatory sequences
XX CC compared to the wild-type. These sequences are then transcribed with less
XX CC frequency compared to the wild-type. In particular, the invention relates
XX CC to altered luciferase sequences. This can be used to detect weak promoter
XX CC activity, to express fusion proteins, to detect and/or measure levels of
XX CC gene expression, subcellular localisation or targeting, in life science
XX CC research, agrogenetics, gene therapy, developmental science and
XX CC pharmaceutical development. The present sequence is an oligonucleotide
XX CC described in the exemplification of the invention
XX SQ
XX Sequence 40 BP; 4 A; 10 C; 16 G; 10 T; 0 U; 0 Other;
XX Query Match 60.8%; Score 14.6; DB 6; Length 40;
XX Best Local Similarity 81.0%; Pred. No. 9.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 3 GCCAACCTGCTCTGGAGGCC 23
XX Db 16 GGCATTCCTGATCTGGAGGCC 36
XX
XX RESULT 15
XX AAF02607
XX ID AAF02607 standard; DNA; 17 BP.
XX XX
XX AC AAF02607;
XX XX
XX DT 16-FEB-2001 (first entry)
XX DE
XX Hammerhead ribozyme substrate #902.
XX KW
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KW interferon alpha; ss.
XX XX
XX OS Homo sapiens.
XX
XX RESULT 16
XX AAC62092
XX ID AAC62092 standard; DNA; 20 BP.
XX XX
XX AC AAC62092;
XX XX
XX DT 06-MAR-2001 (first entry)
XX XX
XX DE Reverse primer used to amplify a human elastase I gene exon 8.
XX XX
XX Human; elastase I; chromosome 12q13; mutant; serine protease; eczema;
XX KW hyperproliferative skin condition; psoriasis; lupus erythematosis;
XX KW erythema; cancer; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200061728-A2.
XX XX
XX PD 19-OCT-2000.
XX XX
XX PF 12-APR-2000; 2000WO-GB001389.
XX XX
XX PR 13-APR-1999; 99GB-00008458.
XX XX
XX PA (QUEB-) QUEEN MARY & WESTFIELD COLLEGE.
XX PI
XX Gerst-Talas U, Dunlop J, Kelsell DP;
XX XX
XX WPI; 2000-679482/66.
XX XX
XX Recombinant polynucleotide encoding human elastase I mutant useful for
XX PT determining the predisposition of a subject to cancer or

```

```

XX WO200061729-A2.
XX PN
XX 19-OCT-2000.
XX PD
XX 11-APR-2000; 2000WO-US009721.
XX PF
XX 12-APR-1999; 99US-0129390P.
XX PR
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX PI
XX WPI; 2000-647423/62.
XX DR
XX Enzymatic and antisenase nucleic acid inhibition of repressor genes,
XX XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PT
XX Claim 37; Page 76; 164pp; English.
XX PS
XX The present invention relates to enzymatic and antisenase nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX CC factor gene, IRF-2 and/or the CAATF Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
XX CC consequently increases expression of) genes involved in the production of
XX CC erythropoietin, granulocyte colony stimulating factor protein and
XX CC interferon alpha
XX CC
XX SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 60.0%; Score 14.4; DB 3; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.1e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 7 ACCCTGCTCTGGAGGC 22
XX Db 1 ACCCGCTCTGGAGGC 16
XX
XX RESULT 17
XX AAC62092
XX ID AAC62092 standard; DNA; 20 BP.
XX XX
XX AC AAC62092;
XX XX
XX DT 06-MAR-2001 (first entry)
XX XX
XX DE Reverse primer used to amplify a human elastase I gene exon 8.
XX XX
XX Human; elastase I; chromosome 12q13; mutant; serine protease; eczema;
XX KW hyperproliferative skin condition; psoriasis; lupus erythematosis;
XX KW erythema; cancer; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200061728-A2.
XX XX
XX PD 19-OCT-2000.
XX XX
XX PF 12-APR-2000; 2000WO-GB001389.
XX XX
XX PR 13-APR-1999; 99GB-00008458.
XX XX
XX PA (QUEB-) QUEEN MARY & WESTFIELD COLLEGE.
XX PI
XX Gerst-Talas U, Dunlop J, Kelsell DP;
XX XX
XX WPI; 2000-679482/66.
XX XX
XX Recombinant polynucleotide encoding human elastase I mutant useful for
XX PT determining the predisposition of a subject to cancer or

```

PT hyperproliferative skin condition such as psoriasis, eczema,
XX erythematosis.

XX Disclosure; Page 20; 35pp; English.

XX PCR primers AAC62091-92 were used to amplify a human elastase I gene
CC fragment. The elastase I gene maps to chromosome 12q13. Elastase is a
CC serine protease, and is localised in the basal layer of the mammalian
CC skin. The specification describes a mutant elastase I, with a frame shift
CC mutation in any one of the codons 207-225. The mutation results in the
CC disruption of the carboxy terminal of the protein, and possibly affects
CC substrate binding. An allele encoding a mutant elastase I can be detected
CC to determine the predisposition of a subject to a hyperproliferative skin
CC condition (e.g. psoriasis, eczema, lupus erythematosus and erythema) or
CC cancer

XX Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 3; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.1e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AACCTGCTCTGGAGG 21

DB 5 ACCCTGCTCTGGAGG 20

RESULT 17

AAL29368

ID AAL29368 standard; DNA; 50 BP.

AC AAL29368;

XX 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #2576.

XX

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; histone; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX Homo sapiens.

OS WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.

XX Claim 1; Page 2121; 4143pp; English.

XX

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms

SQ Sequence 50 BP; 6 A; 21 C; 15 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 4; Length 50;

Best Local Similarity 93.8%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGCCAACCCCTGCTCTG 17

DB 22 TGCCAGCCCTGCTCTG 37

RESULT 18

AAL34152/C

ID AAL34152 standard; DNA; 50 BP.

XX AAL34152;

AC AAL34152;

XX 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #7360.

XX

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; histone; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

XX Homo sapiens.

OS WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.

XX Claim 1; Page 3504; 4143pp; English.

XX

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms

XX SQ Sequence 50 BP; 10 A; 21 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 4; Length 50;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ATGCCAACCTGCTCTGGAGGCT 24

Db 39 ATGCTGACCTGGCTGGAGGCTT 16

RESULT 19

ADG86318
 ID ADG86318 standard; DNA; 20 BP.

XX AC ADG86318;

XX DT 11-MAR-2004 (first entry)

XX DE Human SMRT chimeric phosphorothioate oligonucleotide SEQ ID NO:32.

XX KW SMRT; silencing mediator for retinoid and thyroid hormone action;
 KW SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic;
 KW antirheumatic; antisense therapy; inflammatory disorder;
 KW rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia;
 KW breast cancer; human; phosphorothioate; ss; chimeric.

OS Chimeric.

OS Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate linkages, and all cytidine
 residues are 5-methylcytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyls"

XX WO2003106645-A2.

XX PD 24-DEC-2003.

XX PF 17-JUN-2003; 2003WO-US018923.

XX PR 17-JUN-2002; 2002US-00174014.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM, Dobie KW;

XX DR WPI; 2004-082184/08.

XX Novel antisense compound targeted to nucleic acid encoding SMRT
 XX (silencing mediator for retinoid and thyroid hormone action), useful for
 XX treating animal having disease associated with SMRT such as cancer,

PT rheumatoid arthritis.

XX Example 15; SEQ ID NO 32; 260pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding SMRT (silencing mediator for
 CC retinoid and thyroid hormone action), where (I) specifically hybridises
 CC with the nucleic acid molecule encoding SMRT and inhibits expression of a
 CC SMRT. (I) specifically hybridises with at least 8-nucleobase portion of a
 CC preferred target region on nucleic acid molecule encoding SMRT. Also
 CC described is a composition (II) comprising (I) and a carrier or diluent.
 CC (I) and (II) have cytostatic, antiinflammatory, antiarthritic and
 CC antirheumatic activities, and can be used in antisense therapy, and as
 CC SMRT expression inhibitors. (I) is useful for inhibiting the expression
 CC of SMRT in cells or tissues. (I) is also useful for treating an animal
 CC having a disease or condition associated with SMRT, e.g., inflammatory
 CC disorder such as rheumatoid arthritis; or a hyperproliferative disorder
 CC such as cancer chosen from leukaemia and breast cancer, by inhibiting the
 CC expression of SMRT. (I) is useful for diagnostics, therapeutics,
 CC prophylaxis and as research reagents and kits. The present sequence
 CC represents a chimeric phosphorothioate antisense oligonucleotide which
 CC inhibits human SMRT, which is used in an example from the present
 CC invention. N.B. The present sequence is designated as SEQ ID NO:30 in
 CC example 15 but corresponds to SEQ ID NO:32 in the Sequence Listing.

XX SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 12; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.3e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCAACCTGCTCTGGAGG 21

Db 2 GCCCACCTGCTCTGCATG 20

RESULT 20

ADG86349/c

ID ADG86349 standard; DNA; 20 BP.

XX AC ADG86349;

XX DT 11-MAR-2004 (first entry)

XX DE Human SMRT target region SEQ ID NO:63.

XX KW SMRT; silencing mediator for retinoid and thyroid hormone action;
 KW SMRT inhibitor; cytostatic; antiinflammatory; antiarthritic;
 KW antirheumatic; antisense therapy; inflammatory disorder;
 KW rheumatoid arthritis; hyperproliferative disorder; cancer; leukaemia;
 KW breast cancer; human; ss; target.

OS Synthetic.

OS Homo sapiens.

XX WO2003106645-A2.

XX PD 24-DEC-2003.

XX PF 17-JUN-2003; 2003WO-US018923.

XX PR 17-JUN-2002; 2002US-00174014.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM, Dobie KW;

XX DR WPI; 2004-082184/08.

XX Novel antisense compound targeted to nucleic acid encoding SMRT
 XX (silencing mediator for retinoid and thyroid hormone action), useful for
 XX treating animal having disease associated with SMRT such as cancer,
 XX rheumatoid arthritis.

```
XX PS Example 15; SEQ ID NO 63; 260pp; English.
XX CC The present invention describes a compound (I) 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding SMRT (silencing mediator for
CC retinoid and thyroid hormone action), where (I) specifically hybridises
CC with the nucleic acid molecule encoding SMRT and inhibits expression of a
CC SMRT. (I) specifically hybridises with at least 8-nucleobase portion of a
CC preferred target region on nucleic acid molecule encoding SMRT. Also
CC described is a composition (II) comprising (I) and a carrier or diluent.
CC (I) and (II) have cytostatic, antiinflammatory, antiproliferative and
CC antirheumatic activities, and can be used in anticancer therapy, and as
CC SMRT expression inhibitors. (I) is useful for inhibiting the expression
CC of SMRT in cells or tissues. (I) is also useful for treating an animal
CC having a disease or condition associated with SMRT, e.g., inflammatory
CC disorder such as rheumatoid arthritis; or a hyperproliferative disorder
CC such as cancer chosen from leukaemia and breast cancer, by inhibiting the
CC expression of SMRT. (I) is useful for diagnostics, therapeutics,
CC prophylaxis and as research reagents and kits. The present sequence
CC represents a human SMRT target region sequence, which is used in an
CC example from the present invention. N.B. The present sequence is
CC designated as SEQ ID NO:61 in example 15 but corresponds to SEQ ID NO:63
CC in the Sequence Listing.
XX CC
XX SQ Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
      Query Match      59.2%; Score 14.2; DB 12; Length 20;
      Best Local Similarity 84.2%; Pred. No. 1.3e+04;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCCAACCTGCTCTGAGG 21
Db 19 GCCACCTGCTCTGCATG 1
      |||||
RESULT 21
ADP17501/c
ID ADP17501 standard; DNA; 25 BP.
XX AC ADP17501;
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #3906.
XX KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLON/) SLONI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX CC
```

```
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 4237; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX CC
XX SQ Sequence 25 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
      Query Match      59.2%; Score 14.2; DB 12; Length 25;
      Best Local Similarity 84.2%; Pred. No. 1.4e+04;
      Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGCCAACCTGCTCTGGA 19
Db 19 ATGCCATCTCAGCTCTGGA 1
      |||||
RESULT 22
AAV68288
ID AAV68288 standard; DNA; 24 BP.
XX AC AAV68288;
XX DT 01-MAR-1999 (first entry)
XX DE Penicillium chrysogenum primer 24.
XX KW ss; PCR; amplification; primer; filamentous fungus; recombinant DNA;
KW DNA domain; fermentation.
XX OS Synthetic.
XX OS Penicillium chrysogenum.
XX PN WO9846772-A2.
XX PD 22-OCT-1998.
XX PF 09-APR-1998; 98WO-EP002070.
XX PR 11-APR-1997; 97EP-00201091.
XX PA (KONN ) GIST-BROCADES BV.
XX PI Selten GCM, Swinkels BW, Bovenberg RAL;
XX PI WPI; 1998-609917/51.
XX DR Recombinant filamentous fungus produced by gene conversion - has DNA
XX integrated into two or more mostly homologous DNA domains of its
XX chromosomes, used in the fermentation industry.
XX PT Example; Page 33; 171pp; English.
XX PS
XX CC The primers AAV68265-V68314 are used in examples of the construction of
XX new filamentous fungus with a recombinant DNA molecule integrated into at
XX least 2 substantially homologous DNA domains of its chromosome(s), and
```

CC where the DNA domains are not the ribosomal DNA repeats. The recombinant
CC fungus is used in the fermentation industry, and the DNA domains can be
CC further multiplied with integrated recombinant DNA through gene
CC conversion or amplification. The new fungi provide greater versatility
CC compared with available systems, because the fungus is not confined to
CC the use of deficient selectable marker genes for transformation, and is
CC not confined to the use of only ribosomal DNA as target sequences for
CC integration. Also, the fungi provide greater genetic stability of the
CC integrated multiple copies compared with conventional recombinant fungi
CC in which recombinant DNA are randomly integrated in tandem arrays. The
CC genotype of the fungi can be completely defined, facilitating regulatory
CC approval, and the phenotype will be more predictable
XX
SQ Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 24;
Best Local Similarity 77.3%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGGCT 24
Db 1 GCCTACTCTGTTCTGGAGGCT 22

RESULT 23
ADC06568/c
ID ADC06568 standard; DNA; 25 BP.
XX
AC ADC06568;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Na/H exchanger-like protein 1 gene oligonucleotide #3015.
XX
KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS Homo sapiens.
XX
PN EP1273660-A2.
XX
PD 08-JAN-2003.
XX
PF 25-JAN-2002; 2002EP-00001160.
XX
PR 30-JAN-2001; 2001WO-US000666.
PR 23-MAY-2001; 2001US-00864761.
PR 21-DEC-2001; 2001US-0343331P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y;
XX
DR WPI; 2003-302724/30.
XX
PT New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHELP1.
XX
PS Example 2; SEQ ID NO 3055; 468pp; English.

XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHELP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in

CC diagnostic methods. This sequence corresponds to a 256-mer
CC oligonucleotide spanning the sequence of the human NHELP1 gene
CC (ADC03514).

SQ Sequence 25 BP; 4 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 10; Length 25;
Best Local Similarity 77.3%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGC 22
Db 25 ACGCCAACTCTGATCTGAAGCC 4

RESULT 24
ADC06569/c
ID ADC06569 standard; DNA; 25 BP.
XX
AC ADC06569;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human Na/H exchanger-like protein 1 gene oligonucleotide #3016.
XX
KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS Homo sapiens.
XX
PN EP1273660-A2.
XX
PD 08-JAN-2003.
XX
PF 25-JAN-2002; 2002EP-00001160.
XX
PR 30-JAN-2001; 2001WO-US000666.
PR 23-MAY-2001; 2001US-00864761.
PR 21-DEC-2001; 2001US-0343331P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y;
XX
DR WPI; 2003-302724/30.
XX
PT New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHELP1.
XX
PS Example 2; SEQ ID NO 3056; 468pp; English.

XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHELP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 256-mer
CC oligonucleotide spanning the sequence of the human NHELP1 gene
CC (ADC03514).

SQ Sequence 25 BP; 4 A; 4 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 10; Length 25;
Best Local Similarity 77.3%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QV 1 ATGCCAACCTGCTCTGGAGGC 22
 Db 24 ACGCCCACTGCTGATCTGAAGCC 3

RESULT 25
 ID AAQ70259/c
 AC AAQ70259;
 XX AAQ70259;
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1995 (first entry)
 XX
 DE T. gondii P30.291 PCR primer.
 XX
 KW Toxoplasma gondii; toxoplasmosis; P30; P30.291; nP30.873; trachyzoite;
 KW surface antigen; vaccine; alpha-virus; vector; PCR;
 KW polymerase chain reaction; amplification; primer; secretion; ss.
 XX
 OS Synthetic.
 XX
 PN WO9417813-Al.
 XX
 PD 18-AUG-1994.
 XX
 PF 08-FEB-1994; 94WO-US001398.
 XX
 PR 08-FEB-1993; 93US-00015414.
 XX
 PA (PARA-) PARAVAX INC.
 XX
 PI Grieve RB, Xiong C;
 XX
 XX WPI; 1994-279381/34.
 DR
 XX
 XX Use of packaging defective alpha-virus expression vectors - for prodn. of
 PT protective cpds. for protecting animals from disease, partic.
 PT toxoplasmosis.
 XX
 XX Example; Page 81; 128pp; English.
 PS
 XX A sequence is provided (AAQ70254) that contains the entire coding region
 CC for the T. gondii tachyzoite major surface antigen P30 (AARS7065). DNA
 CC fragment nP30.873 encoding T. gondii antigen P30.291 was obtained by PCR
 CC amplification of a clone encoding the P30 gene using the primers given in
 CC AAQ70259-60. P30.291 comprises amino acids 46-336 of P30, but is
 CC functionally equivalent to the natural protein. Deletion of the N-
 CC terminal hydrophobic region of P30 allows improved secretion from
 CC producer cells, for use in toxoplasmosis vaccine production. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 35 BP; 6 A; 13 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 2; Length 35;
 Best Local Similarity 77.3%; Pred. No. 1.7e-04;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QV 1 ATGCCAACCTGCTCTGGAGGC 22
 Db 25 ATGCCATCCCGGCTAGAGTC 4

RESULT 26
 ADP71324/c
 ID ADP71324 standard; DNA; 36 BP.
 XX
 AC ADP71324;
 XX
 DT 23-SEP-2004 (first entry)
 DT
 XX Human INSP105 PCR primer INSP105-exon4R.

XX human; INSP105; growth hormone; antinflammatory; cytostatic;
 KW neuroprotective; virucide; osteopathic; antibacterial; fungicide;
 KW anorectic; nephrotropic; cardiant; reproductive disorder;
 KW pregnancy disorder; gestational trophoblastic disease;
 KW developmental disorder; Silver-Russell syndrome; growth disorder;
 KW growth hormone deficiency; Cushing's disease; endocrine disorder;
 KW cell proliferative disorder; neoplasm; carcinoma; tumour; melanoma;
 KW adenocarcinoma; choriocarcinoma; osteosarcoma; angiogenesis;
 KW myeloproliferative disorder; autoimmune disorder; inflammatory disorder;
 KW cardiovascular disorder; neurological disorder; pain; metabolic disorder;
 KW diabetes mellitus; osteoporosis; obesity; cachexia; AIDS; renal disease;
 KW lung injury; ageing; infection; PCR; primer; ss; chromosome 17.
 XX
 OS Homo sapiens.
 XX
 PN WO2004056863-A2.
 XX
 PD 08-JUL-2004.
 XX
 PF 19-DEC-2003; 2003WO-GB005594.
 XX
 PR 20-DEC-2002; 2002GB-00029850.
 XX
 PA (ARES-) ARES TRADING SA.
 XX
 PI Fagan RJ, Phelps CB, Rodrigues TM, Power C, De Tiani M;
 XX
 XX WPI; 2004-500284/47.
 DR
 XX New INSP105 polypeptides, useful in preparing a composition for treating
 PT or preventing a disease associated with growth hormone proteins, e.g.
 PT cell proliferative, inflammatory or neurological disorders or infections.
 XX
 XX Example 2; Page 55; 84pp; English.
 PS
 XX The present invention describes an INSP105 polypeptide comprising: (a) a
 CC 199 amino acid sequence given in SEQ ID NO:8 (ADP71313); (b) a fragment
 CC of (1) that functions as a growth hormone, or having an antigenic
 CC determinant in common with (1); or (c) a functional equivalent of (1) or
 CC the polypeptide; (2) a purified nucleic acid molecule which encodes
 CC (2). Also described: (1) a vector comprising the nucleic acid molecule; (3) a
 CC host cell transformed with the vector; (4) a ligand which binds
 CC specifically to the growth hormone polypeptide; (5) a compound that
 CC either increases or decreases the level of expression or activity of the
 CC polypeptide; (6) a method of diagnosing a disease in a patient; (7) a
 CC pharmaceutical composition comprising the polypeptide, nucleic acid
 CC molecule, vector, host cell, ligand or compound; (8) a vaccine
 CC composition comprising the polypeptide or nucleic acid molecule; (9) a
 CC method of treating a disease in a patient; (10) a method of monitoring
 CC the therapeutic treatment of disease in a patient; (11) a method for
 CC identifying a compound for treating or diagnosing a disease; (12) a kit
 CC useful for diagnosing disease; (13) a transgenic or knockout non-human
 CC animal that has been transformed to express higher, lower or absent
 CC levels of the polypeptide; and (14) a method for screening for a compound
 CC for treating a disease. INSP105 has antiinflammatory, cytostatic,
 CC neuroprotective, virucide, osteopathic, antibacterial, fungicide,
 CC anorectic, nephrotropic and cardiant activities. The INSP105 polypeptide
 CC is useful as a growth hormone or as a modulator of growth hormone
 CC activity. The polypeptide, nucleic acid molecule, vector, host cell,
 CC ligand or compound can be used in preparing a composition for treating or
 CC preventing a disease associated with growth hormone proteins, e.g.,
 CC reproductive disorders; pregnancy disorder such as gestational
 CC trophoblastic disease; developmental disorders such as Silver-Russell
 CC syndrome; growth disorders; growth hormone deficiency; Cushing's disease;
 CC endocrine disorders; cell proliferative disorders, including neoplasm,
 CC carcinoma, pituitary tumour, ovary tumour, melanoma, lung, colorectal,
 CC breast, pancreas, head and neck, placental site trophoblastic tumour;
 CC adenocarcinoma, choriocarcinoma, osteosarcoma and other solid tumours;
 CC angiogenesis; myeloproliferative disorders; autoimmune/inflammatory
 CC disorders; cardiovascular disorders; neurological disorders; pain;
 CC metabolic disorders including diabetes mellitus; osteoporosis; obesity;
 CC cachexia; AIDS; renal disease; lung injury; ageing; or infections

QY 1 ATGCCAACCTGCTCTGGAGGC 22
DB 5 ATCCAAACGCTGATGTGGAGGC 26

RESULT 29
ABZ49539
ID ABZ49539 standard; DNA; 42 BP.
AC ABZ49539;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human glutathione-S-transferase MGST1 gene polymorphic site, #6322.
DE
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(20..23,Ct)
FT /*tag= a
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
DR WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
XX
XX Claim 23; Page 192; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for

CC clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 42 BP; 13 A; 16 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 58.3%; Score 14; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCCTGCTCTGGAG 20
DB 19 ACCCTGCTCTGGAG 32

RESULT 30
ABZ45912
ID ABZ45912 standard; DNA; 42 BP.
XX
XX AC ABZ45912;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Human glutathione-S-transferase MGST1 gene polymorphic site, #2696.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; ds.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(20..23,Ct)
FT /*tag= a
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
DR WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
XX
XX Claim 23; Page 109; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of

CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy

XX
SQ Sequence 42 BP; 13 A; 16 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 42;
Best Local Similarity 100.0%; Pred.No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCTGCTCTGGAG 20
|||||
Db 19 ACCCTGCTCTGGAG 32

RESULT 31
ACH66436/c
ID ACH66436 standard; DNA; 20 BP.
XX
AC ACH66436;
XX
DT 16-OCT-2003 (first entry)
XX
DE Sense PCR primer used to amplify AOC3.
XX
KW Promoter; ss: genomic DNA; gDNA; untranslated region; UTR;
KW DNA high-density microarray; biosite; large scale production; gDNA probe;
KW microarray; type I primer; PCR; primer.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /label= OTHER
FT /note= "OTHER= linked to the bacteriophage T7 promoter
FT (ACH66426)"
XX
FN US2003073085-A1.
XX
PD 17-APR-2003.
XX
PF 05-OCT-2001; 2001US-00972469.
XX
PR 05-OCT-2001; 2001US-00972469.
XX
XX (LAIF/) LAI F.
PA (ZHOU/) ZHOU D.
XX
PI Lai F, Zhou D;

XX WPI; 2003-555942/52.
DR
XX Amplifying expressed genetic sequences from genomic DNA of mammalian or
PT higher order plant species for printing on DNA microarrays, involves
PT using the 3' untranslated region of the gene sequence.
XX
PS Disclosure; Page 6; 15pp; English.
XX
CC The invention discloses a method for amplifying expressed genetic
CC sequences from genomic DNA (gDNA) from mammalian or higher order plant
CC species. The method involves identifying a 3' untranslated region (UTR)
CC of a gDNA sequence, designing probe, performing PCR, separating the
CC product by size differentiation and performing a second PCR to amplify
CC the predetermined sequence. Also claimed is a biological analysis device,
CC comprising a substrate and an array of a set of expressed genetic
CC sequences, located on the substrate, which are generated by the method
CC above and a DNA high-density microarray comprising a substrate upon which
CC are deposited an array of biosites of genomic DNA fragments having the
CC sequence of at least one exon, and absent polyadenine and vector
CC sequences, where the genomic DNA fragments have a sequence length of from
CC about 75-2000 nucleotides. The method is efficient for amplifying gene
CC sequences, enables large-scale production of gDNA sequences, generates
CC large quantities of gDNA probes, which enables greater efficiency for
CC printing in microarray formats, fabricates high-density DNA arrays of
CC enhanced, widely varying genetic content and abstains from using RNA-
CC derived sequences by simple PCR amplifications without cloning. The
CC method produces amplified sequences that have greater specificity and
CC size consistency than that observed with cDNA fragments, and allows for
CC greater signal sensitivity than oligonucleotides. The sequence presented
CC is a Type I gene specific primer which is linked at its 5' termini to the
CC bacteriophage T7 promoter

XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 9; Length 20;
Best Local Similarity 88.2%; Pred.No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCAACCCCTGCTCTGG 18
|||||
Db 17 TGCCAACCCCTACTCTGG 1

RESULT 32
ABZ84928
ID ABZ84928 standard; DNA; 20 BP.
XX
AC ABZ84928;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Claim 15; SEQ ID NO 170; 872pp; English.
 XX
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ublquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: the sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 10; Length 20;
 Best Local Similarity 88.2%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGGCCACCCTGCTCTGG 18
 DB 3 TGGCCACCCTGCTCTGG 19
 RESULT 33
 ABD211158
 ID ABD211158 standard; DNA; 20 BP.
 XX
 AC ABD211158;
 DT
 DT 29-JUL-2004 (first entry)
 XX
 DE Human transglutaminase-derived oligo SEQ ID 170.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 XX Homo sapiens.
 OS
 XX WO200285309-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013143.
 PF
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX

PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-093058/08.
 DR
 DR Pharmaceutical composition for treating asthma, has antisense
 XX oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 170; 763pp; English.
 PS
 PS This invention describes a novel composition (a) a first active agent,
 XX comprising oligonucleotides, effective for alleviating
 XX bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 XX Sequence 20 BP; 1 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 11; Length 20;
 Best Local Similarity 88.2%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TGGCCACCCTGCTCTGG 18
 DB 3 TGGCCACCCTGCTCTGG 19
 RESULT 34
 ABD31281
 ID ABD31281 standard; DNA; 20 BP.
 XX
 AC ABD31281;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human XT-II gene fragment for glucosaminoglycan reduction in glial scars.
 XX
 KW ss; vulneryary; cell therapy; glial scar; primary proteoglycan;
 KW chain initiation enzyme; elongation enzyme; neuronal regeneration;
 KW glucosaminoglycan.
 XX
 OS Homo sapiens.
 XX
 XX WO2004041197-A2.
 PN

```
XX PD 21-MAY-2004.
XX PF 31-OCT-2003; 2003WO-US034806.
XX PR 01-NOV-2002; 2002US-0423082P.
XX PR 16-MAY-2003; 2003US-0471447P.
XX (UYCA-) UNIV CASE WESTERN RESERVE.
XX PA Grimpe B, Silver J;
XX PI WPI; 2004-400518/37.
XX DR
XX PT Reducing GAG content in a glial scar comprises inhibiting the expression
XX PT of primary proteoglycans or the expression and/or activity of a chain
XX PT initiation or elongation enzyme.
XX PS Example 12; SEQ ID NO 103; 265pp; English.
XX CC The invention relates to a method of reducing glucosaminoglycan (GAG)
XX CC content in a glial scar by inhibiting the expression of primary
XX CC proteoglycans or the expression and/or activity of a chain initiation or
XX CC elongation enzyme. The method is useful in reducing GAG content in a
XX CC glial scar and promoting neuronal regeneration. This sequence corresponds
XX CC to a fragment of the human XT-II gene used to identify sequences to which
XX CC antisense oligos, ribozymes, RNAi constructs can designed.
XX SQ Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 57.5%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CCCTGCTCTGGAGGCCT 24
DB 4 CCCTGGCTCGAGGCCT 20
RESULT 35
ID AAX05223/c
XX ID AAX05223 standard; DNA; 25 BP.
XX AC AAX05223;
XX DT 22-APR-1999 (first entry)
XX DE Murine ICE mutagenic PCR primer m8p/s.
XX KW ICE; ALS; SOD gene; interleukin-1 converting enzyme; mutant; cell death;
XX KW amyotrophic lateral sclerosis; transgenic; ICE-like caspase; apoptosis;
XX KW traumatic brain injury; TBI; neurological; neurodegenerative; kidney;
XX KW heart disease; immune system; intestinal; aging; viral infection; AIDS;
XX KW acquired immune deficiency syndrome; gene therapy; PCR primer; ss.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9857664-A1.
XX PD 23-DEC-1998.
XX PF 18-JUN-1998; 98WO-US012716.
XX PR 19-JUN-1997; 97US-0050242P.
XX (YUAN/) YUAN J.
XX (FRIE/) FRIEDLANDER R M.
XX Yuan J, Friedlander RM;
XX WPI; 1999-095294/08.
XX
XX PT Treating amyotrophic lateral sclerosis (ALS) or ALS-like symptoms -
XX PT comprises inhibiting interleukin-1 converting enzyme (ICE) by gene
XX PT therapy, useful for treating central nervous system damage.
XX PS Example 1; Page 29; 96pp; English.
XX CC The invention relates to methods of treating amyotrophic lateral
XX CC sclerosis (ALS) or ALS-like symptoms that comprises inhibiting
XX CC interleukin-1 converting enzyme (ICE) by gene therapy. A mutant ICE gene
XX CC product can also be used for modulating programmed cell death
XX CC accompanying ALS. Transgenic non-human animal (including progeny)
XX CC containing a mutant ICE and SOD (ALS phenotype) gene are used to screen
XX CC compounds for treating ALS. Inhibitors of an ICE-like caspase are used to
XX CC attenuate or prevent apoptosis resulting from traumatic brain injury
XX CC (TBI), and to reduce the formation of reactive oxygen species following
XX CC TBI. Diseases caused by acute and chronic dysregulation of cell death,
XX CC which are treated by the ICE gene product, include malignant and pre-
XX CC malignant conditions, neurological, neurodegenerative disorders, heart
XX CC disease, immune system disorders, intestinal disorders, kidney disease,
XX CC aging, viral infections and acquired immune deficiency syndrome (AIDS).
XX CC The methods, mutant genes and inhibitors of ICE enable a better
XX CC understanding of the role of cell death and what triggers cell death in
XX CC ALS, which allow treatment of the disease. They also enable understanding
XX CC of the pathways mediating post traumatic apoptosis, which lead to novel
XX CC pharmacotherapy of TBI. Sequences AAX05223-27 represent PCR mutagenic
XX CC primers of mouse ICE cDNA used for constructing vectors containing mutant
XX CC ICE sequences
XX SQ Sequence 25 BP; 9 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 57.5%; Score 13.8; DB 2; Length 25;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CCCTGCTCTGGAGGCCT 24
DB 21 CTCTCCTCTGGAGGCCT 5
RESULT 36
ID ABS55668
XX ID ABS55668 standard; DNA; 33 BP.
XX AC ABS55668;
XX DT 27-DEC-2002 (first entry)
XX DE cAMP dependent kinase regulation subunit 8.8 PCR primer #2.
XX KW Human; cAMP dependent kinase regulation subunit 8.8; cyclic AMP;
XX KW malignant tumour; inflammation; antagonist; reverse transcriptase PCR;
XX KW RT-PCR; primer; ss.
XX OS Homo sapiens.
XX PN CNI352179-A.
XX PD 05-JUN-2002.
XX PF 10-NOV-2000; 2000CN-00127387.
XX PR 10-NOV-2000; 2000CN-00127387.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
XX WPI; 2002-733428/80.
XX New human cAMP dependent protein kinase regulation subunit 8.8
XX PT polypeptide for treating diseases, such as, malignant tumors and
XX PT inflammations.
```

PS Example 4; Page 19 (Disclosure); Opp; Chinese.

XX The present invention discloses a new kind of polypeptide, human cAMP

CC dependent kinase regulation subunit 8.8, polynucleotides encoding the

CC polypeptide and a DNA recombination process to produce the polypeptide.

CC The present invention also discloses applying the polypeptide in treating

CC various diseases, such as malignant tumours, and inflammations. The

CC present invention also discloses the antagonist resisting the polypeptide

CC and its treatment effect. This sequence represents a PCR primer used to

CC amplify DNA encoding the human cAMP dependent kinase regulation subunit

CC 8.8 protein

XX

SQ Sequence 33 BP; 8 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 33;

Best Local Similarity 88.2%; Pred. No. 2.1e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGGC 22

DB 6 ATCCCTACTCTGGAGGC 22

RESULT 37

ABK11966/c

ID ABK11966 standard; DNA; 41 BP.

XX AC ABK11966;

XX

DT 05-JUN-2002 (first entry)

XX

DE Human TIM23 specific oligonucleotide probe #1.

XX

KW Human; mitochondrial endomembrane transferase; TIM 23 11.66;

KW mitochondrial disease; tumour; developmental disorder; inflammation;

KW immune disorder; gene therapy; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200210397-A1.

XX

PD 07-FEB-2002.

XX

PF 29-JUN-2001; 2001WO-CN001077.

XX

PR 30-JUN-2000; 2000CN-00116939.

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-241621/29.

XX

PT New human mitochondrial endomembrane transferase TIM 23 11.66 for

PT diagnosing and treating tumors, inflammation, and immune disorders.

XX

PS Example 6; Page 22; 37pp; Chinese.

XX

CC This invention relates to a novel isolated polypeptide of human

CC mitochondrial endomembrane transferase TIM 23 11.66, the polynucleotide

CC encoding the protein and a method for producing the recombinant protein.

CC The protein of the invention and the nucleic acid encoding the protein

CC may be used in diagnosis and treatment of mitochondrial disease, tumours,

CC developmental disorders, inflammation, and immune disorders by gene

CC therapy. The invention also discloses an antagonist of the TIM23 protein

CC and therapeutic uses thereof. The present sequence represents the human

CC mitochondrial endomembrane transferase specific oligonucleotide probe #1.

CC This probe is used to probe the mitochondrial endomembrane transferase

CC cDNA of the invention

XX

SQ Sequence 41 BP; 12 A; 10 C; 16 G; 3 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 41;

Best Local Similarity 88.2%; Pred. No. 2.1e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGGC 22

DB 6 ATCCCTACTCTGGAGGC 22

RESULT 39

AAI73671

ID AAI73671 standard; DNA; 50 BP.

XX AC AAI73671;

XX

DT 09-NOV-2001 (first entry)

XX

PS Example 4; Page 19 (Disclosure); Opp; Chinese.

XX The present invention discloses a new kind of polypeptide, human cAMP

CC dependent kinase regulation subunit 8.8, polynucleotides encoding the

CC polypeptide and a DNA recombination process to produce the polypeptide.

CC The present invention also discloses applying the polypeptide in treating

CC various diseases, such as malignant tumours, and inflammations. The

CC present invention also discloses the antagonist resisting the polypeptide

CC and its treatment effect. This sequence represents a PCR primer used to

CC amplify DNA encoding the human cAMP dependent kinase regulation subunit

CC 8.8 protein

XX

SQ Sequence 33 BP; 8 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 33;

Best Local Similarity 88.2%; Pred. No. 2.1e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AACCTGCTCTGGAGGC 22

DB 6 ATCCCTACTCTGGAGGC 22

RESULT 38

ABK11967/c

ID ABK11967 standard; DNA; 41 BP.

XX AC ABK11967;

XX

DT 05-JUN-2002 (first entry)

XX

DE Human TIM23 specific oligonucleotide probe #2.

XX

KW Human; mitochondrial endomembrane transferase; TIM 23 11.66;

KW mitochondrial disease; tumour; developmental disorder; inflammation;

KW immune disorder; gene therapy; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200210397-A1.

XX

PD 07-FEB-2002.

XX

PF 29-JUN-2001; 2001WO-CN001077.

XX

PR 30-JUN-2000; 2000CN-00116939.

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-241621/29.

XX

PT New human mitochondrial endomembrane transferase TIM 23 11.66 for

PT diagnosing and treating tumors, inflammation, and immune disorders.

XX

PS Example 6; Page 22; 37pp; Chinese.

XX

CC This invention relates to a novel isolated polypeptide of human

CC mitochondrial endomembrane transferase TIM 23 11.66, the polynucleotide

CC encoding the protein and a method for producing the recombinant protein.

CC The protein of the invention and the nucleic acid encoding the protein

CC may be used in diagnosis and treatment of mitochondrial disease, tumours,

CC developmental disorders, inflammation, and immune disorders by gene

CC therapy. The invention also discloses an antagonist of the TIM23 protein

CC and therapeutic uses thereof. The present sequence represents the human

CC mitochondrial endomembrane transferase specific oligonucleotide probe #2.

CC This probe is used to probe the mitochondrial endomembrane transferase

CC cDNA of the invention

XX

SQ Sequence 41 BP; 12 A; 11 C; 15 G; 3 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 41;

Best Local Similarity 88.2%; Pred. No. 2.1e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAG 20

DB 41 CCAGCCCTGCTCTGGAG 25

RESULT 39

AAI73671

ID AAI73671 standard; DNA; 50 BP.

XX AC AAI73671;

XX

DT 09-NOV-2001 (first entry)

XX

```
XX DE Human silent SNP containing nucleic acid SEQ:612.
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX KW protein therapy; vaccine; probe; diagnostic assay; detection;
XX KW quantitation; restorative therapy; polymorphic; ds.
XX OS Homo sapiens.
XX XX
XX FN WO200140521-A2.
XX PD 07-JUN-2001.
XX XX
XX PF 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX XX
XX PA (CURA-) CURAGEN CORP.
XX XX
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 241; 2653pp; English.
XX XX
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AA153114 to AA153329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides. For
XX CC example, (I) may be used to treat disorders by rectifying mutations or
XX CC deletions in a patient's genome that affect the activity of polypeptides
XX CC by expressing inactive proteins or to supplement the patient's own
XX CC production of polypeptide. Additionally, (I) and its complementary
XX CC sequences may also be used as DNA probes in diagnostic assays to detect
XX CC and quantitate the presence of similar nucleic acids in samples, and
XX CC therefore which patients may be in need of restorative therapy. The
XX CC polypeptides encoded by (I) may be used as antigens in the production of
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also
XX CC be used to down regulate expression and activity. The antibodies may also
XX CC be used as diagnostic agents for detecting the presence of polymorphic
XX CC polypeptides in samples
XX SQ Sequence 50 BP; 8 A; 16 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 4; Length 50;
Best Local Similarity 88.2%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CCCTGCTCTGGAGGCCT 24
Db 33 CCATGCTCTGGAGGCCT 49

RESULT 40
ADP22838/c
ID ADP22838 standard; DNA; 20 BP.
XX AC ADP22838;
XX XX
XX DT 26-AUG-2004 (first entry)
XX DE Human BUB1-beta target sequence ISIS 196160.
XX KW ss; BUB1-beta; hyperproliferative disorder; cancer; human.
XX OS Homo sapiens.
```

```
XX US2004110149-A1.
XX 10-JUN-2004.
XX 10-DEC-2002; 2002US-00316459.
XX 10-DEC-2002; 2002US-00316459.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Jain R;
XX WPI; 2004-440338/41.
XX New oligonucleotide compound that inhibits expression of BUB1-beta,
XX useful for preparing a composition for treating hyperproliferative
XX disorder, e.g. cancer.
XX Example 15; SEQ ID NO 104; 92pp; English.
XX The invention relates to a new compound, having a sequence targeted to a
XX nucleic acid encoding BUB1-beta, which specifically hybridises with the
XX nucleic acid encoding BUB1-beta and inhibits expression of BUB1-beta. The
XX oligonucleotide compound is useful for preparing a composition for
XX treating a hyperproliferative disorder, e.g. cancer. The present sequence
XX represents a human BUB1-beta target sequence.
XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 56.7%; Score 13.6; DB 12; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CAACCCCTGCTCTGGAGGCCT 24
Db 20 CCACTGCTCTAGAGGCCT 1

Search completed: November 18, 2005, 11:52:22
Job time : 167.262 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTGCTCTGGAGCCT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.6	60.8	35	7 T73795	YC54a06.s1
C 2	14.4	60.0	31	1 A1323319	mh78a09.x
C 3	14.4	60.0	50	1 AU102721	AU102721
C 4	14	58.3	45	7 T71655	YC62e05.s1
C 5	14	58.3	48	8 BH865457	BH865457
C 6	13.6	56.7	31	8 AZ809714	2M0073P16
C 7	13.6	56.7	33	7 T73421	YC35a08.s1
C 8	13.6	56.7	45	8 A2768397	1M0568D23
C 9	13.4	55.8	37	4 B034402	B034402
C 10	13.4	55.8	41	9 BX209782	Danio rer
C 11	13.4	55.8	45	7 T69149	YC32e08.s1
C 12	13.4	55.8	49	1 AA917511	OL52c07.s
C 13	13.2	55.0	40	4 B0339939	B0339939
C 14	13.2	55.0	50	1 AU103163	AU103163
C 15	13.2	55.0	50	1 AU103164	AU103164
C 16	13.2	55.0	50	1 AU103168	AU103168
C 17	13.2	55.0	50	1 AU103176	AU103176
C 18	13	54.2	38	8 A2961550	2M0230H05
C 19	13	54.2	42	9 CG720584	1119062H0
C 20	13	54.2	43	8 A2785692	2M0029P14
C 21	13	54.2	43	9 CS869098	AC0059.Sa
C 22	13	54.2	46	7 C0784990	BL282B.A0
C 23	13	54.2	49	8 BH796330	1008093E1
C 24	12.8	53.3	35	9 DR8L23T	Danio rer

25	12.8	53.3	49	9 AG191198	Pan trogl
26	12.8	53.3	50	1 AU102722	AU102722
27	12.8	53.3	50	1 AU102724	AU102724
28	12.6	52.5	40	1 AU1021601	ub09f01.f
29	12.6	52.5	43	8 A2474035	1M0290F18
30	12.6	52.5	48	8 A2475962	1M0294I21
C 31	12.6	52.5	50	1 AU103032	AU103032
C 32	12.4	51.7	25	1 A1397039	fb25e02.Y
33	12.4	51.7	34	1 AU255522	AU255522
34	12.4	51.7	37	6 CA796933	Cac.BL_39
35	12.4	51.7	40	8 AZ775757	2M0008B24
36	12.4	51.7	46	7 N83841	KK3617F.Hum
37	12.4	51.7	50	8 A2766605	1M0564L13
38	12.4	51.7	50	9 CG724386	1119081A0
C 39	12.4	51.7	50	9 CL528330	ASV5801.f
C 40	12.2	50.8	31	4 B1522142	603081524
C 41	12.2	50.8	43	1 AA482116	zv43c12.s
C 42	12.2	50.8	46	7 R48775	Y769C01.B1
C 43	12.2	50.8	47	8 A2621187	1M0454F18
C 44	12	50.0	32	8 A2827691	2M0104H13
C 45	12	50.0	32	8 AZ830592	2M0109K23

ALIGNMENTS

RESULT 1
T73795/c
LOCUS
DEFINITION
YC54a06.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:84466.3, similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR
(HUMAN); mRNA sequence.
T73795
T73795.1 GI:690470
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
1 (bases 1 to 35)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 965
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL this clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 965 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:501523"
/db_xref="taxon:9606"
/clone="IMAGE:84466"

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 965
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL this clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 965 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:501523"
/db_xref="taxon:9606"
/clone="IMAGE:84466"

```

/dev_scages="49 years old"
/lab_host="SOUR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/notes="Organ: liver; Vector: pBluescript SK; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Hepatotomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match      60.8%; Score 14.6; DB 7; Length 35;
Best Local Similarity 73.9%; Pred. No. 8.e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCACCCCTGCTCTGGAGGCC 23
Db 25 ANGCCACCCCGCGCTCGAGGNC 3

RESULT 2
AI323319/c
LOCUS
DEFINITION
mh78a09.xi Soares mouse placenta 4NDMP13.5 14.5 Mus musculus CDNA
clone IMAGE:457048 3' similar to TR:Q64366 Q64366 SYNAPTOTAGMIN
VIII ;, mRNA sequence.
ACCESSION
AI323319
VERSION
AI323319.1 GI:4057748
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 31)
AUTHORS
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
Waterston R.
TITLE
The WashU-HMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:273936
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequenced stop: 1.
Location/Qualifiers
1. 31
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457048"
/sex="unknown"
/tissue type="placenta"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="Soares mouse placenta 4NDMP13.5 14.5"
/notes="Organ: placenta; Vector: p7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',

```

```

TGTACCAATCTCAAGTCGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match      60.0%; Score 14.4; DB 1; Length 31;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AACCTGCTCTGGAGG 21
Db 27 AAACCTGCTCTGGAGG 12

RESULT 3
AUI02721
LOCUS
DEFINITION
AUI02721 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01205, mRNA sequence.
ACCESSION
AUI02721
VERSION
AUI02721.1 GI:13552242
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 50)
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01205"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES
source
1. 50
Query Match      60.0%; Score 14.4; DB 1; Length 50;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCACCCCTGCTCTGGAGGCC 24
Db 23 ATGCCGCCCATCTCTGGAGAACT 46

RESULT 4
T71655/c
LOCUS
DEFINITION
T71655 yc62605.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:85280 3' similar to gb:X02162 APOLIPROTEIN A-I PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
T71655
VERSION
T71655.1 GI:686176

```


High quality sequence stop: 31.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClm library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source
Query Match 56.7%; Score 13.6; DB 8; Length 31;
Best Local Similarity 80.0%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN
QY 1 ATGCCAACCCCTGCTCGGAG 20
|||||||
Db 12 ATGCCAACCCCTGGGTGGT 31
|||||||

RESULT 7
T73421/c
LOCUS
DEFINITION YC35a08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82646 3' similar to gb:X02162 APOLIPROTEIN A-I PRECURSOR (HUMAN); mRNA sequence.

ACCESSION T73421.1 GI:690096
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 33)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoso,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Lee,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PubMed 8889549

COMMENT Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 993

High quality sequence stops: 18 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found
Insert Length: 993 Std Error: 0.00
Seq primer: -21mi3
High quality sequence stop: 18.
Location/Qualifiers
1..33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:499703"
/db_xref="taxon:9606"
/clone="IMAGE:82646"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOAR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb, Uni-ZAP XR Vector; ~5' adaptor sequence: 5' CTCAGATTTTTTTTTTTT 3'"

FEATURES
source
Query Match 56.7%; Score 13.6; DB 7; Length 33;
Best Local Similarity 76.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ORIGIN
QY 1 ATGCCAACCCCTGCTCGGAG 21
|||||||
Db 22 ANGCAAGCCGCCTCGAGG 2
|||||||

RESULT 8
A2768397
LOCUS
DEFINITION IM0568D23F Mouse 10Kb plasmid UUGClm library Mus musculus genomic clone UUGClm0568D23 F, genomic survey sequence.

ACCESSION A2768397
VERSION
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0568 row: D column: 23
Seq primer: CGTTGTAACACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0568D23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 [gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 56.7%; Score 13.6; DB 8; Length 45;
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGG 21
 |||||
 Db 22 TGCCAACCTGGACTGATGG 41

RESULT 9

BJ034402/c
 LOCUS BJ034402 37 bp mRNA linear EST 26-SEP-2003
 DEFINITION BJ034402 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL028h05 5', mRNA sequence.

ACCESSION BJ034402.1 GI:17391943
 VERSION BJ034402.1
 KEYWORDS EST.

SOURCE

ORGANISM Xenopus laevis (African clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE

AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.

TITLE

Expressed genes in X. laevis embryo

JOURNAL

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp

The information of this clone is available through the following URL.

http://xenopus.nibb.ac.jp.

FEATURES

source

Location/Qualifiers
 1..37
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL028h05"
 /tissue_type="whole embryo"
 /dev_stages="stage 15"
 /clone_lib="NIBB Mochii normalized Xenopus neurula library"

ORIGIN

Query Match 55.8%; Score 13.4; DB 4; Length 37;
 Best Local Similarity 93.3%; Pred. No. 3e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 TGCCAACCTGCTCT 16
 |||||
 Db 15 TGCCAACCTGTCTCT 1

RESULT 10

BJ209782

LOCUS

BJ209782 41 bp DNA linear GSS 29-JAN-2003

DEFINITION

BJ209782 Danio rerio genomic clone DKEY-250L15, genomic survey sequence.

ACCESSION

BJ209782

VERSION

BJ209782.1 GI:28041668

KEYWORDS

GSS.

SOURCE

ORGANISM Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.

TITLE

Direct Submission

JOURNAL

Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished

COMMENT

This sequence was generated from the T7 end of BAC 250L15. 250L15 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

Location/Qualifiers
 1..41
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEY-250L15"
 /tissue_type="Testis"
 /note="vector pIndigoBAC-536"

ORIGIN

Query Match 55.8%; Score 13.4; DB 9; Length 41;
 Best Local Similarity 73.9%; Pred. No. 3e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 2 TGCCAACCTGCTCTGGAGGCT 24
 |||||
 Db 19 TCCAAACTCTGCTCTGGAGGCT 41

RESULT 11

T69149/c

LOCUS

T69149 45 bp mRNA linear EST 23-FEB-1995

DEFINITION

yc32e08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82406 3' similar to gb.X02162 APOLIPOPROTEIN A-I PRECURSOR (HUMAN); mRNA sequence.

ACCESSION

T69149

VERSION

T69149.1 GI:680297

KEYWORDS

EST.

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 45)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.


```

Qy      3  GCCAACCTGCTCTGGAGG 21
Db      21  GNGACCTGCTCTAGAGG 39

RESULT 14.
AUI03163/c
LOCUS   AUI03163 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03163 50 bp mRNA linear EST 28-JAN-2004
COLF1812, mRNA sequence.
ACCESSION AUI03163
VERSION   AUI03163.1 GI:13552684
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    source           1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="COLF5980"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      7  ACCCTGCTCTGGAGGCCT 24
Db      22  ACCCAGCTCTGGCGTCCT 5

RESULT 16.
AUI03168/c
LOCUS   AUI03168 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03168 50 bp mRNA linear EST 28-JAN-2004
HRC02059, mRNA sequence.
ACCESSION AUI03168
VERSION   AUI03168.1 GI:13552689
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    source           1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="COLF1812"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      7  ACCCTGCTCTGGAGGCCT 24
Db      22  ACCCAGCTCTGGCGTCCT 5

RESULT 15.
AUI03164/c
LOCUS   AUI03164 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
AUI03164 50 bp mRNA linear EST 28-JAN-2004
COLF5980, mRNA sequence.
ACCESSION AUI03164
VERSION   AUI03164.1 GI:13552685
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.,
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL  EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE  21270072
PUBMED   11375929
COMMENT  Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    source           1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="HRC02059"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      7  ACCCTGCTCTGGAGGCCT 24
Db      22  ACCCAGCTCTGGCGTCCT 5

```

```

Db      28 ACCGAGCTCTGGCGTCCT 11
||||| ||||| ||||| |||||
RESULT 17
AU1031176/c
LOCUS   AU1031176 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION
HMA00666, mRNA sequence.
ACCESSION AU1031176
VERSION   AU1031176.1 GI:13552697
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL ENBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yzuku@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HMA0066"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      55.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 ACCCTGCTCTGGAGGCTT 24
||||| ||||| ||||| |||||
Db      48 ACCGAGCTCTGGCGTCCT 31

RESULT 18
AZ961550
LOCUS   AZ961550 38 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0230H05F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0230H05 F, genomic survey sequence.
ACCESSION AZ961550
VERSION   AZ961550.1 GI:13832777
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: H column: 05
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source           1..38
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0230H05"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      54.2%; Score 13; DB 8; Length 38;
Best Local Similarity 76.2; Pred. No. 4.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATGCCAACCTGCTCTGGAGG 21
||||| ||||| ||||| |||||
Db      14 ATGCANAAACGTCTTTGGATG 34

RESULT 19
CG720584
LOCUS   CG720584 42 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119062H06.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG720584
VERSION   CG720584.1 GI:37753618
KEYWORDS GSS.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 42)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

```


humquery@sanger.ac.uk Unpublished
 This sequence was generated from the T7 end of BAC 8L23. 8L23 is
 part of the Dariokey BAC Library created by R. Plasterk and N.V.
 Keygene.
 Further details: http://www.sanger.ac.uk/Projects/D_dario/.

FEATURES

source
 1..35
 /location=Qualifiers
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKXY-8L23"
 /tissue_type="Testis"
 /note="Vector pIndigoBAC-536"

ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 35;
 Best Local Similarity 70.8%; Pred. No. 5.5e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCT 24
 ||||| ||||| ||||| ||||| |||||
 Db 2 ATGCAAGCTCGTCTCTGGAGGCT 25

RESULT 25

AG191198 49 bp DNA linear GSS 06-MAR-2004
 LOCUS Pan troglodytes DNA, clone: RP43-067A16.T7, genomic survey
 DEFINITION sequence.

ACCESSION

AG191198 GI:45223374

VERSION

GSS.

KEYWORDS

Pan troglodytes

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

BAC end sequences of Library RP-43

Unpublished

2 (bases 1 to 49)

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIBB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail: redstone@mail.kribb.re.kr, URL: <http://phs.grc.kribb.re.kr/>,

Tel: 82-42-866-7181, Fax: 82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43. This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R Site 1 : EcoRI

R Site 2 : EcoRI

Location/Qualifiers

1..49

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-067A16.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 49;

Best Local Similarity 87.5%; Pred. NO. 5.6e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

7 ACCCTGCTCTGGAGGC 22

Db

6 ACCCTGCTCTAGGC 21

RESULT 26

AU102722

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yuuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAS02544"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 50;

Best Local Similarity 70.8%; Pred. No. 5.6e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCT 24

||||| ||||| ||||| ||||| |||||

Db 23 ATGCAGCCATCTCTGGAGAACT 46

RESULT 27

AU102724

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

AU102722 50 bp mRNA linear EST 28-JAN-2004
 LOCUS Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION CAS02544, mRNA sequence.

ACCESSION AU102722

VERSION AU102722.1 GI:13552243

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yuuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAS02544"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 50;

Best Local Similarity 70.8%; Pred. No. 5.6e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGCT 24

||||| ||||| ||||| ||||| |||||

Db 23 ATGCAGCCATCTCTGGAGAACT 46

RESULT 27

AU102724

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

[illegible]

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* Xli10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	52.5%;	Score 12.6;	DB 8;	Length 48;
Best Local Similarity	78.9%;	Pred. NO. 6.8e+05;		
Matches 15; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	5	CAACCCCTGCTCGAGGCC	23	
Dh	2	CACCCCTTATCTGGGTGCC	20	

RESULT 31					
AU103032/c					
LOCUS	50 bp	mRNA	linear	EST 28-JAN-2004	
DEFINITION	AU103032 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone				
	CAS05571. mRNA sequence.				

ACCESSION	AF010302
VERSION	AF010302.1
KEYWORDS	GI:13552553
EST.	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
PUBMED	11375929
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki.Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES	Location/Qualifiers 1..50 /organism="Homo sapiens"
source	

```

/organism="homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="CAS05571"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      52.5%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 CAACCTGCTGTGAGGCC 23
      ||| ||||| |||
Db      40 CAACCTGCTCGTCAGCC 22

```

```

RESULT 32
AI397039/c
LOCUS
DEFINITION
fb2se02.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3712922 5' similar to SW:IQGA.HUMAN P46940 RAS
GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 ;, mRNA sequence.
ACCESSION
AI397039
VERSION
AI397039.1 GI:42266932
KEYWORDS
EST
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 25)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1
POLYA=No.

FEATURES
Location/Qualifiers
1..25
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3712922"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'pGACTAGTCTTAGATCGGACGCGCGCCCTTTTCTTTT3];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

ORIGIN
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178
2179
2180
2181
2182
2183
2184
2185
2186
2187
2188
2189
2190
2191
2192
2193
2194
2195
2196
2197
2198
2199
2200
2201
2202
2203
2204
2205
2206
2207
2208
2209
2210
2211
2212
2213
2214
2215
2216
2217
2218
2219
2220
2221
2222
2223
2224
2225
2226
2227
2228
2229
2230
2231
2232
2233
2234
2235
2236
2237
2238
2239
2240
2241
2242
2243
2244
2245
2246
2247
2248
2249
2250
2251
2252
2253
2254
2255
2256
2257
2258
2259
2260
2261
2262
2263
2264
2265
2266
2267
2268
2269
2270
2271
2272
2273
2274
2275
2276
2277
2278
2279
2280
2281
2282
2283
2284
2285
2286
2287
2288
2289
2290
2291
2292
2293
2294
2295
2296
2297
2298
2299
2300
2301
2302
2303
2304
2305
2306
2307
2308
2309
2310
2311
2312
2313
2314
2315
2316
2317
2318
2319
2320
2321
2322
2323
2324
2325
2326
2327
2328
2329
2330
2331
2332
2333
2334
2335
2336
2337
2338
2339
2340
2341
2342
2343
2344
2345
2346
2347
2348
2349
2350
2351
2352
2353
2354
2355
2356
2357
2358
2359
2360
2361
2362
2363
2364
2365
2366
2367
2368
2369
2370
2371
2372
2373
2374
2375
2376
2377
2378
2379
2380
2381
2382
2383
2384
2385
2386
2387
2388
2389
2390
2391
2392
2393
2394
2395
2396
2397
2398
2399
2400
2401
2402
2403
2404
2405
2406
2407
2408
2409
2410
2411
2412
2413
2414
2415
2416
2417
2418
2419
2420
2421
2422
2423
2424
2425
2426
2427
2428
2429
2430
2431
2432
2433
2434
2435
2436
2437
2438
2439
2440
2441
2442
2443
2444
2445
2446
2447
2448
2449
2450
2451
2452
2453
2454
2455
2456
2457
2458
2459
2460
2461
2462
2463
2464
2465
2466

```

PUBMED
COMMENT
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.

FEATURES

Location/Qualifiers
1..37
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 3999"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonado type Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."

ORIGIN

Query Match 51.7%; Score 12.4; DB 6; Length 37;
Best Local Similarity 69.6%; Pred. No. 8.3e+05;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 TGCCAACCTGCTCTGGAGGCT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 9 TGCCAACNCCTCTGCGCTTGCT 31

RESULT 35

AZ775757
LOCUS
DEFINITION 2M0008B24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0008B24 R, genomic survey sequence.
ACCESSION AZ775757
VERSION AZ775757.1 GI:12902623
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: B column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008B24"

FEATURES

Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008B24"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.7%; Score 12.4; DB 8; Length 40;
Best Local Similarity 72.7%; Pred. No. 8.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 GCCAACCTGCTCTGGAGGCT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 9 GTCTACCTGCTGCAGATGCT 30

RESULT 36

N83841
LOCUS
DEFINITION KK3617F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK3617 5' similar to STAT4, mRNA sequence.
ACCESSION N83841
VERSION N83841.1 GI:1259466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Liew, C.C.
COMMENT CDNAS from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliu@rics.bwh.harvard.edu
Seq primer: GAAATTAACCTCTACTAAGGG.
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KK3617"
/lab_host="E. coli XL1-Blue"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

ORIGIN

Query Match 51.7%; Score 12.4; DB 7; Length 46;
 Best Local Similarity 72.7%; Pred. No. 8.4e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGCCAACTCTGCTGGAGGCC 23
 |||||
 Db 16 TGCCAACTCTGCTGGAGGCC 37

RESULT 37
 AZ766605
 LOCUS
 DEFINITION 50 bp DNA linear GSS 16-FEB-2001
 clone UUGC1M0564L13 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (Bases 1 to 50)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Muscle whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0364 row: L column: 13

Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 50.

Location/Qualifiers

FEATURES
 source

1..50
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC1M0564L13"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 51.7%; Score 12.4; DB 8; Length 50;
 Best Local Similarity 92.9%; Pred. No. 8.4e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTCTGGAGG 21
 |||||
 Db 26 CCTGCTCTGGTGG 39

RESULT 38
 CG724386
 LOCUS

DEFINITION 50 bp DNA linear GSS 20-OCT-2003
 1119081A01.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
 survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Zea mays
 Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 AUTHORS
 1 (Bases 1 to 50)
 Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon
 Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1119081 row: A column: 01

Class: transposon-tagged.

Location/Qualifiers

FEATURES
 source

1..50
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
 was extracted from leaf strips, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 50;
 Best Local Similarity 72.7%; Pred. No. 8.4e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGC 22
 |||||

Db 26 ATGCCAACCTCTCTCTGTCGC 47

RESULT 39

LOCUS

DEFINITION 50 bp DNA linear GSS 17-MAY-2004
 ASV5B01.fwd ASLV-vector integration sites in human 293T-TVA cells
 Homo sapiens genomic clone ASV5B01.fwd, genomic survey sequence.

ACCESSION: CL528330
VERSION: CL528330.1 GI:47421526
KEYWORDS: GSS.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 50)
AUTHORS: Mitchell, R.S., Beitzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H.,
Berry, C.C., Ecker, J.R. and Bushman, F.
TITLE: Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target
Site Preferences
JOURNAL: Unpublished (2004)
COMMENT: Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.

FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="ASV5B01.fwd"
/clone_lib="ASLV-vector integration sites in human
293T-TVA cells"
/note="Human 293T cells expressing the subgroup A avian
retrovirus receptor (293T-TVA) were infected with an
ASLV-based vector. DNA was isolated and cleaved with
restriction enzymes; linkers were ligated onto the cleaved
DNA and DNAs were amplified using one primer that bound to
the linker DNA and one that bound to the ASLV cDNA.
Junctions between integrated ASLV proviruses and cellular
DNA were cloned and sequenced."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 50;
Best Local Similarity 92.9%; Pred. No. 8.4e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ACCCTGCTCTGGAG 20
|||||
Db 19 ACCCGGCTCTGGAG 6

RESULT 40
BI522142
LOCUS: BI522142 31 bp mRNA linear EST 29-AUG-2001
DEFINITION: 60308152471 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221084 3',
mRNA sequence.
ACCESSION: BI522142
VERSION: BI522142.1 GI:15346934
KEYWORDS: EST.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE: 1 (bases 1 to 31)
AUTHORS: NIH-MGC <http://mgi.nci.nih.gov/>.
JOURNAL: National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT: Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM1555 row: 0 column: 05
High quality sequence start: 7
High quality sequence stop: 31.
FEATURES
source
1..31
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5221084"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 50.8%; Score 12.2; DB 4; Length 31;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCCAACCCCTGCTCTGGA 19
|||||
Db 14 GCTGACTCTGCTCTGGA 30
Search completed: November 18, 2005, 21:12:40
Job time : 1150.98 secs

This Page Blank (uspto)


```
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-58956

Query Match      61.7%; Score 14.8; DB 4; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGG 21
    ||||| ||||| |||||
Db 3 CCAAGCCTGCTCTGAAG 20
    ||||| ||||| |||||

RESULT 7
US-09-671-317-812
; Sequence 812, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 812
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-138-141 : polymorphic base G or A
US-09-671-317-812

Query Match      61.7%; Score 14.8; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
    ||||| ||||| |||||
Db 8 ATGCCAAGGCTGATCTRGAG 27
    ||||| ||||| |||||

RESULT 8
US-09-396-196G-2325
; Sequence 2325, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124901
```

```
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-2325

Query Match      60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCCT 24
    ||||| ||||| |||||
Db 1 CCAACCCCTGCTCAGGGCTCCT 21
    ||||| ||||| |||||

RESULT 9
US-09-396-196G-8574
; Sequence 8574, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-8574

Query Match      60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCCT 24
    ||||| ||||| |||||
Db 2 CCAACACTGCTAATGAGGCCT 22
    ||||| ||||| |||||

RESULT 10
US-09-396-196G-124901/c
; Sequence 124901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124901
```

Query Match 60.8%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAAACCTGCTCTGGAGGC 22
| | | | | | | | | | | | | | | | | | | | |
Db 21 TGCCACACAGATCTGGAGGC 1

RESULT 11
US-09-422-978-2994
; Sequence 2994, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density....
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2994
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21492-310 : polymorphic base C or T
US-09-422-978-2994

Query Match 60.8%; Score 14.6; DB 4; Length 47;
Best Local Similarity 73.9%; Pred. No. 2e+03;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGCC 23
| | | | | | | | | | | | | | | | | | | | |
Db 11 ATGCCAAGGCTGCTTGATCCC 33

RESULT 12
US-09-396-196G-57276
; Sequence 57276, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-57276

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCAAACCTGCTCTGGAG 20
| | | | | | | | | | | | | | | | | | | | |
Db 3 TGCCAACTCTGCTCTACAG 21

RESULT 13
US-09-396-196G-70618
; Sequence 70618, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70618

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCTGGAGGCC 23
| | | | | | | | | | | | | | | | | | | | |
Db 7 CAACATGCTCTGGAGACC 25

RESULT 14
US-09-396-196G-76806/c
; Sequence 76806, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76806
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-76806

Query Match 59.2%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCAAACCTGCTCTGGAG 20
| | | | | | | | | | | | | | | | | | | | |
Db 21 TGCCTTCCCTGCGCTGGAG 3

RESULT 15
US-09-402-631A-24
; Sequence 24, Application US/09402631A

; Patent No. 6432672
; GENERAL INFORMATION:
; APPLICANT: Gist-Brocades B. V.
; APPLICANT: Selten, Gerardus
; APPLICANT: Swinkels, Bart
; APPLICANT: Bovenberg, Roelof
; TITLE OF INVENTION: Gene Conversion as a Tool for the Construction of Recombinant
; TITLE OF INVENTION: Organisms
; FILE REFERENCE: 99/757
; CURRENT APPLICATION NUMBER: US/09/402,631A
; CURRENT FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/EP98/02070
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: EP 97201091.2
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: misc feature
; OTHER INFORMATION: PCR primer
US-09-402-631A-24

Query Match 58.3%; Score 14; DB 3; Length 24;
Best Local Similarity 77.3%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGGCT 24
Db 1 GCCTACTCTGTCTGGAGGCT 22

RESULT 16
US-08-375-235-6/c
; Sequence 6, Application US/08375235
; Patent No. 5766602
; GENERAL INFORMATION:
; APPLICANT: Xiong Ph.D., Cheng
; APPLICANT: Grieve Ph.D., Robert B.
; TITLE OF INVENTION: "RECOMBINANT VIRAL PARTICLE VACCINES"
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESS: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 Lincoln St., #3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,235
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,414
; FILING DATE: 08-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik Esq., Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2618-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; TELEX: 467377
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Toxoplasma gondii
; INDIVIDUAL ISOLATE: P30 antigen gene
; IMMEDIATE SOURCE:
; CLONE: Primer #5
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..18
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 19..35
US-08-375-235-6

Query Match 58.3%; Score 14; DB 1; Length 35;
Best Local Similarity 77.3%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAGGC 22
Db 25 ATGCCATCCCGGCTCTAGATC 4

RESULT 17
US-09-396-196G-58955
; Sequence 58955, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-58955

Query Match 57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAG 20
Db 9 CCAAGCCTGCTCTGAAG 25

RESULT 18
US-08-987-326-13
; Sequence 13, Application US/08987326
; Patent No. 6057105
; GENERAL INFORMATION:
; APPLICANT: NGI/Cancer Tech Company, LLC
; TITLE OF INVENTION: Detection of Melanoma or Breast Metastasis with a
; TITLE OF INVENTION: Multiple Marker Assay
; FILE REFERENCE: NGI 20823-701 CIP
; CURRENT APPLICATION NUMBER: US/08/987,326
; CURRENT FILING DATE: 1997-12-09

```
; EARLIER APPLICATION NUMBER: 08/406,307
; EARLIER FILING DATE: 1995-03-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: sequence
US-08-987-326-13

Query Match          56.7%; Score 13.6; DB 3; Length 22;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
    ||||| ||| ||| |||||
Db 1 ATGCCAACCCCTGCTCTGGAG 20

RESULT 19
US-08-991-862-15
; Sequence 15, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/08/991,862
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/863,862
; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-08-991-862-15

Query Match          56.7%; Score 13.6; DB 3; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 20
US-09-813-156-15
; Sequence 15, Application US/09813156
; Patent No. 6670183
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-813-156-15

Query Match          56.7%; Score 13.6; DB 4; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 21
US-09-456-886-15
; Sequence 15, Application US/09456886
; Patent No. 6720159
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/456,886
; CURRENT FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-456-886-15

Query Match          56.7%; Score 13.6; DB 4; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CCAACCCCTGCTCTGGAGGCC 23
    ||| ||||| ||| |||||
Db 5 CCAGCCCTGCTGTTAAGGCC 24

RESULT 22
US-09-824-647-15
; Sequence 15, Application US/09824647
; Patent No. 6824775
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z9996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/824,647
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
```

; NAME/KEY: primer
; LOCATION: (1)..(24)
; OTHER INFORMATION: Antisense oligonucleotide to human GP88
US-09-824-647-15

Query Match 56.7%; Score 13.6; DB 4; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCAACCCCTGCTCTGGAGGCC 23
||| ||||| ||||| |||||
Db 5 CCAGCCCTGCTGTAAAGGCC 24

RESULT 23
US-09-396-196G-71340
; Sequence 71340, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71340
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71340

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTGCTCTGGAG 20
||| ||||| ||||| |||||
Db 3 ATCCAGCACTGCTCTGCAG 22

RESULT 24
US-09-396-196G-74893
; Sequence 74893, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-74893

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CCAACCCCTGCTCTGGAGGCC 23
||| ||||| ||||| |||||
Db 5 CCAGTCCTGCTCTGCATGCC 24

RESULT 25
US-09-396-196G-124900/c
; Sequence 124900, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124900

Query Match 56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCAACCCCTGCTCTGGAGGCC 22
||| ||||| ||||| |||||
Db 25 GCCCACACAGATCTGGAGGCC 6

RESULT 26
US-09-907-794A-16/c
; Sequence 16, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414

;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 16
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-907-794A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 27
US-09-905-125A-16/c
; Sequence 16, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.

;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Macher, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,125A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 16
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-125A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 28
US-09-902-775A-16/c
; Sequence 16, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTCTGCTCTGGAG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 29

US-09-906-700-16/c
Sequence 16, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

```
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-906-700-16

Query Match      56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGAG 20
        ||||| ||||| |||||
Db      22 ATGCCACAGCTGCTGTGGAG 3

RESULT 30
US-09-903-603A-16/c
; Sequence 16, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.16182C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-903-603A-16

Query Match      56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGAG 20
        ||||| ||||| |||||
Db      22 ATGCCACAGCTGCTGTGGAG 3

RESULT 31
US-09-904-920A-16/c
; Sequence 16, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
```

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-920A-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTCTCTGGAG 20
|||||
Db 22 ATGCCACAGCTGCTGGAG 3

RESULT 32
US-09-064-16/c
Sequence 16, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-909-064-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCCCTCTCTGGAG 20
|||||
Db 22 ATGCCACAGCTGCTGGAG 3

RESULT 33
US-09-905-381A-16/c
Sequence 16, Application US/09905381A
Patent No. 6818746

```

1 / GENERAL INFORMATION:
2 / APPLICANT: Genentech, Inc.
3 / APPLICANT: Ashkenazi, Avi
4 / APPLICANT: Botstein, David
5 / APPLICANT: Desnoyers, Luc
6 / APPLICANT: Eaton, Dan L.
7 / APPLICANT: Ferrara, Napoleone
8 / APPLICANT: Filvaroff, Ellen
9 / APPLICANT: Fong, Sherman
10 / APPLICANT: Gao, Wei-Qiang
11 / APPLICANT: Gerber, Hanspeter
12 / APPLICANT: Gerritsen, Mary E.
13 / APPLICANT: Goddard, A.
14 / APPLICANT: Godowski, Paul J.
15 / APPLICANT: Grimaldi, Christopher J.
16 / APPLICANT: Gurney, Austin L.
17 / APPLICANT: Hillan, Kenneth, J.
18 / APPLICANT: Kljavin, Ivar J.
19 / APPLICANT: Mather, Jennie P.
20 / APPLICANT: Pan, James
21 / APPLICANT: Paoni, Nicholas F.
22 / APPLICANT: Roy, Margaret Ann
23 / APPLICANT: Stewart, Timothy A.
24 / APPLICANT: Tumas, Daniel
25 / APPLICANT: Williams, P. Mickey
26 / APPLICANT: Wood, William, I.
27 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
28 / TITLE OF INVENTION: Acids Encoding the Same
29 / FILE REFERENCE: 10466-14
30 / CURRENT APPLICATION NUMBER: US/09/905,381A
31 / CURRENT FILING DATE: 2001-07-13
32 / PRIOR APPLICATION NUMBER: PCT/US00/04414
33 / PRIOR FILING DATE: 2000-02-22
34 / PRIOR APPLICATION NUMBER: US 60/143,048
35 / PRIOR FILING DATE: 1993-07-07
36 / PRIOR APPLICATION NUMBER: US 60/145,698
37 / PRIOR FILING DATE: 1993-07-26
38 / PRIOR APPLICATION NUMBER: US 60/146,222
39 / PRIOR FILING DATE: 1993-07-28
40 / PRIOR APPLICATION NUMBER: PCT/US99/20594
41 / PRIOR FILING DATE: 1993-09-08
42 / PRIOR APPLICATION NUMBER: PCT/US99/20944
43 / PRIOR FILING DATE: 1993-09-13
44 / PRIOR APPLICATION NUMBER: PCT/US99/21090
45 / PRIOR FILING DATE: 1993-09-15
46 / PRIOR APPLICATION NUMBER: PCT/US99/21547
47 / PRIOR FILING DATE: 1993-09-15
48 / PRIOR APPLICATION NUMBER: PCT/US99/23089
49 / PRIOR FILING DATE: 1993-10-05
50 / PRIOR APPLICATION NUMBER: PCT/US99/28214
51 / PRIOR FILING DATE: 1993-11-29
52 / PRIOR APPLICATION NUMBER: PCT/US99/28313
53 / PRIOR FILING DATE: 1993-11-30
54 / PRIOR APPLICATION NUMBER: PCT/US99/28564
55 / PRIOR FILING DATE: 1993-12-02
56 / PRIOR APPLICATION NUMBER: PCT/US99/28565
57 / PRIOR FILING DATE: 1993-12-02
58 / PRIOR APPLICATION NUMBER: PCT/US99/30095
59 / PRIOR FILING DATE: 1993-12-16
60 / PRIOR APPLICATION NUMBER: PCT/US99/30911
61 / PRIOR FILING DATE: 1993-12-20
62 / PRIOR APPLICATION NUMBER: PCT/US99/30999
63 / PRIOR FILING DATE: 1993-12-20
64 / PRIOR APPLICATION NUMBER: PCT/US00/00219
65 / PRIOR FILING DATE: 2000-01-05
66 / NUMBER OF SEQ ID NOS: 423
67 / SEQ ID NO 16
68 / LENGTH: 50
69 / TYPE: DNA
70 / ORGANISM: Artificial Sequence
71 / FEATURE:
72 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
73 / OTHER INFORMATION: oligonucleotide probe

```

US-09-905-381A-16

Query Match 56.7% Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred.No.5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps

Qy 1 ATGCCAACCTGCTCTGGAG 20
 ||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 34
US-09-906-618-16/c
; Sequence 16, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 16
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-906-618-16

Query Match 56.7%; Score 13.6; DB 4; Length 50;
Best Local Similarity 80.0%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCCCTGCTCTGGAG 20
||||| ||||| |||||
Db 22 ATGCCACAGCTGCTGTGGAG 3

RESULT 35

US-08-222-619-24
; Sequence 24, Application US/08222619
; Patent No. 5652352

; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-222-619-24

Query Match 55.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGA 19
||||| ||||| |||||
Db 1 CAACCCCTGCTGTGGA 15

RESULT 36

US-09-906-618-16

PCT-US95-04075-24
; Sequence 24, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
PCT-US95-04075-24

Query Match 55.8%; Score 13.4; DB 5; Length 18;
Best Local Similarity 93.3%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAACCCCTGCTCTGGA 19
||||| ||||| |||||
Db 1 CAACCCCTGCTGTGGA 15

RESULT 37

US-09-657-472-2169/c
; Sequence 2169, Application US/09657472
; Patent No. 6727063

; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2169
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2169

Query Match 55.8%; Score 13.4; DB 4; Length 21;
Best Local Similarity 93.3%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      9 CCTGCTCTGGAGGCC 23
Db     18 CCTGCTCRGGAGGCC 4

RESULT 38
US-09-396-196G-3026
; Sequence 3026, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3026

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGAGGCC 23
Db      2 ATCCAGACATGCTCTGTAGGGC 24

RESULT 39
US-09-396-196G-3027
; Sequence 3027, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3027
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3027

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGAGGCC 23
Db      1 ATCCAGACATGCTCTGTAGGGC 23

RESULT 40
US-09-396-196G-15020
; Sequence 15020, Application US/09396196G
```

```
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15020
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15020

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CAACCCCTGCTCTGGA 19
Db      9 CAAGCCTGCTCTGGA 23

Search completed: November 18, 2005, 11:21:58
Job time : 47.6312 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-3

Perfect score: 24

Sequence: 1 ATGCCAACCTGCTCTGGAGGCT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

```

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10I_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-08-469-172-3
2	24	100.0	24	20	US-10-788-779-3
3	19.2	80.0	25	26	US-11-036-317-8035
4	17.8	74.2	25	26	US-11-036-317-18356
5	17.8	74.2	25	26	US-11-036-317-584705

```

6 16.6 69.2 25 22 US-10-719-900-833111 Sequence 833111,
7 16.6 69.2 25 22 US-10-719-900-924760 Sequence 924760, A
8 16.6 69.2 25 22 US-10-809-189-54586 Sequence 54586, A
9 16.6 69.2 25 24 US-10-719-956-188380 Sequence 188380,
c 10 16.2 67.5 25 26 US-10-719-900-174561 Sequence 174561,
c 11 16.2 67.5 25 26 US-11-036-317-584704 Sequence 584704,
c 12 16.2 67.5 25 26 US-11-060-756-77825 Sequence 77825, A
c 13 15.8 65.8 25 22 US-10-719-900-53167 Sequence 53167, A
c 14 15.8 65.8 25 22 US-10-809-189-54585 Sequence 54585, A
c 15 15.8 65.8 41 19 US-10-035-833A-1677 Sequence 1677, Ap
c 16 15.8 65.8 41 19 US-10-035-833A-7225 Sequence 7225, Ap
c 17 15.6 65.0 45 22 US-10-887-230-21 Sequence 21, Appl
c 18 15.4 64.2 25 26 US-11-036-317-327390 Sequence 327390,
c 19 15.2 63.3 25 22 US-10-719-900-170847 Sequence 170847,
c 20 15.2 63.3 25 22 US-10-719-900-170848 Sequence 170848,
c 21 15.2 63.3 25 22 US-10-719-900-352179 Sequence 352179,
c 22 15.2 63.3 25 22 US-10-719-900-513335 Sequence 513335,
c 23 15.2 63.3 25 22 US-10-719-900-796279 Sequence 796279,
c 24 15.2 63.3 25 22 US-10-956-157-196604 Sequence 196604,
c 25 15.2 63.3 25 24 US-10-719-956-26759 Sequence 26759, A
c 26 15.2 63.3 25 24 US-10-719-956-95487 Sequence 95487, A
c 27 15.2 63.3 25 24 US-10-719-956-671714 Sequence 671714,
c 28 15.2 63.3 25 26 US-11-036-317-52603 Sequence 52603, A
c 29 15.2 63.3 25 26 US-11-036-317-194782 Sequence 194782,
c 30 15.2 63.3 25 26 US-11-036-317-257640 Sequence 257640,
c 31 15.2 63.3 25 26 US-11-036-317-294807 Sequence 294807,
c 32 15.2 63.3 25 26 US-11-036-317-305597 Sequence 305597,
c 33 15.2 63.3 25 26 US-11-036-317-311815 Sequence 311815,
c 34 15.2 63.3 25 26 US-11-036-317-322925 Sequence 322925,
c 35 15.2 63.3 25 26 US-11-036-317-443709 Sequence 443709,
c 36 15.2 63.3 25 26 US-11-060-756-256216 Sequence 256216,
c 37 15.2 63.3 29 24 US-10-885-190B-2 Sequence 2, Appli
c 38 15 62.5 25 20 US-10-775-169-2685 Sequence 2685, Ap
c 39 15 62.5 25 22 US-10-719-900-13488 Sequence 13488, A
c 40 15 62.5 25 22 US-10-719-900-408446 Sequence 408446,
c 41 15 62.5 25 22 US-10-719-900-833110 Sequence 833110,
c 42 15 62.5 25 22 US-10-719-900-924759 Sequence 924759, A
c 43 15 62.5 25 22 US-10-809-189-63266 Sequence 63266, A
c 44 15 62.5 25 22 US-10-809-189-127234 Sequence 127234,
c 45 15 62.5 25 24 US-10-719-956-188382 Sequence 188382,

```

ALIGNMENTS

```

RESULT 1
US-08-469-172-3
; Sequence 3, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```



```
RESULT 5
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 924760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-924760

Query Match          69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAGGCT 23
    |||||
Db 3 ATGCCAACCTGCTCTGGAGGCT 25
    |||||

RESULT 6
; US-10-809-189-54586
; Sequence 54586, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54586
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-10-809-189-54586

Query Match          69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGGCT 24
    |||||
Db 1 TGCCAACCTGCTCTAGAGTCT 23
    |||||

RESULT 7
; US-10-719-900-924760
; Sequence 924760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 188380
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-188380

Query Match          69.2%; Score 16.6; DB 24; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGGCT 24
    |||||
Db 3 TGCCAACCTGCTCTAGAGTCT 25
    |||||

RESULT 8
; US-10-719-900-924760
; Sequence 924760, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 584705
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-036-317-584705

Query Match          74.2%; Score 17.8; DB 26; Length 25;
Best Local Similarity 90.5%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAACCTGCTCTGGAGGCT 24
    |||||
Db 1 CCAACCTACTCTGATGCT 21
    |||||

RESULT 9
; US-10-719-900-833111
; Sequence 833111, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 833111
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-833111

Query Match          69.2%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGGCT 24
    |||||
Db 3 TGCCAACCTGCTCTAGAGTCT 25
    |||||

RESULT 9
; US-10-719-900-924760
; Sequence 924760, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
```

```
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77825
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-77825

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCCT 24
      ||| ||| ||| ||| ||| ||| |||
Db      23 CCATCCCTTCTCTGGAGTCCT 3

RESULT 10
US-10-719-900-174561/c
; Sequence 174561, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 174561
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-174561

Query Match      67.5%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGCCACCCCTCTCTGGAGGC 22
      ||| ||| ||| ||| ||| ||| |||
Db      22 TGCCACACTGATCTGGAGGC 2

RESULT 11
US-11-036-317-584704
; Sequence 584704, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 584704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-584704

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCCT 24
      ||| ||| ||| ||| ||| ||| |||
Db      1 CCAACCCCTACTCAGGATGCCT 21

RESULT 12
US-11-060-756-77825/c
; Sequence 77825, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
```

```
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77825
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-77825

Query Match      67.5%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CCAACCCCTGCTCTGGAGGCCT 24
      ||| ||| ||| ||| ||| ||| |||
Db      23 CCATCCCTTCTCTGGAGTCCT 3

RESULT 13
US-10-719-900-53167
; Sequence 53167, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-53167

Query Match      65.8%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCCAACCCCTGCTCTGGA 19
      ||| ||| ||| ||| ||| ||| |||
Db      1 AAGCCATCCCTGCTCTGGA 19

RESULT 14
US-10-809-189-54585
; Sequence 54585, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
```

US-10-809-189-54585

Query Match 65.8%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAAACCTGCTCTGGAG 20
||||| ||||| ||||| |||||
DB 7 TGCCAAACCTGCTCTAGAG 25

RESULT 15

US-10-035-833A-1677/c
; Sequence 1677, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuhio
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1677
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-1677

Query Match 65.8%; Score 15.8; DB 19; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
DB 25 CCAAYCCTACTCTGGGCT 5

RESULT 16

US-10-035-833A-7225/c
; Sequence 7225, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuhio
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7225
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-7225

Query Match 65.8%; Score 15.8; DB 19; Length 41;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCAACCTGCTCTGGAGGCT 24
||||| ||||| ||||| |||||
DB 25 CCAAYCCTACTCTGGGCT 5

RESULT 17

US-10-887-230-21/c

; Sequence 21, Application US/10887230
; Publication No. US20050042218A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: MHC Class I - Peptide-Antibody Conjugates with Modified
; FILE REFERENCE: B2-Microglobulin
; CURRENT APPLICATION NUMBER: US/10/887,230
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/485,716
; PRIOR FILING DATE: 2003-7-10
; PRIOR APPLICATION NUMBER: US 60/513,043
; PRIOR FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer used in Production of VH Cassette/CH1/hinge
US-10-887-230-21

Query Match 65.0%; Score 15.6; DB 22; Length 45;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGCTCTGGAGGC 22
||||| ||||| ||||| |||||
DB 40 ATGCCAACCTGCTGGAGGC 19

RESULT 18

US-11-036-317-327390/c
; Sequence 327390, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 327390
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-327390

Query Match 64.2%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCCTGCTCTGGAGGCC 23
||| ||||| ||||| |||||
DB 17 ACTCTGCTCTGGAGGCC 1

RESULT 19

US-10-719-900-170847
; Sequence 170847, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170847
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-170847

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGGC 22
|||||
Db 2 GCCAACCTGCTTTGAGGC 21

RESULT 20

US-10-719-900-170848
; Sequence 170848, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-170848

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGGC 22
|||||
Db 2 GCCAACCTGCTTTGAGGC 21

RESULT 21

US-10-719-900-352179/c
; Sequence 352179, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 352179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-352179

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCTGGAGGCCT 24
|||||

Db 23 CAACCAAGCTCTGGAGACCT 4

RESULT 22

US-10-719-900-513335
; Sequence 513335, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 513335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-513335

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGCCAACCTGCTCTGGAG 20
|||||
Db 2 ATGCCATCTTGTCTCAGGAG 21

RESULT 23

US-10-719-900-796279
; Sequence 796279, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 796279
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-796279

Query Match 63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCTGGAGGCCT 24
|||||
Db 2 CAACGCTGCGCTGGAGCCT 21

RESULT 24

US-10-956-157-196604/c
; Sequence 196604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04

```

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred.No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCCAACCTGTCTCGGAG 20
    |||||
Db 23 ATGCCAGCCTGTCTCGGAAG 4
    |||||

```

```

RESULT 29
US-11-036-317-194782/c
; Sequence 194782, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639

```

```
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 194782
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-194782

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCCAACCCCTGCTCTGGAGGC 22
Db      23 GCCCACCCCTGCTCTGCATGC 4

RESULT 30
US-11-036-317-257640/c
; Sequence 257640, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 257640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-257640

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCCAACCCCTGCTCTGGAGGC 22
Db      21 GCCCACCCCTGCTCTGCATGC 2

RESULT 31
US-11-036-317-294807/c
; Sequence 294807, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 294807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-294807

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 GCCAACCCCTGCTCTGGAGGC 22
Db      24 GCCCACCCCTGCTCTGCATGC 5

RESULT 32
US-11-036-317-305597/c
; Sequence 305597, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 305597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-305597

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCCAACCCCTGCTCTGGAGGC 22
Db      20 GCCCACCCCTGCTCTGCATGC 1

RESULT 33
US-11-036-317-311815/c
; Sequence 311815, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 311815
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-311815

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GCCAACCCCTGCTCTGGAGGC 22
Db      22 GCCCACCCCTGCTCTGCATGC 3

RESULT 34
US-11-036-317-322925/c
; Sequence 322925, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
```

FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 322925
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-322925

Query Match 63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGCC 22
Db 25 GCCAACCTGCTCTGCATGC 6

RESULT 35

US-11-036-317-443709
Sequence 443709, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 443709
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-443709

Query Match 63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAACCTGCTCTGGAGCCT 24
Db 2 CAACCTGCTCTGGTGACT 21

RESULT 36

US-11-060-756-256216/c
Sequence 256216, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 256216
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-256216

Query Match 63.3%; Score 15.2; DB 26; Length 25;

Best Local Similarity 85.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CCACCCCTGCTCTGGAGCC 23
Db 20 CCATCCCTTCTCTGGAGTCC 1

RESULT 37

US-10-885-190B-2/c
Sequence 2, Application US/10885190B
Publication No. US20050202548A1
GENERAL INFORMATION:
APPLICANT: Hoffmann-La Roche Inc.
TITLE OF INVENTION: Crystal structure of OSC
FILE REFERENCE: Case 21797
CURRENT APPLICATION NUMBER: US/10/885,190B
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human oxidosqualene synthase nucleotide probe with XbaI site inserted
US-10-885-190B-2

Query Match 63.3%; Score 15.2; DB 24; Length 29;
Best Local Similarity 85.0%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCAACCTGCTCTGGAGCC 22
Db 20 GCCAACCTGATCTAGAGCC 1

RESULT 38

US-10-775-169-2685/c
Sequence 2685, Application US/10775169
Publication No. US2004017543A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dörner, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2685
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-10-775-169-2685

Query Match 62.5%; Score 15; DB 20; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGCCAACCTGCTCTGGAGCCT 24
Db 25 TGTCACCTGCTCTGGGTACCT 3

RESULT 39

US-10-719-900-13488
Sequence 13488, Application US/10719900
Publication No. US2005026164A1

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13488

Query Match      62.5%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. NO. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATGCCAACCTGCTCTGGAGGCC 23
        | | | | | | | | | | | | | |
Db      2 AAGCCAGACCTGCGCTGGAGGAC 24

RESULT 40
US-10-719-900-408446
; Sequence 408446, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 408446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-408446

Query Match      62.5%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. NO. 5.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATGCCAACCTGCTCTGGAGGCC 23
        | | | | | | | | | | | | | |
Db      3 AAGCCAGACCTGCGCTGGAGGAC 25

Search completed: November 18, 2005, 15:41:04
Job time : 323.586 secs
```


Result No.	Query			DB	ID	Description
	Score	Match	%			
1	24	100.0	24	6	I12897	Sequence 4
2	16.2	67.5	34	6	A52065	Sequence 21
3	16.2	67.5	34	6	AR067674	Sequence 21
4	16.2	67.5	34	6	AR169819	Sequence 21
5	16	66.7	35	6	E22424	Method for
6	16	66.7	35	6	E58671	Novel metal
7	15.2	63.3	25	6	AX663329	Sequence
8	14.8	61.7	49	6	CQ818593	Sequence
9	14.6	60.8	27	6	BD074127	Compositi
10	14.4	60.0	30	6	CQ857208	Sequence
11	14.4	60.0	30	6	AX793975	Sequence
12	14.2	59.2	28	6	CQ874317	Sequence
13	14	58.3	36	6	AR120382	Sequence
14	14	58.3	36	6	BD274040	Identific
15	14	58.3	36	6	BD274049	Identific
16	14	58.3	36	6	AR341073	Sequence
17	14	58.3	36	6	BD063391	Streptoco
18	14	58.3	38	6	AX061955	Sequence
19	14	58.3	41	6	AX514615	Sequence

```

TITLE      HUMAN PHOSPHODIESTERASE TYPE IVC, AND ITS PRODUCTION AND USE
JOURNAL    Patent: WO 9620281-A 21 04-JUL-1996;
COMMENT    CELTECH THERAPEUTICS LTD (GB)
FEATURES   Other publication AU 4270596 960719.
SOURCE     Location/Qualifiers
           1. 34
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

ORIGIN
Query Match      67.5%; Score 16.2; DB 6; Length 34;
Best Local Similarity 85.7%; Pred. No. 6.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  TTTCATGTTTCCAAAGTGCATG 22
    ||| ||| ||| ||| ||| ||| ||| |||
Db  3  TTTAAGCTTCCAAAGTGCATG 23
    ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
AR067674
LOCUS      AR067674          34 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5851784.
ACCESSION AR067674
VERSION    AR067674.1 GI:5998896
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.

REFERENCE   1 (bases 1 to 34)
AUTHORS    Owens,R.John., Perry,M.John. and Lumb,S.Mark.
TITLE      Human phosphodiesterase type IVC, and its production and use
JOURNAL    Patent: US 5851784-A 21 22-DEC-1998;
FEATURES   Location/Qualifiers
SOURCE     1. 34
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      67.5%; Score 16.2; DB 6; Length 34;
Best Local Similarity 85.7%; Pred. No. 6.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  TTTCATGTTTCCAAAGTGCATG 22
    ||| ||| ||| ||| ||| ||| ||| |||
Db  3  TTTAAGCTTCCAAAGTGCATG 23
    ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
AR169819
LOCUS      AR169819          34 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 21 from patent US 6291199.
ACCESSION AR169819
VERSION    AR169819.1 GI:17907735
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.

REFERENCE   1 (bases 1 to 34)
AUTHORS    Owens,R.John., Perry,M.John. and Lumb,S.Mark.
TITLE      Human phosphodiesterase type IVC, and its production and use
JOURNAL    Patent: US 6291199-A 21 18-SEP-2001;
FEATURES   Location/Qualifiers
SOURCE     1. 34
           /organism="unknown"
           /mol_type="unassigned DNA"

ORIGIN
Query Match      67.5%; Score 16.2; DB 6; Length 34;
Best Local Similarity 85.7%; Pred. No. 6.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy  2  TTTCATGTTTCCAAAGTGCATG 22
    ||| ||| ||| ||| ||| ||| ||| |||
Db  3  TTTAAGCTTCCAAAGTGCATG 23
    ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
E22424
LOCUS      E22424          35 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for gene cloning of protein.
ACCESSION  E22424
VERSION     E22424.1 GI:13024066
KEYWORDS    JP 1999032779-A/4.
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 35)
AUTHORS    Yoshikazu,I. and Akira,A.
TITLE      Method for gene cloning of protein
JOURNAL    Patent: JP 1999032779-A 4 09-FEB-1999;
            EDUCATIONAL FOUNDATION FUJITA GAKUEN,RYUJI HUNAKOSHI
COMMENT     OS Unidentified
            PN JP 1999032779-A/4
            PD 09-FEB-1999
            PF 24-JUL-1997 JP 1997214074
            PR
            PI YOSHIKAZU ICHIHARA,AKIRA AWAYA
            PC C12N15/09,C07K14/47,C12P21/02//(C12P21/02,C12R1:91),C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source 1..35
            /organism="Unidentified".

FEATURES   source
           1..35
           /organism="unidentified"
           /mol_type="genomic DNA"
           /db_xref="taxon:32644"

ORIGIN
Query Match      66.7%; Score 16; DB 6; Length 35;
Best Local Similarity 79.2%; Pred. No. 8.4e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  CTTTCATGTTTCCAAAGTGCATGAT 24
    ||| ||| ||| ||| ||| ||| ||| |||
Db  6  CTTTCATGTTTCCAAAGGAGGAGGCT 29
    ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
E58671
LOCUS      E58671          35 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Novel metallic protease.
ACCESSION  E58671
VERSION     E58671.1 GI:18629893
KEYWORDS    JP 2001017183-A/19.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 35)
AUTHORS    Yamaji,N., Nishimura,K. and Sasamata,M.
TITLE      Novel metallic protease
JOURNAL    Patent: JP 2001017183-A 19 23-JAN-2001;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS Homo sapiens (human)
            PN JP 2001017183-A/19
            PD 23-JAN-2001
            PF 09-JUL-1999 JP 1999196584
            PR
            PI NOBORU YAMAJI,KOICHI NISHIMURA,MIHO SASAMATA
            PC C12N15/09,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC
            C12N9/50,C12Q1/37,
            PC C12N15/00,C12N5/00

```

```
CC
FH Key Location/Qualifiers
FT source 1..35
FT /organism='Homo sapiens (human)'.

FEATURES
    source
        Location/Qualifiers
            1..35
            /organism='Homo sapiens'
            /mol_type='genomic DNA'
            /db_xref='taxon:9606'

ORIGIN
    Query Match 66.7%; Score 16; DB 6; Length 35;
    Best Local Similarity 79.2%; Pred. No. 8.4e+03;
    Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTCCAAAGTCATGAT 24
    ||||| ||||| ||||| |||||
Db 7 CCTCATCTTCTAGGTGATGAT 30
    ||||| ||||| ||||| |||||

RESULT 7
AX663329/c
LOCUS AX663329 25 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 36 from Patent WO20061086.
ACCESSION AX663329
VERSION AX663329.1 GI:29163676
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        other sequences; artificial sequences.
REFERENCE
    1 Fedér,J., Ramanathan,C. and Mintier,G.
    Human leucine-rich repeat containing protein, expressed
    predominantly in small intestine. HLRRS11
    Patent: WO 02061086-A 36 08-AUG-2002;
    Bristol-Myers Squibb Company (US)
FEATURES
    source
        Location/Qualifiers
            1..25
            /organism='synthetic construct'
            /mol_type='unassigned DNA'
            /db_xref='taxon:32630'
            /note='Synthesized oligonucleotide.'

ORIGIN
    Query Match 63.3%; Score 15.2; DB 6; Length 25;
    Best Local Similarity 85.0%; Pred. No. 2.2e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTCCAAAGTCGA 20
    ||||| ||||| ||||| |||||
Db 23 CTTTCGTGGCTCCAAAGTCGA 4
    ||||| ||||| ||||| |||||

RESULT 8
CQ818593/c
LOCUS CQ818593 49 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 23 from Patent WO2004039825.
ACCESSION CQ818593
VERSION CQ818593.1 GI:48427205
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        other sequences; artificial sequences.
REFERENCE
    1 freskg Rd.P.O., Franch,T., Gouliaev,A.H., Lunderof,M.D., Felding,J.,
    Olsen,B.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
    Jensen,K.B. and Pedersen,H.
    Enzymatic encoding
    Patent: WO 2004039825-A 23 13-MAY-2004;
    Nuevolution A/S (DK)
FEATURES
    source
        Location/Qualifiers
            1..49
            /organism='synthetic construct'

/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Artificially produced'

ORIGIN
    Query Match 61.7%; Score 14.8; DB 6; Length 49;
    Best Local Similarity 88.9%; Pred. No. 3.3e+04;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTCATGTTCCAAAGTCG 19
    ||||| ||||| ||||| |||||
Db 40 TTCATGTTCCAAAGTCG 23
    ||||| ||||| ||||| |||||

RESULT 9
BD074127/c
LOCUS BD074127 27 bp DNA linear PAT 27-AUG-2002
DEFINITION Composition binding specifically to colorectal cancer and
utilization thereof.
ACCESSION BD074127
VERSION BD074127.1 GI:22619730
KEYWORDS
SOURCE
    ORGANISM
        unidentified
        unclassified.
REFERENCE
    1 (Bases 1 to 27)
    Waldman,S.A., Pearlman,J.M., Barber,M.T., Schultz,S. and
    Parkinson,S.J.
    Composition binding specifically to colorectal cancer and
    utilization thereof
    Patent: JP 2001512666-A 18 28-AUG-2001;
    THOMAS JEFFERSON UNIVERSITY
    OS Unidentified
    PN JP 2001512666-A/18
    PD 28-AUG-2001
    PR 07-AUG-1998 JP 2000506228
    PF 07-AUG-1997 US 08/908643
    PI SCOTT A WALDMAN, JOSHUA M PEARLMAN, MICHAEL T BARBER, STEPHANIE
    PI SCHULTZ,
    PI SCOTT J PARKINSON
    PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/68, G01N33/
    PC 574//
    PC A61K31/7088, A61K39/00, A61K39/395, A61K48/00, A61P35/
    PC 00, A61P35/04,
    PC C12N15/00, C12N5/00
    CC Strandedness: Double;
    CC Topology: linear;
    CC Composition binding specifically to colorectal cancer and CC
    thereof
    FH Key Location/Qualifiers
    FT source 1..27
    FT /organism='Unidentified'.

FEATURES
    source
        Location/Qualifiers
            1..27
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

ORIGIN
    Query Match 60.8%; Score 14.6; DB 6; Length 27;
    Best Local Similarity 81.0%; Pred. No. 4.4e+04;
    Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTCATGAT 24
    ||||| ||||| ||||| |||||
Db 26 CATATGTTCCAAAGACGAGAT 6
    ||||| ||||| ||||| |||||

RESULT 10
CQ857208/c
LOCUS CQ857208 30 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 550 from Patent WO2004069997.
```

<hr/>							
REFERENCE	1						
AUTHORS	Bruggemann,M.						
TITLE	Genetically modified non-human mammals and cells						
JOURNAL	Patent: WO 2004076618-A 13 10-SEP-2004;						
FEATURES	THE BARHAM INSTITUTE (GB)						
source	Location/Qualifiers						
	1..28						
	/organism="synthetic construct"						
	/db_type="unassigned DNA"						
	/mol_type="taxon:32630"						
	/note="Gamma 2a b reverse primer"						
<hr/>							
ORIGIN							
Query Match	59.2%; Score 14.2; DB 6; Length 28;						
Best Local Similarity	84.2%; Pred.No.6.9e+04;						
Matches	16; Conservative	0; Mismatches	3; Indels	0; Gaps	0;		
<hr/>							
Qy	1 CTTTCATGTTTCCAAAGTGC 19						
Dd	8 CTTTCCTTTTCCCAAGTGC 26						
<hr/>							
RESULT 13							
LOCUS	AR120382 Sequence 258 from patent US 6159469.						
DEFINITION	Sequence 258 from patent US 6159469.						
ACCESSION	AR120382						
VERSION	AR120382.1 GI:14103958						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 36)						
AUTHORS	Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B., Fannon,M.R. and Rosen,C.A.						
TITLE	Streptococcus pneumoniae antigens and vaccines						
JOURNAL	Patent: US 6159469-A 258 12-DEC-2000;						
FEATURES	Location/Qualifiers						
source	1..36						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
<hr/>							
ORIGIN							
Query Match	58.3%; Score 14; DB 6; Length 36;						
Best Local Similarity	77.3%; Pred.No.8.6e+04;						
Matches	17; Conservative	0; Mismatches	5; Indels	0; Gaps	0;		
<hr/>							
Qy	3 TCATGTTTTCCAAAGTGCATGAT 24						
Dd	3 TCAAGCTTCCCAACTGTTGAT 24						
<hr/>							
RESULT 14							
BD274040	BD274040						
LOCUS	Identification of molecular interaction sites in RNA for novel drug discovery.						
DEFINITION	BD274040						
ACCESSION	BD274040.1 GI:33083808						
VERSION	JP 2002526030-A/7.						
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	other sequences; artificial sequences.						
REFERENCE	1 (bases 1 to 36)						
AUTHORS	Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.						
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery						
JOURNAL	Patent: JP 2002526030-A 7 20-AUG-2002;						
COMMENT	ISIS PHARMACEUTICALS INC						
	OS Artificial Sequence						
	PN JP 2002526030-A/7						
	PD 20-AUG-2002						
	PF 12-MAY-1999 JP 2000548510						

PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..36
FT /organism='Artificial Sequence'.
Location/Qualifiers
1..36
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

FEATURES
source

ORIGIN

Query Match 58.3%; Score 14; DB 6; Length 36;
Best Local Similarity 77.3%; Pred. No. 8.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TTCATGTTTCCAAAGTGCATGA 23
||||| ||| ||| ||| ||| |||
Db 3 TTCTGCTTCAACAGTGTGA 24

RESULT 15
BD274049 36 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
discovery.
BD274049

ACCESSION BD274049.1 GI:33083817
VERSION JP 2002526030-A/16.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 36)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 16 20-AUG-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002526030-A/16
PD 20-AUG-2002

PR 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..36
FT /organism='Artificial Sequence'.
Location/Qualifiers
1..36
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'

FEATURES
source

ORIGIN

Query Match 58.3%; Score 14; DB 6; Length 36;
Best Local Similarity 77.3%; Pred. No. 8.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TTCATGTTTCCAAAGTGCATGA 23
||||| ||| ||| ||| ||| |||
Db 3 TTCTGCTTCAACAGTGTGA 24

RESULT 16
AR341073 36 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 258 from patent US 6573082.
DEFINITION AR341073
ACCESSION AR341073
VERSION AR341073.1 GI:33733052

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 17

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PF

PR

PI

C12N15/31

G01N33/68

CC

CC

FH

KEY

LOCATION/QUALIFIERS

1..36

/organism='unidentified'

/mol_type='genomic DNA'

/db_xref='taxon:32644'

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 18

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AX061955

Sequence 3 from Patent WO0100837.

AX061955

AX061955.1

GI:12539939

PAT 24-JAN-2001

```

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    other sequences; artificial sequences.
1
AUTHORS     Thonnard,J.S.
TITLE       Babil11 polypeptide and polynucleotide from moraxella catharrhalis
JOURNAL     Patent: WO 0100817-A 3 04-JAN-2001;
SMITHKLINE BEECHAM BIOLOGICALS (S.A.)
FEATURES    Location/Qualifiers
            1..38
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 38;
Best Local Similarity 77.3%; Pred. No. 8.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TTCATGTTTCCAAAGTGCATGA 23
      ||| ||| ||| ||| ||| ||| |||
Db      35  TTAATTTTACCAAAATTCATGA 14

RESULT 19
AX514615/c
LOCUS      AX514615              41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION Sequence 813 from Patent WO02052044.
ACCESSION  AX514615
VERSION     AX514615.1  GI:23561172
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE       Detection of genetic polymorphisms
JOURNAL     Patent: WO 02052044-A 813 04-JUL-2002;
Riken (JP)
FEATURES    Location/Qualifiers
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 41;
Best Local Similarity 70.8%; Pred. No. 8.5e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1  CTTCATGTTTCCAAAGTGCATGAT 24
      ||| ||| ||| ||| ||| ||| |||
Db      24  CATVATGTTTCCAACTGCTGAAT 1

RESULT 20
AX520557/c
LOCUS      AX520557              41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION Sequence 6755 from Patent WO02052044.
ACCESSION  AX520557
VERSION     AX520557.1  GI:23571178
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE       Detection of genetic polymorphisms
JOURNAL     Patent: WO 02052044-A 6755 04-JUL-2002;
Riken (JP)
FEATURES    Location/Qualifiers
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 41;
Best Local Similarity 70.8%; Pred. No. 8.5e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1  CTTCATGTTTCCAAAGTGCATGAT 24
      ||| ||| ||| ||| ||| ||| |||
Db      24  CATVATGTTTCCAACTGCTGAAT 1

RESULT 21
AX697195
LOCUS      AX697195              46 bp      DNA      linear      PAT 02-APR-2003
DEFINITION Sequence 263 from Patent WO0078961.
ACCESSION  AX697195
VERSION     AX697195.1  GI:29498140
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   synthetic construct
Other sequences; artificial sequences.

REFERENCE   1
AUTHORS     Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
            Eaton,D.L., Gao,W.O., Pan,J., Botstein,D., Fong,S., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
            Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
            Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
            Patent: WO 0078961-A 263 28-DEC-2000;
            Genentech Inc. (US)
FEATURES    Location/Qualifiers
            1..46
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 46;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CTTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| |||
Db      13  CTTCATGATGCTCAAGTACATG 34

RESULT 22
AR355880
LOCUS      AR355880              50 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1998 from patent US 6593114.
ACCESSION  AR355880
VERSION     AR355880.1  GI:33761964
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.
Unclassified.

REFERENCE   1 (bases 1 to 50)
AUTHORS     Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
            Rosen,C.A.
TITLE       Staphylococcus aureus polynucleotides and sequences
JOURNAL     Patent: US 6593114-A 1998 15-JUL-2003;
Rosen,C.A.
FEATURES    Location/Qualifiers
            1..50
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 50;

```

```
Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 23
LOCUS AR537436 50 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1998 from patent US 6737248.
ACCESSION AR537436
VERSION AR537436.1 GI:53928653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 1998 18-MAY-2004;
FEATURES
source
Location/Qualifiers
1..50
/mol_type="genomic DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 50;
Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 24
LOCUS AR533926 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 173 from patent US 6733965.
ACCESSION AR533926
VERSION AR533926.1 GI:53923959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Echt,C.S. and Nelson,C.D.
TITLE Microsatellite DNA markers and uses thereof
JOURNAL Patent: US 6733965-A 173 11-MAY-2004;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTG 18
Db 3 TTGATGTTTCCAAATGT 19

RESULT 25
LOCUS BD002832 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002832
VERSION BD002832.1 GI:18630793

Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 23
LOCUS AR537436 50 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1998 from patent US 6737248.
ACCESSION AR537436
VERSION AR537436.1 GI:53928653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
TITLE Staphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 1998 18-MAY-2004;
FEATURES
source
Location/Qualifiers
1..50
/mol_type="genomic DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 50;
Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 7 TTGATGNTCTCAAGAACATGAT 29

RESULT 24
LOCUS AR533926 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 173 from patent US 6733965.
ACCESSION AR533926
VERSION AR533926.1 GI:53923959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Echt,C.S. and Nelson,C.D.
TITLE Microsatellite DNA markers and uses thereof
JOURNAL Patent: US 6733965-A 173 11-MAY-2004;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTG 18
Db 3 TTGATGTTTCCAAATGT 19

RESULT 25
LOCUS BD002832 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002832
VERSION BD002832.1 GI:18630793

KEYWORDS JP 2000245487-A/498.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 498 12-SEP-2000;
COMMENT
OS Unknown
PN JP 2000245487-A/498
PD 12-SEP-2000
PF 27-JAN-2000 JP 200019392
PI 27-JAN-1999 US 09/238.402
PI NIRA SHA,JANET WALINTON,NIRA PATEL
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..31
/organism='Unknown'.
FEATURES
source
Location/Qualifiers
1..31
/organism='unidentified'
/db_type='genomic DNA'
/mol_xref='taxon:32644'
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 31;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCAAAGTCATGAT 24
Db 1 TGTTCCAAAGTCATGAT 19

RESULT 26
LOCUS AX931884/c 35 bp DNA linear PAT 22-DEC-2003
DEFINITION Sequence 41 from Patent WO03087829.
ACCESSION AX931884
VERSION AX931884.1 GI:40312497
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Thunnissen,F.B., Klaassen,C.H. and Prinsen,C.F.
TITLE Human papilloma virus detection with dna microarray
JOURNAL Patent: WO 03087829-A 41 23-OCT-2003;
JOURNAL Dot Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1..35
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/notes='Description of Artificial Sequence: based on
genomic DNA sequence from Human Papilloma Virus'
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 35;
Best Local Similarity 88.2%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGT 17
Db 33 CTACATGTTTCCAAATGT 17

RESULT 27
LOCUS AR284732 47 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 784 from patent US 6528260.
```

```
ACCESSION AR284732
VERSION AR284732.1 GI:29721636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Blumenfeld, M., Chumakov, I., Bougueleret, L. and Cohen, A.
TITLE Biallelic markers related to genes involved in drug metabolism
JOURNAL Patent: US 6528260-A 784 04-MAR-2003;
FEATURES
    source
        1..47
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 47;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 6 TGTTCCTCAAAAGTCATGAT 24
    ||| ||| ||| ||| ||| ||| |||
Db 9 TGTCTCAAAAGTTGAYGAT 27
    ||| ||| ||| ||| ||| ||| |||
RESULT 28
AR565646
LOCUS AR565646 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 10 from patent US 6767738.
ACCESSION AR565646
VERSION AR565646.1 GI:53981680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gage, F.H., Palmer, T., Safar, F.G., Takahashi, J. and Takahashi, M.
TITLE Method of isolating adult mammalian CNS-derived progenitor stem
cells using density gradient centrifugation
JOURNAL Patent: US 6767738-A 10 27-JUL-2004;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTCATGA 23
    ||| ||| ||| ||| ||| ||| |||
Db 1 CATGTATTCAAAGACCATGA 20
    ||| ||| ||| ||| ||| ||| |||
RESULT 29
CQ880137
LOCUS CQ880137 26 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 1 from Patent EP1464710.
ACCESSION CQ880137
VERSION CQ880137.1 GI:54033904
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yamamoto, N., Ogura, M., Kawaguchi, M., Tsukada, M., Yoshii, H.,
Suzuki, T., Ishii, M. and Fukui, T.
TITLE Infectious etiologic agent detection probe and probe set, carrier,
and genetic screening method
JOURNAL Patent: EP 1464710-A 1 06-OCT-2004;
CANON KABUSHIKI KAISHA (JP)
FEATURES
    Location/Qualifiers
ORIGIN
Query Match 56.7%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTCATGA 23
    ||| ||| ||| ||| ||| ||| |||
Db 20 CATGTTTCCAAAGTGAAGA 1
    ||| ||| ||| ||| ||| ||| |||
RESULT 31
BD170377/c
LOCUS BD170377/c 27 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel formate dehydrogenase and process for producing the same.
ACCESSION BD170377
VERSION BD170377.1 GI:27876189
KEYWORDS WO 0246427-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Takaoka, Y. and Namba, H.
TITLE Novel formate dehydrogenase and process for producing the same
JOURNAL Patent: WO 0246427-A 7 13-JUN-2002;
KANAKA CORP., YASUKO TAKAOKA, HIROKAZU NAMBA
COMMENT OS Artificial Sequence
PN WO 0246427-A/7
PD 13-JUN-2002
PF 04-DEC-2001 WO 2001JP010569
PR 04-DEC-2000 JP 00P 368838
PI YASUKO TAKAOKA, HIROKAZU NAMBA
PC C12N15/53, C12N9/04, C12N1/21
```


CC Description of Artificial Sequence: primer-5
FH Key Location/Qualifiers
FT source 1..27
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATG 22

Db 24 TCATGCTGCGAGGTGCATG 5

RESULT 32

AR290927/c AR290927 47 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 2662 from patent US 6537751.
DEFINITION AR290927
ACCESSION AR290927
VERSION AR290927.1 GI:31678211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 2662 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 56.7%; Score 13.6; DB 6; Length 47;
Best Local Similarity 72.7%; Pred. No. 1.4e+05;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATG 24

Db 33 TCATGAATYAAATTCATGAT 12

RESULT 33

AR190122/c AR190122 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5610 from patent US 6346398.
DEFINITION AR190122
ACCESSION AR190122
VERSION AR190122.1 GI:20236087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5610 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 GTTTCCTCAAGTGCAT 21
Db 16 GTTTCCTCAAGAGCAT 2

RESULT 34

AR190123/c AR190123 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5611 from patent US 6346398.
DEFINITION AR190123
ACCESSION AR190123
VERSION AR190123.1 GI:20236088
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5611 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21

Db 15 GTTTCCTCAAGAGCAT 1

RESULT 35

AR325098/c AR325098 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 2500 from patent US 6566127.
DEFINITION AR325098
ACCESSION AR325098
VERSION AR325098.1 GI:33710906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2500 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCTCAAGTGCAT 21

Db 16 GTTTCCTCAAGAGCAT 2

RESULT 36

AR325099/c AR325099 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 2501 from patent US 6566127.
DEFINITION AR325099
ACCESSION AR325099
VERSION AR325099.1 GI:33710907

Query Match 55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;

```

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2501 20-MAY-2003;
FEATURES    Location/Qualifiers
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCCAAAGGCAT 21
    |||||
Db 15 GTTCCAAAGGCAT 1

RESULT 37
DOGP47701/c
LOCUS       DOGP47701      18 bp      DNA      linear      MAM 19-JAN-1996
DEFINITION Dog (Clone: CXK.477) primer for STS 477, 5' end.
ACCESSION   L24354
VERSION     L24354.1 GI:404031
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     1 of 2
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE   1 (bases 1 to 18)
AUTHORS     Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE       One hundred and one new simple sequence repeat-based markers for
            the canine genome
JOURNAL     Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE     95268214
PUBMED      7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EOostrander@bl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile: Denaturation: 94 degrees C for 1.00 minute
            Annealing: 55 or 59 degrees C for 0.45 minutes
            Polymerization: 74 degrees C for 1.00 minutes
            PCR Cycles: 33
            Final Extension: 74 degrees C for 5.00 minutes.
            Location/Qualifiers
            1..18
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /db_xref="taxon:9615"
            /tissue_type="spleen"
            /dev_stages="adult"
            /tissue_lib="E. Ostrander, in pBluescript+"

FEATURES    primer_bind
            1..18
ORIGIN
Query Match      55.8%; Score 13.4; DB 4; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TTTCCAAAGTCATG 22
    |||||
Db 15 TTTCCAAAGGCATG 1

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 2501 20-MAY-2003;
FEATURES    Location/Qualifiers
            1..17
            /organism="unknown"
            /mol_type="unassigned RNA"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTCCAAAGGCAT 21
    |||||
Db 15 GTTCCAAAGGCAT 1

RESULT 38
DOGP47701/c
LOCUS       DOGP47701      20 bp      DNA      linear      PAT 15-JUL-2002
DEFINITION Sequence 239 from Patent EP1217079.
ACCESSION   AX462495
VERSION     AX462495.1 GI:21885708
KEYWORDS
SOURCE      Aegilops tauschii
ORGANISM    Aegilops tauschii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Aegilops.

REFERENCE   1
AUTHORS     Bernard,M., Sourdille,P. and Guyomarch,H.
TITLE       Microsatellite markers from Triticum tauschii
JOURNAL     Patent: EP 1217079-A 239 26-JUN-2002;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES    Location/Qualifiers
            1..20
            /organism="Aegilops tauschii"
            /mol_type="unassigned DNA"
            /db_xref="taxon:37682"

ORIGIN
Query Match      55.8%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TTCCAAAGTCATGA 23
    |||||
Db 4 TTCCAAAGTCATGA 18

RESULT 39
AB166618/c
LOCUS       AB166618      23 bp      DNA      linear      SYN 07-OCT-2004
DEFINITION Synthetic construct DNA, forward primer for microsatellite
            NRD1KM020.
ACCESSION   AB166618
VERSION     AB166618.1 GI:51850034
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    Ithara,N.; Takasuga,A., Mizoshita,K., Takeda,H., Sugimoto,M.,
            Mizoguchi,Y., Hirano,T., Itoh,T., Watanabe,T., Reed,K.M.,
            Snelling,W.M., Kappes,S.M., Beattie,C.W., Bennett,G.L. and
            Sugimoto,Y.
            A comprehensive genetic map of the cattle genome based on 3802
            microsatellites
JOURNAL     Genome Res. 14 (10), 1987-1998 (2004)
PUBMED      15466297
REFERENCE   2 (bases 1 to 23)
AUTHORS     Sugimoto,Y., Ihara,N. and Mizoshita,K.
TITLE       Direct Submission
JOURNAL     Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shirakawa Institute of
            Animal Genetics; Odakura, Nishigo, Nishi-shirakawa, Fukushima
            961-8061, Japan (E-mail:kazusugi@siag.or.jp, Tel:81-248-25-5641,
            Fax:81-248-25-5725)
FEATURES    Location/Qualifiers
            1..23
            /organism="synthetic construct"
            /mol_type="other DNA"
            /db_xref="taxon:32630"
            /chromosome="20"

misc_feature 1..23
            /note="forward primer for microsatellite NRD1KM020"

ORIGIN

```

Query Match 55.8%; Score 13.4; DB 12; Length 23;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAG 16
Db 16 TTCATGTTTCCAAAG 2

RESULT 40
A94624/c A94624 29 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 7 from Patent EP0943679.
ACCESSION A94624
VERSION A94624.1 GI:6778935
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 29)
AUTHORS
TITLE Novel RNase-like protein and its use
JOURNAL Patent: EP 0943679-A 7 22-SEP-1999;
INNOGENETICS NV (BE)
FEATURES
source 1..29
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 55.8%; Score 13.4; DB 6; Length 29;
Best Local Similarity 73.9%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
Db 26 CTTTCATGTTTCCAAAGTGCATGA 4

Search completed: November 18, 2005, 17:42:53
Job time : 667.986 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 165.262 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTCAATGTTCCAAAGTCATCAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	2	AAQ91124
2	24	100.0	24	9	ACA63114
3	24	100.0	24	13	ADR05300
4	16.4	68.3	41	4	AHA46257
5	16.2	67.5	34	2	AAT34642
6	16	66.7	35	2	AAH18400
7	16	66.7	35	4	AAH20236
8	15.2	63.3	25	6	ABS63500
9	15	62.5	38	6	ADP30162
10	14.8	61.7	20	12	ADP21883
11	14.8	61.7	20	12	ADP21988
12	14.6	61.7	49	12	ADO04093
13	14.6	60.8	27	2	AAH27821
14	14.6	60.8	34	12	ADO41360
15	14.6	60.8	41	10	AAH57225
16	14.6	60.8	41	10	AAH57224
17	14.4	60.0	30	6	ABX70212
18	14.4	60.0	30	13	ADR23060
19	14.4	60.0	33	6	AAH45772
20	14.4	60.0	37	8	ABT42676

21	14.2	59.2	20	4	AAF87048	Aaf87048 PCR prime
22	14.2	59.2	20	12	ADL59164	Adl59164 Human ESM
23	14.2	59.2	20	12	ADL58982	Adl58982 Human ESM
24	14.2	59.2	33	6	ABV74729	Abv74729 Human cia
25	14.2	59.2	50	6	ABZ04574	Abz04574 Human leu
26	14.2	59.2	50	10	ADG33666	Adg33666 Human DNA
27	14.2	59.2	50	12	ADP10108	Adp10108 50-mer ol
28	14	58.3	25	9	ACK15268	Ack15268 Human mic
29	14	58.3	27	10	ABX95855	Abx95855 PCR prime
30	14	58.3	28	12	ADH27316	Adh27316 Ferritin
31	14	58.3	28	12	ADH27295	Adh27295 Ferritin
32	14	58.3	28	12	ADH27302	Adh27302 Ferritin
33	14	58.3	28	12	ADH27288	Adh27288 Ferritin
34	14	58.3	29	12	ADH27309	Adh27309 Ferritin
35	14	58.3	32	13	ADR33465	Adr33465 Human nic
36	14	58.3	33	6	ABK11366	Abk11366 NADH dehy
37	14	58.3	36	2	AAV27468	Aav27468 Streptoco
38	14	58.3	36	3	AAA70860	Aaa70860 Molecular
39	14	58.3	36	3	AAA70869	Aaa70869 Molecular
40	14	58.3	36	6	ABQ84936	Abq84936 Streptoco
41	14	58.3	36	10	ADC45339	Adc45339 S. pneumo
42	14	58.3	38	4	AAF30041	Aaf30041 Moraxella
43	14	58.3	41	6	ABS55299	Abs55299 Human leu
44	14	58.3	46	3	AAA37264	Aaa37264 Human PRO
45	14	58.3	46	4	AAF54390	Aaf54390 Primer #7

ALIGNMENTS

RESULT 1
AAQ91124
ID AAQ91124 standard; cDNA; 24 BP.
XX AC AAQ91124;
XX DT 19-FEB-1996 (first entry)
XX DE Beta-cardiac myosin heavy chain PCR primer B'.
XX KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
XX KW diagnosis; primer; mutation; detection; ss.
XX OS Synthetic.
XX FN US429923-A.
XX PD 04-JUL-1995.
XX PF 11-DEC-1992; 92US-00989160.
XX PR 11-DEC-1992; 92US-00989160.
XX PA (HARD) HARVARD COLLEGE.
XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX PA (GEHO-) GEN HOSPITAL SHENYANG MILITARY AREA.
XX PI Seidman J, Seidman C, Watkins H, Rosenzweig A;
XX WPI; 1995-245715/32.
XX PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
XX useful for testing asymptomatic individual(s).
XX PS Example 1; Col 10; 22pp; English.

AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. they are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 24 BP; 6 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCATGTTTCCAAAGTCATCAT 24
DB 1 CTTTCATGTTTCCAAAGTCATCAT 24

RESULT 4
AAH46257/C
ID AAH46257 standard; DNA; 41 BP.
XX
XX AAH46257;
AC
XX
XX 25-SEP-2001 (first entry)
XX
XX Aldehyde/ketone reductase 9 probe, SEQ ID NO:8.
DE
XX Aldehyde/ketone reductase 9; human; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200146433-A1.
XX
XX 28-JUN-2001.
XX
XX 18-DEC-2000; 2000WO-CN0000607.
XX
XX 22-DEC-1999; 99CN-00125681.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-441679/47.
XX
XX Aldehyde/ketone reductase 9 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation.
XX
XX Example 7; Page 16; 39pp; Chinese.

XX The invention relates to aldehyde/ketone reductase 9 (AAH98900), nucleic
CC acids encoding it (AAH46257), and a method for the recombinant production
CC of the protein. The present invention additionally discloses an agonist
CC of aldehyde/ketone reductase 9 for therapeutic use, and an antibody which
CC specifically binds to aldehyde/ketone reductase 9. Aldehyde/ketone
CC reductase 9, and nucleotides which encode it may be used for treating a
CC variety of diseases, such as malignant tumours, blood diseases, HIV
CC (human immunodeficiency virus) infection, immune disorders and
CC inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH46257-AAH46258 represent aldehyde/
CC ketone reductase 9 probes used in an exemplification of the invention
XX

XX Sequence 41 BP; 10 A; 11 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 68.3%; Score 16.4; DB 4; Length 41;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCATGTTTCCAAAGTGCA 20
DB 37 TCATGTTTCCAAAGTGCA 20

RESULT 5
AAT34642
ID AAT34642 standard; DNA; 34 BP.
XX
XX AAT34642;
AC
XX
XX 14-FEB-1997 (first entry)
XX
XX Primer for human phosphodiesterase type IV D.
DE
XX Phosphodiesterase; screening; identification; inhibitor; inhibition; PDE;
KW treatment; prophylaxis; inflammatory disease; inflamed lung; asthma.
KW
XX Synthetic.
OS
XX WO9620281-A1.
XX
XX 04-JUL-1996.
XX
XX 21-DEC-1995; 95WO-GB003006.
XX
XX 23-DEC-1994; 94GB-00026227.
XX
XX 26-JUN-1995; 95GB-00012996.
XX
XX (CLLT) CELLTech THERAPEUTICS LTD.
XX
XX Owens RJ, Perry MJ, Lumb SM;
XX
XX WPI; 1996-321854/32.
XX
XX Human phosphodiesterase type IVC and selective inhibitors - used in the
XX treatment of inflammatory disease, esp. asthma.

XX Disclosure; Page 15; 50pp; English.

XX Recombinant phosphodiesterase (PDE) type IVC may be used to screen for
CC inhibitors of PDE IVC. The inhibitors may be used in pharmaceutical for
CC the treatment and prophylaxis of inflammatory diseases, especially
CC inflamed lung associated with asthma. Multiple isoforms of PDE exist
CC opening the possibility for individual inhibitors of each isoform. The
CC distribution of PDE IV isoform mRNAs in different human tissues was
CC analysed by northern blotting. Human multiple tissue northern blots were
CC hybridised with isoform specific probes generated by PCR from the 3' non-
CC translated region of each gene. Either HL-60 genomic DNA (probes A and C)
CC or a cDNA library prepared from eosinophil enriched mRNA (probes B and D)
CC were used as templates for the PCR reaction with two primers (AAT34642,


```

PD 08-AUG-2002.
XX
XX PF 20-DEC-2001; 2001WO-US049739.
XX PR 22-DEC-2000; 2000US-0257774P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Feder J, Ramanathan C, Mintier G;
XX WPI; 2002-619252/66.
XX
XX PT New isolated nucleic acid molecules encoding HLRRS11 polypeptides, or
XX their fragments and homologues, useful for preventing, treating and
XX ameliorating medical conditions, e.g. proliferative, gastrointestinal, or
XX renal disorders.
XX
XX PS Example 57; Page 287; 336pp; English.
XX
XX CC The invention relates to isolated nucleic acid molecules (I) encoding
XX human leucine-rich repeat small intestine I (HLRRS11) polypeptides. The
XX nucleic acid molecules and polypeptides are useful for preventing,
XX treating and ameliorating medical conditions, such as proliferative,
XX gastrointestinal, renal, neural, or reproductive disorders; or disorders
XX related to aberrant calcium regulation or apoptosis modulation, either
XX directly or indirectly. They are also useful for treating, preventing
XX and/or diagnosing diseases, disorders and/or conditions of: immune system
XX by activating or inhibiting the proliferation, differentiation, or
XX mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,
XX anaemia; immunologic deficiency syndromes, e.g. human immune deficiency
XX virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,
XX e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,
XX myasthenia gravis; asthma or allergic reactions; inflammatory conditions,
XX e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;
XX cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,
XX aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's
XX chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral,
XX bacterial, and fungal infections. The HLRRS11 polypeptides are useful for
XX modulating cytokine production, antigen presentation or other processes
XX such as boosting immune responses. ABS63485-ABS63504 represent HLRRS11
XX coding sequences and PCR primers of the invention
XX
XX SQ Sequence 25 BP; 5 A; 7 C; 7 G; 4 T; 2 U; 0 Other;
Query Match 63.3%; Score 15.2; DB 6; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCA 20
Db 23 CTTTCGTGGCTCCAAAGTGCA 4

RESULT 9
AAD30162/c
ID AAD30162 standard; DNA; 38 BP.
XX
XX AC AAD30162;
XX
XX DT 17-MAY-2002 (first entry)
XX
XX DE HA-tagged human MCIP1 splice variant 4 isolating PCR primer #1.
XX
XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
XX heart failure; cardiomyopathy; heart disease; human; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200204491-A2.
XX
XX XX 17-JAN-2002.
XX
XX PF 06-JUL-2001; 2001WO-US021662.
XX
XX PD 07-JUL-2000; 2000US-0216601P.
XX PR 13-FEB-2001; 2001US-00782953.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX (WILL/) WILLIAMS S R.
XX (ROTH/) ROTHERMEL B.
XX
XX PI Williams SR, Rothermel B;
XX WPI; 2002-179698/23.
XX
XX PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
XX binding, expression or phosphorylation, useful for treating cardiac
XX hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
XX test compound.
XX
XX PS Example 1; Page 78; 174pp; English.
XX
XX CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
XX and nucleic acid molecules encoding such proteins. MCIPs form a physical
XX complex with the catalytic subunit of calcineurin and increased levels of
XX MCIPs correspond to a reduced ability of calcineurin to stimulate
XX transcription of certain target genes. The invention also relates to
XX methods for identifying modulators of MCIP binding, expression or
XX phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
XX may be used for treating cardiac hypertrophy and heart failure.
XX Antibodies to MCIP can be used in characterising the MCIP content of
XX healthy and diseased tissues and subsequently for determining the
XX presence or absence of cardiomyopathy or as predictor of heart disease.
XX The present sequence is a PCR primer used to isolate HA-tagged human
XX MCIP1 splice variant 4
XX
XX SQ Sequence 38 BP; 14 A; 6 C; 5 G; 13 T; 0 U; 0 Other;
Query Match 62.5%; Score 15; DB 6; Length 38;
Best Local Similarity 78.3%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGATGAT 24
Db 26 TTAAGTTTCTAAAGATGATGAT 4

RESULT 10
ADP21883
ID ADP21883 standard; DNA; 20 BP.
XX
XX AC ADP21883;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Ornithine decarboxylase 1 antisense oligonucleotide seqid 31.
XX
XX KW cytosolic; gene therapy; ornithine decarboxylase 1;
XX ornithine decarboxylase 1 associated disorder;
XX hyperproliferative disorder; cancer; human; antisense oligonucleotide;
XX antisense technology; ss.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "OTHER= Phosphorothioate backbone. All cytidines
XX are 5-methylcytidines"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX modified_base 15..20
XX /tag= c

```

```

FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FN US2004110148-A1.
PD 10-JUN-2004.
XX 10-DEC-2002; 2002US-00316244.
XX 10-DEC-2002; 2002US-00316244.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie KW;
XX WPI; 2004-440337/41.
DR New oligonucleotide compound that inhibits expression of ornithine
XX decarboxylase 1, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g. cancer.
XX Example 15; SEQ ID NO 31; 69pp; English.
XX The invention describes a new compound, having a sequence comprising 8-80
XX bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
XX specifically hybridises with the nucleic acid encoding ornithine
XX decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
XX ornithine decarboxylase 1 in cells or tissues; screening for a
XX modulator of ornithine decarboxylase 1; identifying a disease state; a
XX kit or assay device comprising the compound; and treating an animal
XX having a disease or condition associated with ornithine decarboxylase 1.
XX The oligonucleotide compound is useful for preparing a composition for
XX treating hyperproliferative disorder, e.g. cancer. This sequence
XX represents an ornithine decarboxylase 1 antisense oligonucleotide.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 61.7%; Score 14.8; DB 12; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTGCAAT 21
Db 1 CATGTTTCCAAAGAGCAT 18
RESULT 11
ADP21988/c
ID ADP21988 standard; DNA; 20 BP.
XX
AC ADP21988;
XX
DT 26-AUG-2004 (first entry)
XX
DE Ornithine decarboxylase 1 antisense oligonucleotide seqid 136.
XX
KW cytostatic; gene therapy; ornithine decarboxylase 1;
KW ornithine decarboxylase 1 associated disorder;
KW hyperproliferative disorder; cancer; human; antisense oligonucleotide;
KW antisense technology; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER

```

```

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
XX US2004110148-A1.
XX 10-JUN-2004.
XX 10-DEC-2002; 2002US-00316244.
XX 10-DEC-2002; 2002US-00316244.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie KW;
XX WPI; 2004-440337/41.
XX New oligonucleotide compound that inhibits expression of ornithine
XX decarboxylase 1, useful for preparing a composition for treating
XX hyperproliferative disorder, e.g. cancer.
XX Example 16; SEQ ID NO 136; 69pp; English.
XX The invention describes a new compound, having a sequence comprising 8-80
XX bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
XX specifically hybridises with the nucleic acid encoding ornithine
XX decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
XX ornithine decarboxylase 1. Also described are: inhibiting the expression
XX of ornithine decarboxylase 1 in cells or tissues; screening for a
XX modulator of ornithine decarboxylase 1; identifying a disease state; a
XX kit or assay device comprising the compound; and treating an animal
XX having a disease or condition associated with ornithine decarboxylase 1.
XX The oligonucleotide compound is useful for preparing a composition for
XX treating hyperproliferative disorder, e.g. cancer. This sequence
XX represents an ornithine decarboxylase 1 antisense oligonucleotide.
XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 61.7%; Score 14.8; DB 12; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CATGTTTCCAAAGTGCAAT 21
Db 20 CATGTTTCCAAAGAGCAT 3
RESULT 12
AD004093/c
ID AD004093 standard; DNA; 49 BP.
XX
AC AD004093;
XX
DT 29-JUL-2004 (first entry)
XX
DE Identifier oligonucleotide.
XX
KW Bifunctional complex; ss.
XX
OS Synthetic.
XX
XX WO2004039825-A2.
XX 13-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-DK000739.
XX
XX 30-OCT-2002; 2002DK-00001652.
XX 30-OCT-2002; 2002US-0422167P.
XX 19-DEC-2002; 2002DK-00001955.
XX

```

This sequence is a fragment of the CRCA-1 (colorectal cancer associated) transcript of the invention. The CRCA-1 transcript is a specific marker for colorectal cancer cells and detecting it is used to identify/confirm cells as colorectal cancer cells and to examine the extent of which they have migrated, especially for diagnosis, staging and post-operative monitoring, also for screening subjects at risk. The CRCA-1 DNA is used CC to express the corresponding expression products and its fragments are useful as oligonucleotide probes, primers and antisense agents

Sequence 27 BP; 6 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 2; Length 27;
Best Local Similarity 81.0%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 4 CATGTTTCCAAAGTGCGATGAT 24
||| ||| ||| ||| |||
DB 26 CATATGTCCAAGAGCAGGAT 6

RESULT 14
ADO41360
ID ADO41360 standard; DNA; 34 BP.
XX ADO41360;
AC
XX DT 15-JUL-2004 (first entry)
XX Oligo 3-2 used to diagnose Staphylococcus saprophyticus pathogen.
DE Bacterial pathogen; diagnosis; meningitis; therapy; ss.
XX Staphylococcus saprophyticus.
KW US2004010129-A1.
OS
XX 15-JAN-2004.
XX 28-OCT-2002; 2002US-00281845.
XX 01-NOV-2001; 2001TW-00127119.
XX (HSUP/) HSU P.
PA (CHIA/) CHIANG Y.
PA (HUAN/) HUANG H L.
PA (CHAO/) CHAO S Y.
XX Hau P, Chiang Y, Huang HL, Chao SY;
PI WPI; 2004-224188/21.
XX
XX Nucleic acid kit for diagnosis of bacterial pathogens that cause
PT meningitis comprises nucleic acid sequences designed for 20 bacterial
PT pathogens e.g., Staphylococcus aureus, S.epidermidis, Streptococcus
PT saprophyticus, S.agalactiae.
XX
PS Claim 4; SEQ ID NO 10; 9pp; English.

The present invention relates to a nucleic acid kit for bacterial pathogen diagnosis and method for using the same which provideswith a quick diagnosis for 20 species of bacterial pathogens. The invention is useful for diagnosis of bacterial meningitis pathogens or can be conjugated to a substrate (e.g., biochips) and serve as probes. The present sequence is an oligonucleotide used to diagnose Staphylococcus saprophyticus pathogen. This sequence is used in the invention.

Sequence 34 BP; 10 A; 6 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 12; Length 34;
Best Local Similarity 81.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Qy 4 CATGTTTCCAAAGTGCATG 24
|||||
Db 13 CATGTTCTAAAGTGAAGAT 33

RESULT 15

AAL57225/c
ID AAL57225 standard; DNA; 41 BP.

XX AAL57225;

XX 04-DEC-2003 (first entry)

XX Oligonucleotide probe 2 related to human protein 46-53.

XX Human protein 46.53; cancer; HIV infection; probe; ss.

XX Homo sapiens.

XX CN1381487-A.

XX 27-NOV-2002.

XX 18-APR-2001; 2001CN-00112636.

XX 18-APR-2001; 2001CN-00112636.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2003-258240/26.

XX Polypeptide-human protein-46.53 containing bromo structure domain and polynucleotide for coding it.

XX Example 7; Page 23; Opp; Chinese.

XX This invention relates to the novel human protein 46.53, containing a bromo structure, and the cDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleotide probe 2 related to the human 46.53 protein of the invention and used in example 7 of the specification

XX Sequence 41 BP; 17 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 10; Length 41;
Best Local Similarity 81.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22
|||||
Db 37 TTCATGGTGCCAAATTCATG 17

RESULT 16

AAL57224/c

ID AAL57224 standard; DNA; 41 BP.

XX AAL57224;

XX 04-DEC-2003 (first entry)

XX Oligonucleotide probe 1 related to human protein 46-53.

XX Human protein 46.53; cancer; HIV infection; probe; ss.

XX Homo sapiens.

XX CN1381487-A.

XX 27-NOV-2002.

PF 18-APR-2001; 2001CN-00112636.
XX
PR 18-APR-2001; 2001CN-00112636.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;

XX WPI; 2003-258240/26.

XX Polypeptide-human protein-46.53 containing bromo structure domain and polynucleotide for coding it.

XX Example 7; Page 23; Opp; Chinese.

XX This invention relates to the novel human protein 46.53, containing a bromo structure, and the cDNA sequence encoding it. The invention may be useful in the treatment of diseases such as cancer and HIV infection. The present sequence is that of oligonucleotide probe 1 related to the human 46.53 protein of the invention and used in example 7 of the specification

XX Sequence 41 BP; 16 A; 8 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 10; Length 41;
Best Local Similarity 81.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22

|||||
Db 37 TTCATGGTGCCAAATTCATG 17

RESULT 17

ABX70212/c

ID ABX70212 standard; DNA; 30 BP.

XX AC ABX70212;

XX 07-MAY-2003 (first entry)

XX Novel Helicobacter pylori gene PCR primer #3183.

XX Protein-protein interaction; ulcer; selected interacting domain; SID; PCR; primer; ss.

XX Helicobacter pylori.

XX WO200266501-A2.

XX 29-AUG-2002.

XX 28-DEC-2001; 2001WO-EP015428.

XX 02-JAN-2001; 2001US-0259302P.

XX (HVBR-) HYBRIGENICS.

XX (INSP) INST PASTEUR.

XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;

XX WPI; 2002-674910/72.

XX New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.

XX Example 9; Page 587; 642pp; English.

XX The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be

CC used for treating or preventing ulcers in a human or animal. This
 CC sequence represents a primer used to isolate polynucleotides encoding
 CC Helicobacter pylori proteins for studies on protein-protein interactions
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 6; Length 30;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 28 CTTTCATTCATTCTTAGTGCATGAT 5
 RESULT 18
 ADR23060/c
 ID ADR23060 standard; DNA; 30 BP.
 XX
 AC ADR23060;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE DNA/RNA primer 550 used to amplify H. pylori strain typing ORF DNA.
 XX
 KW strain typing; geographical origin; gastric ulcer; duodenal ulcer;
 KW inflammation; stomach cancer; gastric cancer; DNA/RNA hybrid; PCR;
 KW primer; ss.
 XX
 OS Helicobacter pylori.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 1..9
 FT /*tag= a
 FT /note= "RNA bases"
 XX
 FN FR2850667-A1.
 XX
 PD 06-AUG-2004.
 XX
 PF 30-JAN-2003; 2003FR-00001235.
 XX
 PR 30-JAN-2003; 2003FR-00001235.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Thiberge JM, Labigne A, Coppee JY, Lacroix C;
 XX
 DR WPI; 2004-563635/55.
 XX
 PS Disclosure; SEQ ID NO 550; 126pp; French.
 XX
 CC The invention relates to a novel method for preparing a set of DNA
 CC fragments or their expression products that allows typing of Helicobacter
 CC pylori strains. The method comprises preparing genomic DNA components
 CC from clinical isolates and strains of H. pylori that can be
 CC distinguished, particularly from their geographical origin or their
 CC particular associated pathology. Subsequently a set of non-ubiquitous
 CC open reading frames (ORFs) may be identified from amongst the ORFs
 CC present in the genome of a reference strain by comparison with the DNA
 CC prepared in the first stage and a composition may be prepared containing
 CC the identified ORFs, or fragments, their expression products or
 CC antibodies against these expression products. The method of the invention
 CC may be used to provide unequivocal differentiation between clinical
 CC isolates of H. pylori according to their geographical origin and
 CC particular pathologies. H. pylori infection is particularly associated
 CC with gastric and duodenal ulcers or inflammation, as well as cancer of
 CC the stomach or gastric system. The current sequence is that of a DNA/RNA
 CC hybrid PCR primer of the invention which was used to amplify H. pylori

CC ORF DNA for strain typing.
 XX
 SQ Sequence 30 BP; 13 A; 6 C; 5 G; 3 T; 3 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 13; Length 30;
 Best Local Similarity 75.0%; Pred. No. 6.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 28 CTTTCATTCATTCTTAGTGCATGAT 5
 RESULT 19
 AAL45772/c
 ID AAL45772 standard; DNA; 33 BP.
 XX
 AC AAL45772;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Human acid phosphatase family protein 11 cDNA PCR primer #3.
 XX
 KW Human; acid phosphatase family protein 11; cancer; haemopathy;
 KW cytosstatic; haemostatic; virucide; immunomodulatory; antiinflammatory;
 KW immune disease; HIV infection; phlogosis; gene therapy; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200220579-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 19-JUN-2001; 2001WO-CN001011.
 XX
 PR 21-JUN-2000; 2000CN-00116667.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-329869/36.
 XX
 PT Homo acid phosphatase family protein 11 and encoding polynucleotide, used
 PT in diagnosis and treatment of malignant tumors, hemopathy, human
 PT immunodeficiency virus infection, immunological diseases and
 PT inflammation.
 XX
 PS Example 4; Page 13; 39pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC acid phosphatase family protein 11. The sequences can be used in the
 CC treatment of cancer, haemopathy, HIV infection, immune diseases and
 CC phlogosis. The present sequence is a PCR primer for the coding sequence
 CC of the invention
 XX
 SQ Sequence 33 BP; 9 A; 8 C; 5 G; 11 T; 0 U; 0 Other;
 Query Match 60.0%; Score 14.4; DB 6; Length 33;
 Best Local Similarity 75.0%; Pred. No. 6.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 ||||| | | |||||
 Db 33 CTTAATGATGAGAAAGTGCATCAT 10
 RESULT 20
 ABT42676
 ID ABT42676 standard; DNA; 37 BP.
 XX
 AC ABT42676;
 XX

Query Match 59.2%; Score 14.2; DB 12; Length 20;

XX Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
SQ Query Match 59.2%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGC 19
Db 1 CTTTCATGTTTCCCAAGTGC 19
RESULT 24
ABV74729
ID ABV74729 standard; DNA; 33 BP.
XX AC ABV74729;
XX DT 03-FEB-2003 (first entry)
XX DE Human clathrin light chain 13.64 PCR primer #4.
XX KW Human; clathrin light chain 13.64; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; cytostatic; anti-HIV; PCR; primer;
KW ss.
XX OS Homo sapiens.
XX PN CN1352131-A.
XX PD 05-JUN-2002.
XX PF 06-NOV-2000; 2000CN-00127271.
XX PR 06-NOV-2000; 2000CN-00127271.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-644460/70.
XX PT New human clathrin light chain 13.64 polypeptide for treating malignant
PT tumors, hemopathy, human immunodeficiency virus infection, immunological
PT diseases and various inflammations.
XX PS Example 4; Page 18 (Disclosure); 34pp; Chinese.
XX CC The present invention relates to human clathrin light chain 13.64 (see
CC ABB98794). The protein and its coding sequence can be used for treating
CC various diseases, such as malignant tumours, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence is
CC a PCR primer, which was used in an example from the invention
XX SQ Sequence 33 BP; 6 A; 12 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.2; DB 6; Length 33;
Best Local Similarity 84.2%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGC 19
Db 14 CCTGATGTTTCCCAAGTGC 32
RESULT 25
ABZ04574
ID ABZ04574 standard; DNA; 50 BP.
XX AC ABZ04574;
XX DT 09-JAN-2003 (first entry)
XX OS Homo sapiens.

DE Human leukocyte gene expression profiling probe SEQ ID NO 4565.
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX OS Homo sapiens.
XX PN WO200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PR 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.
XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX PI Ly N, Woodward R, Quertermous T, Johnson F;
XX DR WPI; 2002-636525/68.
XX PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX PS Claim 1; Page 473; Opp; English.
XX CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX SQ Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGC 19
Db 10 CTTTCATGTTTCCCAAGTGC 28
RESULT 26
ADG33666
ID ADG33666 standard; DNA; 50 BP.
XX AC ADG33666;
XX DT 26-FEB-2004 (first entry)
XX DE Human DNA probe used to monitor expression of diagnostic genes SeqID990.
XX KW human; ss; autoimmune; chronic inflammatory disease; SLE;
KW systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW diverticulitis; primary biliary sclerosis; probe.
XX OS Homo sapiens.


```

PN WO2003090694-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-US013015.
XX
PR 24-APR-2002; 2002US-00131827.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgenuth J, Fry K, Woodward R, Ly N;
XX
DR WPI; 2003-877243/81.
XX
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
PT colitis, psoriasis and asthma by detecting the expression level of one or
PT more genes.
XX
PS Claim 1; SEQ ID NO 990; 877pp; English.
XX
CC This invention relates to novel methods for diagnosing and monitoring
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to
CC the identification of genes that have a clinical utility as diagnostic
CC tools for the management of, in particular, patients with systemic lupus
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
CC present invention describes a method for determining the levels of
CC multiple differentially expressed genes of a patient, in a concerted
CC manner, in order to achieve an improved diagnostic assay with sensitivity
CC and specificity for the disease in question. As such, these genes are
CC useful for the diagnosis of various other inflammatory disorders
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
CC ankylosing spondylitis, ulcerative colitis, primary sclerosing
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
CC This oligonucleotide is a human DNA probe used to monitor the expression
CC level of the differentially expressed diagnostic genes of the invention.
XX
SQ Sequence 50 BP; 16 A; 12 C; 12 G; 10 T; 0 U; 0 Other;

Query Match          59.2%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTTCATGTTTCCCAAGTGC 19
    ||||| || || || || ||
Db 10 CTTTCATCTTCCCAAGTGC 28

RESULT 27
ADP10108
ID ADP10108 standard; DNA; 50 BP.
XX
XX ADP10108;
AC
XX
XX 12-AUG-2004 (first entry)
XX
XX 50-mer oligonucleotide marker probe of the invention #117.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

Query Match          59.2%; Score 14.2; DB 12; Length 50;
Best Local Similarity 84.2%; Pred. No. 8.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTTCATGTTTCCCAAGTGC 19
    ||||| || || || || ||
Db 10 CTTTCATCTTCCCAAGTGC 28

RESULT 28
ACK15268
ID ACK15268 standard; DNA; 25 BP.
XX
XX ACK15268;
AC
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 115249.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX OS
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (APFY-) AFFYMETRIX INC.
XX
XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.

```

PS Claim 1; SEQ ID NO 115249; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 5 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAA 14
|||||
Db 1 CTTTCATGTTTCCAA 14

RESULT 29

ID ABX95855/c
AC ABX95855 standard; DNA; 27 BP.

XX

AC ABX95855;

XX

DT 01-AUG-2003 (first entry)

XX

DE PCR primer J for detecting DNA derived from cotton event 757.

XX

KW Lepidoptera resistant cotton; transgenic plant; cotton; PV-GHBRK04;
KW cotton event 757 recombinant; progeny; transgene; transgenic; PCR;
KW primer; ss.

XX

OS Gossypium hirsutum.
OS Synthetic.

XX

PN US2003024005-A1.

XX

PD 30-JAN-2003.

XX

PF 16-NOV-2001; 2001US-00990659.

XX

PR 17-NOV-2000; 2000US-0249757P.

XX

PA (HILL/) HILLYARD J R.
PA (ROBE/) ROBERTS J K.
PA (YEMM/) YE M.

XX

PI Hillyard JR, Roberts JK, Ye M;

XX

DR WPI; 2003-456316/43.

XX

PT New cotton plant event PV-GHBRK04 (757) nucleic acid sequences, useful for
PT detecting DNA from the cotton plant event 757 in a sample for determining
PT whether the progeny of a sexual cross contain a transgene of interest.

XX Claim 3; Page 16; 32pp; English.

XX The present invention relates to a Lepidoptera resistant transgenic cotton (Gossypium hirsutum) plant referred to as PV-GHBRK04 or cotton event 757. The invention provides polynucleotide sequences contained within cotton event 757 and methods for detecting DNA from the cotton plant event 757 in a sample. The methods are useful for determining whether the progeny of a sexual cross contain a transgene of interest. The present sequence represents a PCR primer that may be used to detect DNA derived from the cotton event 757 in a sample

XX Sequence 27 BP; 11 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 10; Length 27;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
|||||
Db 23 TTCTTCTTTCGTAAGTGCATCA 2

RESULT 30

ID ADH27316
AC ADH27316 standard; DNA; 28 BP.

XX

AC ADH27316;

XX

DT 11-MAR-2004 (first entry)

XX

DE Ferritin related oligonucleotide Bin#5 structure 3.

XX

KW detection; conserved structure; RNA structural element; fitness; ss.
KW Synthetic.

XX

PN WO2003104478-A2.

XX

PD 18-DEC-2003.

XX

PF 10-JUN-2003; 2003WO-US018573.

XX

PR 10-JUN-2002; 2002US-0387342P.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VM;

XX

DR WPI; 2004-062371/06.

XX

PT Detecting a conserved structures in an RNA sequence by generating an
PT offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.

XX

PS Example 1; Fig 13; 52pp; English.

XX

CC The present invention describes a method for detecting a conserved structure in an RNA sequence. The method comprises: (a) placing 2 structures from structures generated for 2 RNA sequences from 2 organisms into a parent group; (b) generating an offspring group from the parent group; (c) determining fitness of the parent and offspring groups; (d) comparing the fitness of the parent and offspring groups; and (e) selecting at least one group from the parent and offspring groups with the highest fitness, where the conserved structure in the RNA is present within the at least one group. The method is useful for detecting a conserved structure in an RNA sequence. The present sequence is used in the exemplification of the present invention.

XX

SO Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;

```
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 31
ADH27295
ID ADH27295 standard; DNA; 28 BP.
XX
AC ADH27295;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#2 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
DR WPI; 2004-062371/06.
XX
PS Detecting a conserved structures in an RNA sequence by generating an
offspring group from the parent group and selecting at least one group
from the parent and offspring groups with the highest fitness.
XX
Example 1; Fig 13; 52pp; English.
XX
CC The present invention describes a method for detecting a conserved
structure in an RNA sequence. The method comprises: (a) placing 2
structures from structures generated for 2 RNA sequences from 2 organisms
into a parent group; (b) generating an offspring group from the parent
group; (c) determining fitness of the parent and offspring groups; (d)
comparing the fitness of the parent and offspring groups; and (e)
selecting at least one group from the parent and offspring groups with
the highest fitness, where the conserved structure in the RNA is present
within the at least one group. The method is useful for detecting a
conserved structure in an RNA sequence. The present sequence is used in
the exemplification of the present invention.
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 32
ADH27302
ID ADH27302 standard; DNA; 28 BP.
XX
AC ADH27302;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#3 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
DR WPI; 2004-062371/06.
XX
PS Detecting a conserved structures in an RNA sequence by generating an
offspring group from the parent group and selecting at least one group
from the parent and offspring groups with the highest fitness.
XX
Example 1; Fig 13; 52pp; English.
XX
CC The present invention describes a method for detecting a conserved
structure in an RNA sequence. The method comprises: (a) placing 2
structures from structures generated for 2 RNA sequences from 2 organisms
into a parent group; (b) generating an offspring group from the parent
group; (c) determining fitness of the parent and offspring groups; (d)
comparing the fitness of the parent and offspring groups; and (e)
selecting at least one group from the parent and offspring groups with
the highest fitness, where the conserved structure in the RNA is present
within the at least one group. The method is useful for detecting a
conserved structure in an RNA sequence. The present sequence is used in
the exemplification of the present invention.
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
```

```
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
DR WPI; 2004-062371/06.
XX
PS Detecting a conserved structures in an RNA sequence by generating an
offspring group from the parent group and selecting at least one group
from the parent and offspring groups with the highest fitness.
XX
Example 1; Fig 13; 52pp; English.
XX
CC The present invention describes a method for detecting a conserved
structure in an RNA sequence. The method comprises: (a) placing 2
structures from structures generated for 2 RNA sequences from 2 organisms
into a parent group; (b) generating an offspring group from the parent
group; (c) determining fitness of the parent and offspring groups; (d)
comparing the fitness of the parent and offspring groups; and (e)
selecting at least one group from the parent and offspring groups with
the highest fitness, where the conserved structure in the RNA is present
within the at least one group. The method is useful for detecting a
conserved structure in an RNA sequence. The present sequence is used in
the exemplification of the present invention.
XX
SQ Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
Db 1 TTCTGCTTCAACAGTGTCTGA 22

RESULT 33
ADH27288
ID ADH27288 standard; DNA; 28 BP.
XX
AC ADH27288;
XX
DT 11-MAR-2004 (first entry)
XX
DE Ferritin related oligonucleotide Bin#1 structure 3.
XX
KW detection; conserved structure; RNA structural element; fitness; ss.
XX
OS Synthetic.
XX
PN WO2003104478-A2.
XX
PD 18-DEC-2003.
XX
PF 10-JUN-2003; 2003WO-US018573.
XX
PR 10-JUN-2002; 2002US-0387342P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Sampath R, Ecker DJ, Griffey RH, Fogel GB, Porto VW;
```

XX WPI; 2004-062371/06.
XX Detecting a conserved structures in an RNA sequence by generating an
PT offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.
XX
XX Example 1; Fig 13; 52pp; English.
XX
XX The present invention describes a method for detecting a conserved
CC structure in an RNA sequence. The method comprises: (a) placing 2
CC structures from structures generated for 2 RNA sequences from 2 organisms
CC into a parent group; (b) generating an offspring group from the parent
CC group; (c) determining fitness of the parent and offspring groups; (d)
CC comparing the fitness of the parent and offspring groups; and (e)
CC selecting at least one group from the parent and offspring groups with
CC the highest fitness, where the conserved structure in the RNA is present
CC within the at least one group. The method is useful for detecting a
CC conserved structure in an RNA sequence. The present sequence is used in
CC the exemplification of the present invention.
XX
XX Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 14; DB 12; Length 28;
Best Local Similarity 77.3%; Pred. No. 9.4e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
||| ||| ||| ||| ||| |||
Db 1 TTCCTGCTTCAACAGTGTCTGA 22

RESULT 34
ADH27309
ID ADH27309 standard; DNA; 29 BP.
XX
AC ADH27309;
XX
DT 11-MAR-2004 (first entry)
DE Ferritin related oligonucleotide Bin#4 structure 3.
XX detection; conserved structure; RNA structural element; fitness; ss.
XX Synthetic.
XX
XX WO2003104478-A2.
XX
XX 18-DEC-2003.
XX
XX 10-JUN-2003; 2003WO-US018573.
XX
XX 10-JUN-2002; 2002US-0387342P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Sampath R, Becker DJ, Griffey RH, Fogel GB, Porto VW;
XX
XX WPI; 2004-062371/06.
XX
XX Detecting a conserved structures in an RNA sequence by generating an
PT offspring group from the parent group and selecting at least one group
PT from the parent and offspring groups with the highest fitness.
XX
XX Example 1; Fig 13; 52pp; English.
XX
XX The present invention describes a method for detecting a conserved
CC structure in an RNA sequence. The method comprises: (a) placing 2
CC structures from structures generated for 2 RNA sequences from 2 organisms
CC into a parent group; (b) generating an offspring group from the parent
CC group; (c) determining fitness of the parent and offspring groups; (d)
CC comparing the fitness of the parent and offspring groups; and (e)
CC selecting at least one group from the parent and offspring groups with

CC the highest fitness, where the conserved structure in the RNA is present
CC within the at least one group. The method is useful for detecting a
CC conserved structure in an RNA sequence. The present sequence is used in
CC the exemplification of the present invention.
XX
XX Sequence 29 BP; 7 A; 7 C; 6 G; 9 T; 0 U; 0 Other;
SQ

Query Match 58.3%; Score 14; DB 12; Length 29;
Best Local Similarity 77.3%; Pred. No. 9.5e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATGA 23
||| ||| ||| ||| ||| |||
Db 2 TTCCTGCTTCAACAGTGTCTGA 23

RESULT 35
ADR33465/c
ID ADR33465 standard; DNA; 32 BP.
XX
AC ADR33465;
XX
DT 04-NOV-2004 (first entry)
DE Human nicking agent target DNA #1006.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
XX Example 1; Page 87; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for

CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.

XX
 SQ Sequence 32 BP; 10 A; 8 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 13; Length 32;
 Best Local Similarity 77.3%; Pred. No. 9.6e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 29 TCATTTTCCATAGACATGGT 8

RESULT 36

ABK11366

ID ABK11366 standard; DNA; 33 BP.

XX

AC ABK11366;

XX

DT 05-JUN-2002 (first entry)

XX

DE NADH dehydrogenase 51kd subunit 10 PCR primer #1.

XX

KW ss; PCR; NADH dehydrogenase 51kd subunit 10; malignant tumour;
 KW haemopathy; human immunodeficiency virus infection; HIV; primer;
 KW immunological disease; inflammation; cytostatic; haemostatic; virucide;
 KW immunomodulatory; antiinflammatory; metabolic disturbance.

XX

OS Unidentified.

XX

FN WO200202618-A1.

XX

PD 10-JAN-2002.

XX

PF 18-JUN-2001; 2001WO-CN000991.

XX

PR 19-JUN-2000; 2000CN-00116593.

XX

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-090538/12.

XX

NADH-dehydrogenase 51 and encoded polynucleotide, used in diagnosis and
 treatment of malignant tumors, hemopathy, human immunodeficiency virus
 infection, immunological diseases and inflammation.

XX

PS Example 5; Page 13; 35pp; Chinese.

XX

The invention relates to an isolated polypeptide of NADH-dehydrogenase 51
 Kd subunit 10, the cDNA encoding it, and its fragment, analogue or
 derivative. Also included are vectors expressing the protein, a host cell
 comprising the vector, the isolation of modulators of the protein and an
 anti-NADH-dehydrogenase 51 antibody. The protein and nucleic acid are
 used in diagnosis and treatment of a malignant tumour, haemopathy, human
 immunodeficiency virus (HIV) infection, immunological diseases, various
 inflammations, metabolic disturbance of carbohydrate, lipid and protein.
 The present sequence is a PCR primer used to clone the cDNA encoding the
 NADH- dehydrogenase 51kd subunit 10

XX

SQ Sequence 33 BP; 8 A; 8 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 33;

Best Local Similarity 77.3%; Pred. No. 9.7e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 8 TGATGTTTCCCATATACATGAT 29

RESULT 37

AAV27468

ID AAV27468 standard; DNA; 36 BP.

XX

AC AAV27468;

XX

DT 02-OCT-1998 (first entry)

XX

DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.

XX

KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.

XX

OS Synthetic.

OS Streptococcus pneumoniae.

XX

PN WO9818930-A2.

XX

PD 07-MAY-1998.

XX

PF 30-OCT-1997; 97WO-US019422.

XX

PR 31-OCT-1996; 96US-0029960P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Kunsch CA, Choi GH, Johnson LS, Hromockyj A;

XX

DR WPI; 1998-272224/24.

XX

Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae
 - or their epitope-containing fragments, useful in protective or
 therapeutic vaccines, and for diagnosis.

XX

PS Example 1; Page 106; 118pp; English.

XX

The present sequence represents a cloning primer used in an example from
 the present invention which describes proteins from Streptococcus
 pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
 proteins can be useful in vaccines for inducing protective antibodies
 against Streptococcus pneumoniae, for treatment or prevention of
 infection e.g. pneumonia, otitis media or meningitis. Probes based on the
 nucleic acids are used to detect Streptococcus infection (by usual
 hybridisation or amplification methods), also for isolating Streptococcus
 genes or their allelic variants. The proteins can be used similarly to
 detect specific antibodies in standard immunoassays, especially for
 diagnosing or monitoring infections. Antibodies which bind the proteins
 are used to detect corresponding antigens, to purify the proteins and for
 passive immunisation (optionally coupled to a toxin). Vaccines are
 administered, e.g. by injection, orally or through the skin, typically at
 0.01-1000 (especially 10-300) mu g/ml per dose. The cloning primers used
 in the present invention are given in AAV27437 to AAV27562 and AAV39870
 to AAV39969

SQ Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 36;

Best Local Similarity 77.3%; Pred. No. 9.8e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 3 TCAGCTTCCAAACTGGTGTAT 24

RESULT 38

AAA70860

ID AAA70860 standard; DNA; 36 BP.

XX

```

AC AAA70860;
XX
XX 27-APR-2001 (first entry)
XX
XX Molecular interaction site DNA #13.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Xenopus sp.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX
XX Example 2; Fig 63; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUAUCUAGUACAGAAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
XX Sequence 36 BP; 7 A; 11 C; 9 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 58.3%; Score 14; DB 3; Length 36;
XX Best Local Similarity 77.3%; Pred. No. 9.8e+03;
XX Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX Qy 2 TTCATGTTTCAAAAGTCATGA 23
XX ||| ||| ||| ||| |||
XX Db 3 TTCCTGCTTCAACAGTGTCTGA 24
XX
XX RESULT 39
XX AAA70869
XX ID AAA70869 standard; RNA; 36 BP.
XX
XX AC AAA70869;

```

```

XX
XX 27-APR-2001 (first entry)
XX
XX Molecular interaction site RNA #55.
XX
XX Modulator; identification; molecular interaction; virtual library; ss.
XX
XX Xenopus sp.
XX
XX WO9958947-A2.
XX
XX 18-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010361.
XX
XX 12-MAY-1998; 98US-00076404.
XX
XX 12-MAY-1998; 98US-0085092P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX
XX Example 2; Fig 66; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX with members of the virtual library of compounds to generate a hierarchy
XX of the compounds ranked in accordance with their respective ability to
XX form physical interactions with the molecular interaction site. The
XX method also describes (1) RNA comprising a joined sequence of at least 24
XX nucleotides but not more than 70 nucleotides and having secondary
XX structure defined by: (a) 3 nucleotides forming a first side of a first
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX internal loop region; (c) 4 nucleotides forming a first side of a second
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUAUCUAGUACAGAAAAUC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX or industrial compounds
XX
XX Sequence 36 BP; 7 A; 11 C; 9 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 58.3%; Score 14; DB 3; Length 36;
XX Best Local Similarity 45.5%; Pred. No. 9.8e+03;
XX Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX
XX Qy 2 TTCATGTTTCAAAAGTCATGA 23
XX ::| ::| ::| ::| ::|
XX Db 3 UUCUCGCUCAACACAGUCUUGA 24
XX
XX RESULT 40
XX ABQ84936
XX ID ABQ84936 standard; DNA; 36 BP.
XX
XX AC ABQ84936;
XX

```

DT 04-SEP-2002 (first entry)
 XX Streptococcus pneumoniae ORF cloning primer SEQ ID NO:258.
 DE
 XX
 KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
 KW antibacterial; Streptococcal infection; detection; primer; ss.
 XX
 OS Streptococcus pneumoniae.
 OS Synthetic.
 XX
 XX US2002061545-A1.
 FN
 XX
 PD 23-MAY-2002.
 XX
 XX
 PF 22-JAN-2001; 2001US-00765272.
 XX
 XX 30-OCT-1997; 97US-00961083.
 XX
 XX (CHOI/) CHOI G H.
 PA (KUNS/) KUNSCH C A.
 PA (BARA/) BARASH S C.
 PA (DILL/) DILLON P J.
 PA (DOUG/) DOUGHERTY B.
 PA (FANN/) FANNON M R.
 PA (ROSE/) ROSEN C A.
 XX
 PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
 PI Rosen CA;
 XX
 XX WPI; 2002-479261/51.
 DR
 XX
 XX New Streptococcus pneumoniae antigens, useful for detecting Streptococcus
 PT and for preventing or attenuating disease caused by Streptococcus
 PT infection.
 XX
 XX Example 1; Page 62; 70pp; English.
 PS
 XX ABO84792 to ABO84904 represents nucleic acids which encode the
 CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669. The S.
 CC pneumoniae antigens have antibacterial activity and can be used in
 CC vaccines. The S. pneumoniae antigens can also be used to prevent or
 CC attenuate a Streptococcal infection in an animal. The polynucleotides
 CC encoding the S. pneumoniae antigens can be used to detect Streptococcus
 CC nucleic acids. ABO84905 to ABO85130 represent primers used in the cloning
 CC of S. pneumoniae ORFs (open reading frames) which are used in an example
 CC from the present invention
 XX
 SQ Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 58.3%; Score 14; DB 6; Length 36;
 Best Local Similarity 77.3%; Pred. No. 9.8e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 TCATGTTTCCAAAGTCATGAT 24
 ||| ||||| |||||
 Db 3 TCAAGCTTCCAACTGGTTGAT 24
 ||| ||||| |||||

Search completed: November 18, 2005, 11:52:25
 Job time : 168.262 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1147.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTCATGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	65.0	44	BH810239	BH810239 SALK_0482
2	14.2	59.2	42	AV845171	AV845171 SALK_0482
3	14.2	59.2	47	DA945171	DA945171 SALK_0482
4	14	58.3	43	AA423162	AA423162 ve36b01.r
5	14	58.3	48	AA930873	AA930873 vz71e07.s
6	14	58.3	48	AI172854	AI172854 uc10c07.r
7	14	58.3	48	AA386692	AA386692 vb55c05.r
8	13.6	56.7	40	AZ651473	AZ651473 1M0522N07
9	13.4	55.8	26	AZ637079	AZ637079 1M0496F09
10	13.4	55.8	27	TA46H06P	TA46H06P 1M0496F09
11	13.4	55.8	42	T73611	T73611 yc36h11.s1
12	13.2	55.0	31	AZ307496	AZ307496 1M0009F14
13	13.2	55.0	33	AU014420	AU014420 AU014420
14	13.2	55.0	35	CL213211	CL213211 AU014420
15	13.2	55.0	41	AL753405	AL753405 Arabidops
16	13.2	55.0	41	AX891114	AX891114 Arabidops
17	13.2	55.0	45	CC888123	CC888123 SALK_1513
18	13	54.2	29	BZ762504	BZ762504 SALK_1050
19	13	54.2	37	BE548888	BE548888 601073346
20	13	54.2	40	EX572262	EX572262 Arabidops
21	13	54.2	43	BE788148	BE788148 601480079
22	13	54.2	43	BH790838	BH790838 SALK_0580
23	13	54.2	44	BJ076538	BJ076538 BJ076538
24	12.8	53.3	28	W11835	W11835 mb20h01.r1

25	12.8	53.3	36	8	AZ794096	AZ794096 2M0047P10
26	12.8	53.3	36	9	CC796901	CC796901 SALK_1442
27	12.8	53.3	43	1	AA995598	AA995598 os23h03.s
28	12.8	53.3	46	8	CC049873	CC049873 01S0518-0
29	12.6	52.5	26	8	BZ290816	BZ290816 SALK_0915
30	12.6	52.5	31	8	BZ661378	BZ661378 SALK_0248
31	12.6	52.5	32	9	CG712334	CG712334 1119026A1
32	12.6	52.5	37	8	BH850177	BH850177 SALK_0709
33	12.6	52.5	38	5	BW593923	BW593923 BW593923
34	12.6	52.5	40	7	H95706	H95706 yf95g10.s1
35	12.6	52.5	41	9	TA202B01Q	TA202B01Q T. brucei
36	12.6	52.5	43	1	AI280742	AI280742 qw07c06.x
37	12.6	52.5	43	8	BZ766776	BZ766776 SALK_1378
38	12.4	51.7	37	8	AZ388487	AZ388487 1M0148F03
39	12.4	51.7	41	8	BH866468	BH866468 SALK_1013
40	12.4	51.7	42	9	TA232A04Q	TA232A04Q T. brucei
41	12.4	51.7	47	8	AZ830439	AZ830439 2M0109M08
42	12.4	51.7	47	8	BZ584043	BZ584043 3590_1_53
43	12.2	50.8	25	8	AZ826147	AZ826147 2M0101O12
44	12.2	50.8	33	8	AZ762777	AZ762777 1M0558A05
45	12.2	50.8	33	8	BH911010	BH911010 SALK_0645

ALIGNMENTS

RESULT 1
BH810239
LOCUS BH810239 44 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK_048259 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_048259, genomic survey sequence.

ACCESSION BH810239
VERSION BH810239.1 GI:20388057

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 44)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

FEATURES
source

Class: TDNA tagged.

Location/Qualifiers

1..44

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_048259"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

65.0%; Score 15.6; DB 8; Length 44;


```

RGIN
Query Match      58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17: Conservative 0; Mismatches 5; Indels

```

	matches	17; conservative	0; mismatches	5; indels	0; gaps
Qy	3	TCATGTTTCCAAAGTGCATGAT	24		
Db	34	TCATGTCTCCCAAGTGGTTCAT	13		

RESULT 6
AI172854/c
LOCUS AI172854 4

LOCUS	AI172854	48 bp	mRNA	linear	EST 07-OCT-1998
DEFINITION	uc10c07.r1 Soares mammary gland NbMWG Mus musculus cDNA clone IMAGE:1397580 5' similar to gb:M90696 CATHEPSIN S PRECURSOR (HUMAN); mRNA sequence.				

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

Theising, B., Wyllie, I., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:909296

```

1. .48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
source

```

Query Match 58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0

```

QY      3 TCATGTTTCCAAAGTGCATGAT 24
      ||||| ||| ||||| |||
Db      34 TCATGTTTCCCAAGTGGTTCAT 13
      ||||| ||| ||||| |||

RESULT 7
AA386692/c
LOCUS   AA386692                48 bp      mRNA      linear      EST 23-APR-1997
DEFINITION
IMAGE:760904 5' similar to gb:M90696 CATHEPSIN S PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
VERSION  AA386692
KEYWORDS
SOURCE    AA386692.1  GI:2039656
          Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE
The WashU-HHMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:461824
Trace considered overall poor quality
High quality sequence stop: 1.

FEATURES
Location/Qualifiers
1..48
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:760904"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
/clone_lib="Ko mouse embryo 11 5dpc"
/note="Organ: embryo; Vector: pSPORT1; Site 1: SalI;
Site 2: NotI; Total RNAs were extracted from 11.5 dpc
embryos (excluding placenta and yolk sac). The
double-stranded cDNA was synthesized with an oligo (dTp)-1
primer GAGAGAGCTAGTCTCTAGTCGAGCGCGCTTTTTCATTTTTCATTTT
3'. The cDNAs were ligated to LL-Sal3A: 5'
GCTATTGACGTCGATCC 3' and LL-Sal3B: 5'
GGATAGTCGACGTCATCC 3'. The cDNAs were size-selected and
amplified by long-range PCR using Ex Taq polymerase for 18
cycles. The PCR-amplifiable cDNA mixture went through
one round of equalization and was digested with SalI/NotI
and cloned into the SalI/NotI sites of the pSPORT1
plasmid vector (Life Technologies). The library was
constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong
Wang."

ORIGIN
Query Match 58.3%; Score 14; DB 1; Length 48;
Best Local Similarity 77.3%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 TCATGTTTCCAAAGTGCATGAT 24
      ||||| ||| ||||| |||

RESULT 8
AA386692/c
LOCUS   AA386692                40 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION
IMAGE:760904 5' similar to gb:M90696 CATHEPSIN S PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
VERSION  AA386692
KEYWORDS
SOURCE    AA386692.1  GI:11787002
          Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0522 row: N column: 07
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 40.

FEATURES
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0522N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 56.7%; Score 13.6; DB 8; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ATGTTTCCAAAGTGCATGAT 24
      ||||| ||| ||||| |||

```

```

Db          23 ATGTTTCCCAAGTCGATGAT 4
|||||
RESULT 9
AZ637079/c
LOCUS      26 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION clone UUGC1M0496F09 F, genomic survey sequence.
ACCESSION  AZ637079
VERSION     AZ637079.1  GI:11759185
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL    plasmid inserts
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0496 row: F column: 09
Seq primer: CCGTGAATACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES   Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0496F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      55.8%; Score 13.4; DB 8; Length 26;
Best Local Similarity 93.3%; Pred. NO. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db          9  TTCCAAAGTCGATGA 23
|||||
RESULT 9
AZ637079/c
LOCUS      26 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION clone UUGC1M0496F09 F, genomic survey sequence.
ACCESSION  AZ637079
VERSION     AZ637079.1  GI:11759185
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL    plasmid inserts
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0496 row: F column: 09
Seq primer: CCGTGAATACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES   Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0496F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      55.8%; Score 13.4; DB 8; Length 26;
Best Local Similarity 93.3%; Pred. NO. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db          23 ATGTTTCCCAAGTCGATGA 4
|||||
RESULT 10
TA46H06P/c
LOCUS      27 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 46h06, forward sequence,
genomic survey sequence.
ACCESSION  TA46H06P
VERSION     AL454437
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Trypanosoma brucei
REFERENCE  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
AUTHORS    Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="46h06"
ORIGIN
Query Match      55.8%; Score 13.4; DB 9; Length 27;
Best Local Similarity 93.3%; Pred. NO. 2.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  TTTCCAAGTCGATG 22
|||||
Db      27  TTTCACAGTCGATG 13
|||||
RESULT 11
T73611/c
LOCUS      42 bp      mRNA      linear      EST 02-MAR-1995
DEFINITION YC36h11.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:82821 3', similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION  T73611
VERSION     T73611.1  GI:690286
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

```

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, K., Wilson, R., and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 889549

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1676

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality

Insert Length: 1676 Std Error: 0.00

Seq primer: -21ml3

High quality sequence stop: 1.

Location/Qualifiers

1. .42

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:499878"

/db_xref="taxon:9606"

/clone="IMAGE:82821"

/sex="male"

/dev_stage="49 years old"

/lab_host="SOUR cells (kanamycin resistant)"

/clone_lib="Stratagene liver (#937224)"

/note="Organ: liver; Vector: pBluescript SK; Site: 1:

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. Hepatotomy from normal male caucasian. Average

insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATCGCACGAG 3' -3' adaptor sequence: 5'

CTCAGATTTTTTTTTTTTTTTT 3'

ORIGIN

Query Match 55.8%; Score 13.4; DB 7; Length 42;
Best Local Similarity 82.4%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTG 18

| | | | | | | | | | | | | | | | | | | | | |

Db 23 TANANGTTTCCAAAGTG 7

RESULT 12

AZ307496/c

LOCUS

DEFINITION AZ307496 31 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0009F14 F, genomic survey sequence.

ACCESSION AZ307496

VERSION AZ307496.1 GI:10346554

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0009 row: F column: 14

Seq primer: CGTGTAAACGAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

1. .31

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0009F14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWB42 (GI:4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 55.0%; Score 13.2; DB 8; Length 31;
Best Local Similarity 83.3%; Pred. No. 2.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAAAGTGCATGA 23

| | | | | | | | | | | | | | | | | | | | | |

Db 30 TGTTCCTCAAAAGTGCATGA 13

RESULT 13

AU014420

LOCUS

DEFINITION AU014420 33 bp mRNA linear EST 03-AUG-1998
Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc09814, mRNA sequence.

ACCESSION AU014420

VERSION AU014420.1 GI:3369211

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM

Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomyces.

1 (bases 1 to 33)

Moriyomo, M. and Mitu, K.

Identification of expressed sequence tags of Schizosaccharomyces

pombe

Unpublished (1998)

Contact: Mitsuo Moriyo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-ku, Chiba 263-8555, Japan

Email: moriyom@nirs.go.jp

Location/Qualifiers

FEATURES

```

source
1. .33
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc09814"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M3mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M3mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.niers.go.jp)"

ORIGIN
Query Match 55.0%; Score 13.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. NO. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTCATGA 23
|||||
Db 9 TGTTCCTATGATGA 26
|||||

RESULT 14
LOCUS CL213211 35 bp mRNA linear GSS 30-JUN-2004
DEFINITION A045A04 GATC Gene Trap Library GV03C04 Mus musculus cDNA clone
A045A04, mRNA sequence.
ACCESSION CL213211.2 GI:49489584
VERSION
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
TITLE A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
JOURNAL 22810117
MEDLINE 12904583
PUBMED
COMMENT On Jun 30, 2004 this sequence version replaced gi:40730112.
Contact: GATC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
p1ribetageo gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=A045A04' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 08991
Class: Gene Trap.
FEATURES
Location/Qualifiers
source
1. .35
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="A045A04"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: p1ribetageo"

ORIGIN
Query Match 55.0%; Score 13.2; DB 9; Length 35;
Best Local Similarity 83.3%; Pred. NO. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTCGA 20
|||||
Db 1 TCATGTTTGCACAGTCCA 18
|||||

RESULT 15
LOCUS AL753405 41 bp DNA linear GSS 31-MAR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-049G05-013871,
genomic survey sequence.
ACCESSION AL753405
VERSION AL753405.1 GI:21485903
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL 22755829
MEDLINE 12874060
PUBMED
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL 23117147
MEDLINE 14756321
PUBMED
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL 14682050
MEDLINE
PUBMED
REFERENCE 4
AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weishaar, B.
TITLE Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
Details on the protocols used for generation of the sequence are
described in References 1-3. Re-examination of the source from
which this sequence has been produced indicates that the sequence
is of low reliability. Therefore, no information on a potential
insertion site is deduced. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
source
1. .41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-049G05-013871"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.

```

T-DNA derived sequences were removed."

```

ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATGTTTCCAAAGTCATG 22
    ||||| ||||| |||||
Db 21 ATGTTTCTAAAGTTCAAG 4

RESULT 16
BX891114 41 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-446C12-023804,
DEFINITION genomic survey sequence.
ACCESSION BX891114
VERSION BX891114.1 GI:39923609
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
BIOINFORMATICS 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
PUBMED 14756321
REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
PUBMED
Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
K21P3. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-446C12-023804"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The

lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGTTTCCAAAGTCATGA 23
    ||||| ||||| |||||
Db 4 TTTTCCAAATTCAGAGA 21

RESULT 17
CC888123 45 bp DNA linear GSS 31-JUL-2003
LOCUS SALK_151365.21.90.x Arabidopsis thaliana T-DNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_151365.21.90.x, genomic
survey sequence.
ACCESSION CC888123
VERSION CC888123.1 GI:33364479
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmermann, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
T-DNA.
Class: T-DNA tagged.

FEATURES
source
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_151365.21.90.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more T-DNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          55.0%; Score 13.2; DB 9; Length 45;
Best Local Similarity 83.3%; Pred. No. 2.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGTTTCCAAAGTCATGA 23
    ||||| ||||| |||||
Db 24 TGTTTCCCATGTCATGA 7

RESULT 18
BZ762504/c

```


LOCUS BZ762504 29 bp DNA linear GSS 13-MAR-2003
 DEFINITION SALK_105087.19.80.n Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_105087.19.80.n, genomic
 survey sequence.
 ACCESSION BZ762504
 VERSION BZ762504.1 GI:289335057
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 29)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
 1..29
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotye="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_105087.19.80.n"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 29;
 Best Local Similarity 76.2%; Pred. No. 3.3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCAT 21
 Db 27 CATGTGTATCCAAAGTCCAT 7

RESULT 19
 BE548888
 LOCUS BE548888 37 bp mRNA linear EST 09-AUG-2000
 DEFINITION 601073346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3459586 5',
 mRNA sequence.
 ACCESSION BE548888
 VERSION BE548888.1 GI:9777533
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 37)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E.B. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM8452 row: k column: 11
 High quality sequence stop: 37.
 Location/Qualifiers
 1..37
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3459586"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

FEATURES

source

Query Match 54.2%; Score 13; DB 2; Length 37;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22
 Db 8 TTCCTGCTTCAACAGTGCTTG 28

RESULT 20

BE572262

LOCUS BE572262 40 bp DNA linear GSS 04-APR-2004

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-544G08-020964,
 genomic survey sequence.

ACCESSION BX572262

VERSION BX572262.1 GI:33412435

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.

GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

22755829

12874060

REFERENCE 2

AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 Weissshaar,B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

23117147

14756321

REFERENCE 3

AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
 Weissshaar,B.

TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines

JOURNAL BioTechniques 35 (6), 1164-1168 (2003)

14682050

REFERENCE 4

AUTHORS Rosso,M.G., Li,Y., Strizhov,N. and Weissshaar,B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atlg32090. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source
1. .40
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 40;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTCATGA 23
||||| ||||| ||||| ||||| |||||
Db 14 TCATCATTAACAGGAGCATGA 34

RESULT 21
BE788148
LOCUS
DEFINITION 601480079F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882835 5', mRNA sequence.
VERSION BE788148
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 43)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NTH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM9653 row: n column: 20
High quality sequence stop: 43.
Location/Qualifiers

FEATURES

source
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3882835"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.8 kb. Library constructed by Life Technologies. "

ORIGIN

Query Match 54.2%; Score 13; DB 2; Length 43;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTCATG 22
||||| ||||| ||||| ||||| |||||
Db 14 TTCTGCTTCAACAGTCTTG 34

RESULT 22

BE790838/c
LOCUS
DEFINITION BH790838 43 bp DNA linear GSS 02-APR-2002
SALK_058022.27.05.x Arabidopsis thaliana T-DNA insertion lines
Arabidopsis thaliana genomic clone SALK_058022.27.05.x, genomic survey sequence.

ACCESSION BH790838
VERSION BH790838.1 GI:19883973
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 43)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of T-DNA. This sequence lies within an annotated exon of At3g41627.
Class: T-DNA tagged.
Location/Qualifiers
1. .43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_058022.27.05.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES

source
1. .43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_058022.27.05.x"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 43;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCAATGTTTCCAAAGTCATG 22
||||| ||||| ||||| ||||| |||||
Db 37 TTCATCTTACACACTGCTG 17

RESULT 23

BJ076538
LOCUS
DEFINITION BJ076538 NIBB Mochii normalized Xenopus tailbud library Xenopus 44 bp mRNA linear EST 29-SEP-2003

laevis cDNA clone XL051f21 3', mRNA sequence.
 ACCESSION BJ076538
 VERSION BJ076538.1 GI:17521454
 KEYWORDS EST
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 44)
 AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 The information of this clone is available through the following URL:
 http://xenopus.nibb.ac.jp.

FEATURES

source
 1..44
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL051f21"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud library"

ORIGIN

Query Match 54.2%; Score 13; DB 4; Length 44;
 Best Local Similarity 81.2%; Pred. No. 3.5e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTCATGTTCCAAAGT 17
 Db 11 TTNANGTTTCCAAANT 26

RESULT 24

W11835/c
 LOCUS W11835 28 bp mRNA linear EST 02-OCT-1997
 DEFINITION mb20h01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:330001 5', similar to SW:CATK_RABIT P43236 CATHEPSIN K PRECURSOR ;, mRNA sequence.

ACCESSION W11835
 VERSION W11835.1 GI:1286140
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI: 211401
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: mob.REGA+ET
 High quality sequence stop: 1.

FEATURES

source
 1..28
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:330001"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares mouse p3NMF19.5"
 /note="vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

ORIGIN

Query Match 53.3%; Score 12.8; DB 7; Length 28;
 Best Local Similarity 87.5%; Pred. No. 4.1e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTG 18
 Db 20 TCATGTTCTCCCAAGT 5

RESULT 25

AZ794096
 LOCUS AZ794096 36 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0047P10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0047P10 R, genomic survey sequence.

ACCESSION AZ794096
 VERSION AZ794096.1 GI:12939715
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 36)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0047 row: P column: 10
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES

source
 1..36
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:330001"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares mouse p3NMF19.5"
 /note="vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC2M0047P10"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 12.8; DB 8; Length 36;
 Best Local Similarity 70.8%; Pred. No. 4.2e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 Db 2 CTGTATACATCCAAATTCATGAT 25

RESULT 26
 CC796901/c
 LOCUS
 DEFINITION SALK_144210.22.90.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_144210.22.90.x, genomic survey sequence.

ACCESSION
 VERSION CC796901.1 GI:32392124
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.

FEATURES
 source
 1. .36
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"

/ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_144210.22.90.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 36;
 Best Local Similarity 70.8%; Pred. No. 4.2e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGAT 24
 |||||
 Db 30 CATGGTGTAGCCAAAGTCGTGAT 7

RESULT 27

AA995598
 LOCUS
 DEFINITION OS22H03.s1 NCI CGAP Kids Homo sapiens CDNA clone IMAGE:1606133 3'
 Similar to TR:O14949 O14949 LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN. i, mRNA sequence.

ACCESSION
 VERSION AA995598.1 GI:3182087

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 43)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-k@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 475 Std Error: 0.00

Seq primer: -40ml3 fwd. RT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. .43
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1606133"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kids"
 /notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGAGAGATTCGGCGCAATATTTTATTTTATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

```

Query Match      53.3%; Score 12.8; DB 1; Length 43;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TTCATGTTTCCAAAGT 17
      ||||| ||||| |||||
Db   24  TTCATATTTCCAAAGT 39

RESULT 28
CC049873/c
LOCUS      CC049873
DEFINITION 0130518-03B1-B06 UniformMu MutAIL Library Zea mays genomic clone
            01S-518-3-7to12-B06, genomic survey sequence.
ACCESSION  CC049873
VERSION     CC049873.1 GI:29464764
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 46)
AUTHORS   Latschaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
JOURNAL   Unpublished (2003)
COMMENT   Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drmc@ufl.edu
FEATURES   Sequence flanking probable Mu insertion site in UniformMu line:
            01S-518-3
            Class: transposon insertion site.
            Location/Qualifiers
                1..46
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="W22 (ACR, bz1-m9)"
                /cultivar="UniformMu"
                /db_xref="taxon:4577"
                /clone="01S-518-3-7to12-B06"
                /clone_lib="UniformMu MutAIL Library"
                /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
            insertions in Mu inactive lines were extracted from the
            UniformMu maize population by the thermo asymmetric
            interlaced PCR (TAIL) protocol using primers specific for
            the Mu terminal inverted repeat and a set of 16 arbitrary
            primers. Amplicons were size enriched using Sepharose 400
            spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match      53.3%; Score 12.8; DB 8; Length 46;
Best Local Similarity 70.8%; Pred. No. 4.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  1  CTTCATGTTTCCAAAGTCATGAT 24
      ||||| ||||| |||||
Db   36  CCTCATGTTTGATACAGGGCATGTT 13

RESULT 29
BZ290816/c
LOCUS      BZ290816
DEFINITION SALK_091529.28.85.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_091529.28.85.x, genomic
            survey sequence.
ACCESSION  BZ290816
VERSION     BZ290816.1 GI:24334846
KEYWORDS   GSS.

Query Match      53.3%; Score 12.6; DB 8; Length 26;
Best Local Similarity 78.9%; Pred. No. 5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3  TCATGTTTCCAAAGTCAT 21
      ||||| ||||| |||||
Db   26  TAACTTTTAAAGTGCT 8

RESULT 30
BZ661378/c
LOCUS      BZ661378
DEFINITION SALK_024848.36.30.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_024848.36.30.x, genomic
            survey sequence.
ACCESSION  BZ661378
VERSION     BZ661378.1 GI:28174525
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 31)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Query Match      52.5%; Score 12.6; DB 8; Length 26;
Best Local Similarity 78.9%; Pred. No. 5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3  TCATGTTTCCAAAGTCAT 21
      ||||| ||||| |||||
Db   26  TAACTTTTAAAGTGCT 8

RESULT 31
BZ661378
LOCUS      BZ661378
DEFINITION SALK_024848.36.30.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_024848.36.30.x, genomic
            survey sequence.
ACCESSION  BZ661378
VERSION     BZ661378.1 GI:28174525
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 31)
            Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

```

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..31

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_024848.36.30.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES
source

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 31;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21

|||||

Db 25 TCATGTTTCCAAATTGAT 7

RESULT 31

CG712334/c

LOCUS

DEFINITION 1119026A11.2BL.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG712334

VERSION CG712334.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 32)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119026 row: A column: 11

Class: transposon-tagged.

FEATURES

source

1..32

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.fastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 52.5%; Score 12.6; DB 9; Length 32;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTCAATGTTTCCAAAGTGC 19

|||||

Db 23 CTTCTGCTTCCAGATC 5

RESULT 32

BH850177/c

LOCUS

DEFINITION SALK_070912.49.55.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_070912.49.55.x, genomic survey sequence.

ACCESSION BH850177

VERSION BH850177.1

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_070912.49.55.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 52.5%; Score 12.6; DB 8; Length 37;
Best Local Similarity 78.9%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGC 20

|||||

Db 35 TTCATATTTCCTTAATGCA 17

Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyT not found
Insert Length: 597 Std Error: 0.00
Seq primer: Promega -2lmj3.
Location/Qualifiers
1. .40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3962089"
/db_xref="taxon:9606"
/clone="IMAGE:232098"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares pineal gland N3HPG"
/notes="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not 1; Site_2: Eco RI
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTCACCAATCGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo. "

ORIGIN

Query Match 52.5%; Score 12.6; DB 7; Length 40;
Best Local Similarity 78.9%; Pred.No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 2 TTCATGTTTCCAAAGTGCA 20
||||| |||||||
Db 22 TTCATCTTCCCAACTGAA 4

RESULT 35
TA202B010/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
source

TA202B01Q
41 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 202b01, reverse sequence,
genomic survey sequence.
AL477015
AL477015.1 GI:11843470
GSS.
Trypanosoma brucei
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 41)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (REU927/4 Gutat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nleayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .41
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"

```

/strain="TREU927"
/db_xref="taxon:5691"
/clone="202b01"

ORIGIN
Query Match      52.5%; Score 12.6; DB 9; Length 41;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 22
    ||||| ||||| |||||
Db 21 CACGCTTCAGAAGTGCATG 3

RESULT 36
LOCUS      AI280742      43 bp mRNA linear EST 23-NOV-1998
DEFINITION Qw07c06.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:1990378 3'
            similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ; mRNA
            sequence.
ACCESSION  AI280742
VERSION     AI280742.1 GI:3918975
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 43)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            Cloning Distribution by: Washington University Genome Sequencing Center
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             source
    source           1..43
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:1990378"
                    /tissue_type="poorly-differentiated endometrial
                    adenocarcinoma, 2 pooled tumors"
                    /lab_host="DH10B"
                    /clone_lib="NCI-CGAP_Ut3"
                    /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
                    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                    Average insert size 1.45 kb. Life Technologies catalog #:
                    11541-018"

ORIGIN
Query Match      52.5%; Score 12.6; DB 1; Length 43;
Best Local Similarity 78.9%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCAT 21
    ||||| ||||| ||||| |||||
Db 16 TCATCTTTTCAAGAGCTT 34

RESULT 37
BZ766776/c
```

```

LOCUS      BZ766776      43 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_137836.19.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_137836.19.55.x, genomic
            survey sequence.
ACCESSION  BZ766776
VERSION     BZ766776.1 GI:28939329
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
            1 (bases 1 to 43)
AUTHORS     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gardinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
            source     1..43
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="SALK_137836.19.55.x"
                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                    each of which contains one or more TDNA insertion
                    elements. The resultant fragment for each line was
                    directly sequenced to determine the genomic sequence at
                    the site of insertion. Details of the protocols used can
                    be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      52.5%; Score 12.6; DB 8; Length 43;
Best Local Similarity 78.9%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ATGTTTCCAAAGTGCATGA 23
    ||||| ||||| ||||| |||||
Db 37 ATGTAGCCAAAGTGAGTGA 19

RESULT 38
AZ388487/c
LOCUS      AZ388487      37 bp DNA linear GSS 02-OCT-2000
DEFINITION LM0148F03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            Clone UUGC1M0148F03 R, genomic survey sequence.
ACCESSION  AZ388487
VERSION     AZ388487.1 GI:10502195
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 37)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```


JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0148 row: F column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

FEATURES
source

1..37
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0148F03"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.7%; Score 12.4; DB 8; Length 37;
Best Local Similarity 72.7%; Pred. No. 6.5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 23 TCCTATACCAAGTACATGGT 2

RESULT 39

BH866468
LOCUS
DEFINITION
SAUK_101369 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SAUK_101369, genomic survey sequence.

ACCESSION

BH866468

VERSION

BH866468.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 41)

REFERENCE

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At3g60570.
Class: TDNA tagged.

FEATURES
source

1..41
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK 101369"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.7%; Score 12.4; DB 8; Length 41;
Best Local Similarity 72.7%; Pred. No. 6.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24

Db 6 TCGCTTACCAAGCCCATGAT 27

RESULT 40

TA232A04Q/c

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 232a04, reverse sequence, genomic survey sequence.

ACCESSION

AL481755

VERSION

AL481755.1

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

1 (bases 1 to 42)

REFERENCE

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/

Location/Qualifiers

1..42

/organism="Trypanosoma brucei"

```
/mol_type="genomic DNA"  
/strain="REU927"  
/db_xref="taxon:5691"  
/clone="232a04"
```

ORIGIN

```
Query Match      51.7%; Score 12.4; DB 9; Length 42;  
Best Local Similarity 72.7%; Pred. No. 6.6e+05;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      3 TCATGTTTCCAAAGTGCATGAT 24  
        |||  |  |||||  |||||  
Db     23 TCACTATACCAAGGTATGAT 2
```

Search completed: November 18, 2005, 21:12:43
Job time : 1150.98 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 46.6312 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTGCATGAT 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUB_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	1	US-07-989-160-4
2	16.2	67.5	34	2	US-08-577-492-21
3	16.2	67.5	34	3	US-09-079-630-21
C 4	15.6	65.0	25	4	US-09-396-196G-53744
C 5	14.8	61.7	25	4	US-09-396-196G-21176
C 6	14.8	61.7	25	4	US-09-396-196G-21177
C 7	14.8	61.7	25	4	US-09-396-196G-21178
C 8	14.6	60.8	25	4	US-09-396-196G-23224
C 9	14.6	60.8	27	3	US-08-908-643C-34
C 10	14	58.3	25	4	US-09-396-196G-59686
C 11	14	58.3	25	4	US-09-396-196G-122551
C 12	14	58.3	36	3	US-08-961-083-258
C 13	14	58.3	36	4	US-09-536-784-258
C 14	14	58.3	50	4	US-08-956-171E-1998
C 15	14	58.3	50	4	US-08-781-986A-1998
C 16	13.8	57.5	25	4	US-09-232-785-173
C 17	13.8	57.5	25	4	US-09-396-196G-21175
C 18	13.8	57.5	25	4	US-09-396-196G-109424
C 19	13.8	57.5	25	4	US-09-396-196G-109425
C 20	13.8	57.5	47	4	US-09-671-317-784
C 21	13.6	56.7	20	4	US-09-913-192A-10
C 22	13.6	56.7	25	3	US-08-544-381B-80
C 23	13.6	56.7	25	4	US-09-396-196G-41037
C 24	13.6	56.7	25	4	US-09-396-196G-59155
C 25	13.6	56.7	25	4	US-09-396-196G-122534
C 26	13.6	56.7	47	4	US-09-422-978-2662
C 27	13.4	55.8	17	3	US-08-584-040-5610

Sequence 5611, Ap
Sequence 2500, Ap
Sequence 2501, Ap
Sequence 2501, Ap
Sequence 2501, Ap
Sequence 10, Appl
Sequence 30572, A
Sequence 33631, A
Sequence 33632, A
Sequence 45409, A
Sequence 45410, A
Sequence 70209, A
Sequence 3015, Ap
Sequence 3250, Ap
Sequence 835, Appl
Sequence 9, Appl
Sequence 5610, Ap
Sequence 12297, A

ALIGNMENTS

RESULT 1
US-07-989-160-4
; Sequence 4, Application US/07989160
; Patent No. 542923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-989-160-4

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.07; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTCATGTTTCCAAAGTGCATGAT 24
|||||||

```
Db      1  CTTTCATGTTTCCAAAGTGCATG 24

RESULT 2
US-08-577-492-21
; Sequence 21, Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,492
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-577-492-21

Query Match      67.5%; Score 16.2; DB 2; Length 34;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| ||| |||
Db      3  TTTAAGCTTCCAAAGTGCATG 23

RESULT 3
US-09-079-630-21
; Sequence 21, Application US/09079630
; Patent No. 6291199
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199ris
; STREET: One Liberty Place, 46th floor

Db      1  CTTTCATGTTTCCAAAGTGCATG 24

RESULT 2
US-08-577-492-21
; Sequence 21, Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,492
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-577-492-21

Query Match      67.5%; Score 16.2; DB 2; Length 34;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2  TTCATGTTTCCAAAGTGCATG 22
      ||| ||| ||| ||| ||| ||| ||| |||
Db      3  TTTAAGCTTCCAAAGTGCATG 23

RESULT 4
US-09-396-196G-53744/c
; Sequence 53744, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-53744

Query Match      65.0%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TTCATGTTTCCAAAGTGCATGA 23
      ||| ||| ||| ||| ||| ||| ||| |||
```

Db 25 TTCAACTTCCCAAGTGCATCA 4

RESULT 5

US-09-396-196G-21176/c

; Sequence 21176, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21176

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21176

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

Db 23 TGTTCCTCAAGTGCATGA 6

RESULT 6

US-09-396-196G-21177/c

; Sequence 21177, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21177

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21177

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

Db 22 TGTTCCTCAAGTGCATGA 5

RESULT 7

US-09-396-196G-21178/c

; Sequence 21178, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21178

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-21178

Query Match 61.7%; Score 14.8; DB 4; Length 25;

Best Local Similarity 88.9%; Pred. No. 1.3e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCAAGTGCATGA 23

Db 20 TGTTCCTCAAGTGCATGA 3

RESULT 8

US-09-396-196G-23224/c

; Sequence 23224, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23224

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-23224

Query Match 60.8%; Score 14.6; DB 4; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTGCATG 22

Db 24 TTCATGTTTCCAAAGGCTTG 4

RESULT 9

US-08-908-643C-34/c

; Sequence 34, Application US/08908643C

; Patent No. 6120995

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; APPLICANT: Pearlman, Joshua M.

; APPLICANT: Barber, Michael T.

; APPLICANT: Schultze, Stephanie

; APPLICANT: Parkinson, Scott J.

; TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO COLORECTAL CANCER CELLS AND METHODS OF USING THE SAME

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908.643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-08-908-643C-34

Query Match 60.8%; Score 14.6; DB 3; Length 27;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 24

Db 26 CATATGTCCAAAGACGAGAT 6

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908.643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-08-908-643C-34

Query Match 60.8%; Score 14.6; DB 3; Length 27;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 24

Db 26 CATATGTCCAAAGACGAGAT 6

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908.643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-08-908-643C-34

Query Match 60.8%; Score 14.6; DB 3; Length 27;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 24

Db 26 CATATGTCCAAAGACGAGAT 6

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908.643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-08-908-643C-34

Query Match 60.8%; Score 14.6; DB 3; Length 27;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATG 24

Db 26 CATATGTCCAAAGACGAGAT 6

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

```
;
; TOPOLOGY: linear
; US-08-961-083-258
;
; Query Match 58.3%; Score 14; DB 3; Length 36;
; Best Local Similarity 77.3%; Pred. No. 3.1e+03;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 3 TCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 3 TCAAGCTTCCAAACTGGTTGAT 24
; ||| ||||| |||||
;
; RESULT 13
; US-09-536-784-258
; Sequence 258, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 258:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 258:
;
; US-09-536-784-258
;
; Query Match 58.3%; Score 14; DB 4; Length 36;
; Best Local Similarity 77.3%; Pred. No. 3.1e+03;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 3 TCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 3 TCAAGCTTCCAAACTGGTTGAT 24
; ||| ||||| |||||
;
; RESULT 14
; US-08-956-171E-1998
; Sequence 1998, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
;
; INFORMATION FOR SEQ ID NO: 1998:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1998:
;
; US-08-956-171E-1998
;
; Query Match 58.3%; Score 14; DB 4; Length 50;
; Best Local Similarity 73.9%; Pred. No. 3.3e+03;
; Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 2 TTCATGTTTCCAAAGTGCATGAT 24
; ||| ||||| |||||
; Db 7 TTGATGNTCTCAAGAACATGAT 29
; ||| ||||| |||||
;
; RESULT 15
; US-08-781-986A-1998
; Sequence 1998, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
;
; INFORMATION FOR SEQ ID NO:
; LENGTH:
; TYPE:
; STRANDEDNESS:
; TOPOLOGY:
; SEQUENCE DESCRIPTION:
;
; US-08-781-986A-1998
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1998:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-1998

Query Match      58.3%; Score 14; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 TTTCATGTTTCCAAAGTGCATGAT 24
      ||||| ||| ||||| |||||
Db      7 TTGATGTTCTCAAGAACATGAT 29

RESULT 16
US-09-232-785-173
; Sequence 173, Application US/09232785
; Patent No. 673365
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig S
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 4481/1E188US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 173
; LENGTH: 20;
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-173

Query Match      57.5%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TTTCATGTTTCCAAAGTG 18
      ||||| ||||| |||||
Db      3 TTTCATGTTTCCAAATGT 19

RESULT 17
US-09-396-196G-21175/c
; Sequence 21175, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-109425

; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21175
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-21175

Query Match      57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 GTTCCAAAGTGCATGA 23
      ||||| ||||| |||||
Db      25 GTTTCAAACTGCATGA 9

RESULT 18
US-09-396-196G-109424/c
; Sequence 109424, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-109424

Query Match      57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 TTTCCTAAGTGCATGAT 24
      ||||| ||||| |||||
Db      23 TTTCCTAAGTGCAGAT 7

RESULT 19
US-09-396-196G-109425/c
; Sequence 109425, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-109425
```



```
Query Match          57.5%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TTTCCAAAGTGCATGAT 24
        ||||| ||||| |||||
DB      17 TTTCTTAAGTGCAGGAT 1

RESULT 20
US-09-671-317-784
; Sequence 784, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 784:
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-266-203 : polymorphic base C or T
US-09-671-317-784

Query Match          57.5%; Score 13.8; DB 4; Length 47;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 TGTTCCTCAAGTTCGATGAT 24
        ||||| ||||| |||||
DB      9 TGTTCCTCAAGTTCGATGAT 27

RESULT 21
US-09-913-192A-10
; Sequence 10, Application US/09913192A
; Patent No. 6767738
; GENERAL INFORMATION:
; APPLICANT: GAGE, FRED H.
; APPLICANT: PALMER, THEO
; APPLICANT: SAFAR, FRANCIS G.
; APPLICANT: TAKAHASHI, JUN
; APPLICANT: TAKAHASHI, MASAYO
; TITLE OF INVENTION: ISOLATION OF STEM CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: SALK2250-1
; CURRENT APPLICATION NUMBER: US/09/913,192A
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: PCT/US00/03596
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/119,642
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/155,871
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 18
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-913-192A-10

Query Match          56.7%; Score 13.6; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 CATGTTTCCAAAGTGCATGA 23
        ||||| ||||| |||||
DB      1 CATGTATTCAAGACCATGA 20

RESULT 22
US-08-544-381B-80
; Sequence 80, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; DETECTING CYSTIC FIBROSIS
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-80

Query Match          56.7%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CATGTTTCCAAAGTGCATGA 23
Db 4 CATTTTGCAAAGTTCATTA 23

RESULT 23
US-09-396-196G-41037/c
; Sequence 41037, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-41037

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTCATGTTTCCAAAGTGCA 20
Db 24 CTACAGATTTCAAAGTGCA 5

RESULT 24
US-09-396-196G-59155
; Sequence 59155, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59155
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-59155

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTCATGTTTCCAAAGTGCA 20
Db 24 CTACAGATTTCAAAGTGCA 5

RESULT 25
US-09-396-196G-122534
; Sequence 122534, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-122534

Query Match          56.7%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATG 22
Db 1 TCATTCTTCCAAAGTGCTTG 20

RESULT 26
US-09-422-978-2662/c
; Sequence 2662, Application US/09422978
; Patent No. 8537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2662
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-13113-234 : polymorphic base G or A
US-09-422-978-2662

Query Match          56.7%; Score 13.6; DB 4; Length 47;
Best Local Similarity 72.7%; Pred. No. 5e+03;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCATGAT 24
```

Db 33 TCATGAATTAATAATTCATGAT 12
||||| | : ||| | |||||

RESULT 27

US-08-584-040-5610/c
; Sequence 5610, Application US/08584040
; Patent No. 6346398

; GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: TREATMENT OF DISEASES OR

; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR

; NUMBER OF SEQUENCES: 8502

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 5610:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-584-040-5610

Query Match

Best Local Similarity 55.8%; Score 13.4; DB 3; Length 17;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21

Db 16 GTTTCCAAAGAGCAT 2

RESULT 28

US-08-584-040-5611/c

; Sequence 5611, Application US/08584040

; Patent No. 6346398

; GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James

; APPLICANT: Stinchcomb, Dan T.

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/584,040

; FILING DATE: January 11, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974

; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 5611:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-584-040-5611

Query Match 55.8%; Score 13.4; DB 3; Length 17;

Best Local Similarity 93.3%; Pred. No. 5.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21

Db 15 GTTTCCAAAGAGCAT 1

RESULT 29

US-09-371-772B-2500/c

; Sequence 2500, Application US/09371772B

; Patent No. 6566127

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MEHB00,876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 14225

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2500
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2500

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTTCCAAAGAGCAT 2

RESULT 30

US-09-371-772B-2501/c
; Sequence 2501, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2501
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2501

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 15 GTTTCCAAAGAGCAT 1

RESULT 31

US-09-685-664B-2500/c
; Sequence 2500, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2500
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2500

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 16 GTTTCCAAAGAGCAT 2

RESULT 32

US-09-685-664B-2501/c
; Sequence 2501, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2501
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2501

Query Match 55.8%; Score 13.4; DB 4; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GTTTCCAAAGTGCAT 21
| | | | | | | | | | | | | | | | | | | | |
Db 15 GTTTCCAAAGAGCAT 1

RESULT 33

US-07-768-437-10
; Sequence 10, Application US/07768437
; Patent No. 5371009
; GENERAL INFORMATION:
; APPLICANT: NEUBERGER, MICHAEL S.
; APPLICANT: MEYER, KERSTIN B.
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO ENHANCERS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,437
FILING DATE: 19910925
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 92374/HCM/JNF/C6734M
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-768-437-10

Query Match 55.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAG 16
Db 3 TTCAAGTTTCCAAAG 17

RESULT 34
US-09-396-196G-30572/c
Sequence 30572, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30572
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-30572

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 5.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TTCATGTTTCCAAAGTCATGAT 24
Db 25 TGCCTTCTTCCAAAGTCATGAT 3

RESULT 35
US-09-396-196G-33631/c
Sequence 33631, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33631
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-33631

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCCAAAGTCATGAT 24
Db 18 TCCAAAGTCATCAT 4

RESULT 36
US-09-396-196G-33632/c
Sequence 33632, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33632
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-33632

Query Match 55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCCAAAGTCATGAT 24
Db 15 TCCAAAGTCATCAT 1

RESULT 37
US-09-396-196G-45409
Sequence 45409, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45409

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-45409

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAA 15
Db 11 CTTTCATGTTTACAAA 25

RESULT 38
US-09-396-196G-45410
; Sequence 45410, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-45410

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAA 15
Db 5 CTTTCATGTTTACAAA 19

RESULT 39
US-09-396-196G-70209/c
; Sequence 70209, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70209
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-70209

Query Match      55.8%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 5.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
   ||||| ||||| ||||| |||||
Db 24 CTTTCATGTTTATAAAGAACATGA 2

RESULT 40
US-09-422-978-3015/c
; Sequence 3015, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3015
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21687-313 : polymorphic base G or A
US-09-422-978-3015

Query Match      55.8%; Score 13.4; DB 4; Length 47;
Best Local Similarity 73.9%; Pred. No. 6.2e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATGA 23
   ||||| ||||| ||||| |||||
Db 23 CTTTCATCTTCCAGAGACTAAGA 1

Search completed: November 18, 2005, 11:21:59
Job time : 47.6312 Secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 322.586 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-4

Perfect score: 24

Sequence: 1 CTTTCATGTTTCCAAAGTCATGAT 24

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10K_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10L_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10M_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10N_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10O_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10P_PUBCOMB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US10Q_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US10R_PUBCOMB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US10S_PUBCOMB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US10T_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-08-469-172-4
2	24	100.0	24	20	US-10-788-779-4
3	18.2	75.8	25	22	US-10-956-157-125280
4	16.8	70.0	25	26	US-11-036-317-256437
5	15.8	65.8	25	24	US-10-719-956-403636

6	15.8	65.8	25	25	US-11-036-317-363552	Sequence 363552,
7	15.8	65.8	25	26	US-11-036-317-478233	Sequence 478233,
8	15.8	65.8	25	26	US-11-060-756-27538	Sequence 27538, A
9	15.8	65.8	25	26	US-11-060-756-27539	Sequence 27539, A
10	15.8	65.8	25	26	US-11-060-756-27549	Sequence 27549, A
11	15.8	65.8	25	26	US-11-060-756-170463	Sequence 170463,
12	15.8	65.8	25	26	US-11-060-756-180820	Sequence 180820,
13	15.6	65.0	25	22	US-10-719-900-394513	Sequence 394513,
14	15.6	65.0	25	22	US-10-809-189-53744	Sequence 53744, A
15	15.6	65.0	25	22	US-10-809-189-53744	Sequence 53744, A
16	15.6	65.0	25	26	US-10-719-956-219368	Sequence 219368,
17	15.4	64.2	25	26	US-11-036-317-606061	Sequence 606061,
18	15.2	63.3	25	21	US-10-973-783-180	Sequence 180, Appl
19	15.2	63.3	25	21	US-10-882-761-37	Sequence 37, Appl
20	15.2	63.3	25	22	US-10-719-900-199176	Sequence 199176,
21	15.2	63.3	25	22	US-10-719-900-413418	Sequence 413418,
22	15.2	63.3	25	22	US-10-956-157-132433	Sequence 132433,
23	15.2	63.3	25	24	US-10-843-527-50302	Sequence 50302, A
24	15.2	63.3	25	24	US-10-843-527-51276	Sequence 51276, A
25	15.2	63.3	25	24	US-10-843-527-51277	Sequence 51277, A
26	15.2	63.3	25	24	US-10-843-527-185436	Sequence 185436,
27	15.2	63.3	25	24	US-10-843-527-185437	Sequence 185437,
28	15.2	63.3	25	26	US-11-036-317-81554	Sequence 186411, A
29	15.2	63.3	25	26	US-11-036-317-47524	Sequence 147524,
30	15.2	63.3	25	26	US-11-036-317-472576	Sequence 472576,
31	15.2	63.3	25	26	US-11-036-317-551468	Sequence 551468,
32	15.2	63.3	25	25	US-11-036-317-771700	Sequence 771700,
33	15	62.5	25	22	US-10-719-900-247281	Sequence 247281,
34	15	62.5	25	24	US-10-681-773-115420	Sequence 115420,
35	15	62.5	25	24	US-10-681-773-120711	Sequence 120711,
36	15	62.5	25	26	US-11-036-317-989895	Sequence 989895,
37	14.8	61.7	20	20	US-10-316-244-31	Sequence 31, Appl
38	14.8	61.7	20	20	US-10-316-244-136	Sequence 136, Appl
39	14.8	61.7	25	22	US-10-719-900-48069	Sequence 48069, A
40	14.8	61.7	25	22	US-10-719-900-262242	Sequence 262242,
41	14.8	61.7	25	22	US-10-719-900-827966	Sequence 827966,
42	14.8	61.7	25	22	US-10-719-900-838178	Sequence 838178,
43	14.8	61.7	25	22	US-10-809-189-21176	Sequence 21176, A
44	14.8	61.7	25	22	US-10-809-189-21177	Sequence 21177, A
45	14.8	61.7	25	22	US-10-809-189-21178	Sequence 21178, A

ALIGNMENTS

RESULT 1
US-08-469-172-4
; Sequence 4, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:


```
RESULT 5
US-10-719-956-403636
; Sequence 403636, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403636
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-403636
Query Match      65.8%; Score 15.8; DB 24; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTCCCAAAGTGCAT 21
||||| |||||||
Db 5 TCATGTTACCAAGTGCCT 23

RESULT 6
US-11-036-317-363552
; Sequence 363552, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 363552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-363552
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGTTCCCAAAGTGCAT 21
||||| |||||||
Db 7 TCATGTTACCGAAGTGCAT 25

RESULT 7
US-11-036-317-478233
; Sequence 478233, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 478233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-478233
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 3 TGTTCCTCCAAAGTGCATGTT 21

RESULT 8
US-11-060-756-27538
; Sequence 27538, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27538
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 6 TGTTCCTCCAAAGTGCATGAT 24

RESULT 9
US-11-060-756-27539
; Sequence 27539, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27539
Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGTTCCTCCAAAGTGCATGAT 24
||||| |||||||
Db 7 TGTTCCTCCAAAGTGCATGAT 25
```

```
RESULT 10
US-11-060-756-27549
; Sequence 27549, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-27549

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      5 TGTTCCTCCAAAGTCATGAT 23

RESULT 11
US-11-060-756-170463
; Sequence 170463, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-170463

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      5 TGTTCCTCCAAAGTCATGAT 23

RESULT 12
US-11-060-756-180820
; Sequence 180820, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180820
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-180820

Query Match      65.8%; Score 15.8; DB 26; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 TGTTCCTCCAAAGTCATGAT 24
      ||||| ||||| ||||| |||||
Db      7 TGTTCCTCCAAAGTCATGAT 25

RESULT 13
US-10-719-900-394513
; Sequence 394513, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 394513
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-394513

Query Match      65.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTCATG 22
      ||||| ||||| ||||| |||||
Db      1 CTTTCATGTTTTCATTTGTGCAAG 22

RESULT 14
US-10-809-189-53744/c
; Sequence 53744, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-53744

Query Match      65.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2 TTTCATGTTTCCAAAGTGCATGA 23
|||||
Db 25 TTCAACTTCCCAAGTGCATCA 4

RESULT 15

US-10-719-956-219368/c
; Sequence 219368, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-219368

Query Match 65.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
|||||
Db 22 CTGCTGTGTCCAAAGTCTTG 1

RESULT 16

US-11-036-317-606061/c
; Sequence 606061, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 606061
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-606061

Query Match 65.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGCATG 22
|||||
Db 24 CTTTCATCTGTACAAAGTCTTG 3

RESULT 17

US-10-973-783-180
; Sequence 180, Application US/10973783
; Publication No. US20050164246A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Bibikova, Marina
; TITLE OF INVENTION: Methods and Compositions For Diagnosing
; TITLE OF INVENTION: Lung Cancer with Specific DNA Methylation Patterns

; FILE REFERENCE: 67234-100
; CURRENT APPLICATION NUMBER: US/10/973,783
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 10/845,667
; PRIOR FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/471,488
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 1513
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-973-783-180

Query Match 64.2%; Score 15.4; DB 24; Length 48;
Best Local Similarity 94.1%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGC 19
|||||
Db 5 TCAIGTTTCCAAAGTCC 21

RESULT 18

US-10-882-761-37/c
; Sequence 37, Application US/10882761
; Publication No. US20040265890A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRS11
; FILE REFERENCE: D0066DIV
; CURRENT APPLICATION NUMBER: US/10/882,761
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 10/029,347
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 25
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Synthesized oligonucleotide.
US-10-882-761-37

Query Match 63.3%; Score 15.2; DB 21; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTTCATGTTTCCAAAGTGC 20
|||||
Db 23 CTTGCTGCTCCAAAGTGC 4

RESULT 19

US-10-719-900-199176/c
; Sequence 199176, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 199176
; LENGTH: 25
; TYPE: DNA

```

; ORGANISM: Mus musculus
US-10-719-900-199176

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCATGTTTCCAAAGTGCA 22
   ||||| ||||| |||||
Db 24 TAAAGTTTACAAAGTGCTG 5

RESULT 20
US-10-719-900-413418/c
; Sequence 413418, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 413418
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-413418

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ATGTTTCCAAAGTGCA 24
   ||| ||||| ||||| |||||
Db 21 ATGCTTCCAAAGTGCTGTT 2

RESULT 21
US-10-956-157-132433
; Sequence 132433, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132433
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-132433

Query Match      63.3%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ATGTTTCCAAAGTGCA 24
   ||||| ||||| |||||
Db 1 ATGTTTCCAAAGTACCTGAT 20

RESULT 22
US-10-843-527-50302/c
; Sequence 50302, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50302
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-50302

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTCATGTTTCCAAAGTGCA 20
   ||||| ||||| |||||
Db 22 CTTCATGTTTATAAAGTGAA 3

RESULT 23
US-10-843-527-51276/c
; Sequence 51276, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51276
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-51276

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTCATGTTTCCAAAGTGCA 20
   ||||| ||||| |||||
Db 24 CTTCATGTTTCCAAAGTGAA 5

RESULT 24
US-10-843-527-51277/c
; Sequence 51277, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-51277
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-51277

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      23  CTTTCATGTTTCCAAAGTGAA 4

RESULT 25
US-10-843-527-185436
; Sequence 185436, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 185436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-185436

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      3  CTTTCATGTTTCCAAAGTGAA 22

RESULT 26
US-10-843-527-185437
; Sequence 185437, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 185437
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-185437

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      2  CTTTCATGTTTCCAAAGTGAA 21

RESULT 27
US-10-843-527-186411
; Sequence 186411, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 186411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-186411

Query Match      63.3%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CTTTCATGTTTCCAAAGTGCA 20
         ||||| ||||| ||||| |||||
Db      4  CTTTCATGTTTATAAAGTGAA 23

RESULT 28
US-11-036-317-81554/c
; Sequence 81554, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-81554

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  TCATGTTTCCAAAGTGCA 22
         ||||| ||||| ||||| |||||
Db      20  TCAGTTTCCAAAGCGCTTG 1

RESULT 29
US-11-036-317-147524/c
; Sequence 147524, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

```
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 147524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-147524

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTGCA 20
Db      20 CTTTCAGGTTTCCCAAGTCCA 1

RESULT 30
US-11-036-317-472576/c
; Sequence 472576, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 472576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-472576

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTGCA 20
Db      20 CTTTCATGTCGCAAAAGTGA 1

RESULT 31
US-11-036-317-551468/c
; Sequence 551468, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 551468
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-551468

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 TCATGTTTCCAAAGTGCA 22
Db      20 TCAGGTTTCCAAAGCGCTTG 1

RESULT 32
US-11-036-317-771700/c
; Sequence 771700, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 771700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-771700

Query Match      63.3%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTGCA 20
Db      20 CTTTCATGTCGCAAAAGTGA 1

RESULT 33
US-10-719-900-247281
; Sequence 247281, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247281
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-247281

Query Match      62.5%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CTTTCATGTTTCCAAAGTGCA 23
Db      3 CTACATGGTTCCAAAGTCCGTA 25

RESULT 34
US-10-681-773-115420/c
; Sequence 115420, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
```

```
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115420
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-115420
```

```
Query Match 62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTTTCATGTTTCCAAAGTGCATCA 23
    ||||| ||||| ||||| |||||
Db 24 CTTTCATGTTTCCAGAGTGACGA 2
```

```
RESULT 35
US-10-681-773-120711/c
; Sequence 120711, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 120711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-120711
```

```
Query Match 62.5%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CTTTCATGTTTCCAAAGTGCATCA 23
    ||||| ||||| ||||| |||||
Db 25 CTTTCATGTTTCCAGAGTGACGA 3
```

```
RESULT 36
US-11-036-317-989895
; Sequence 989895, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 989895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-989895
```

```
Query Match 62.5%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 TTCATGTTTCCAAAGTGCATCAT 24
    ||||| ||||| ||||| |||||
Db 2 TTCATCCTTCAGAAAGTACATCAT 24
```

```
RESULT 37
US-10-316-244-31
; Sequence 31, Application US/10316244
; Publication No. US20040110148A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF ORNITHINE DECARBOXYLASE 1 EXPRESSION
; FILE REFERENCE: HTS-0096
; CURRENT APPLICATION NUMBER: US/10/316,244
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 219
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-244-31
```

```
Query Match 61.7%; Score 14.8; DB 20; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 CATGTTTCCAAAGTGCAT 21
    ||||| ||||| |||||
Db 1 CATGTTTCCAAAGAGCAT 18
```

```
RESULT 38
US-10-316-244-136/c
; Sequence 136, Application US/10316244
; Publication No. US20040110148A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF ORNITHINE DECARBOXYLASE 1 EXPRESSION
; FILE REFERENCE: HTS-0096
; CURRENT APPLICATION NUMBER: US/10/316,244
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 219
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-316-244-136
```

```
Query Match 61.7%; Score 14.8; DB 20; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 CATGTTTCCAAAGTGCAT 21
    ||||| ||||| ||||| |||||
Db 20 CATGTTTCCAAAGAGCAT 3
```

RESULT 39
 US-10-719-900-48069
 ; Sequence 48069, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 48069
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-48069

Query Match 61.7%; Score 14.8; DB 22; Length 25;
 Best Local Similarity 88.9%; Pred. No. 6.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 7 GTTTCCAAAGTGCATGAT 24
 ||||| ||||| |||||
 Db 7 GTTTCAGAGTGCATGAT 24

RESULT 40
 US-10-719-900-262242
 ; Sequence 262242, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 262242
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-262242

Query Match 61.7%; Score 14.8; DB 22; Length 25;
 Best Local Similarity 88.9%; Pred. No. 6.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CTTTCATGTTTCCAAAGTG 18
 ||||| ||||| |||||
 Db 4 CTTTCATGTTTCTGAGTG 21

Search completed: November 18, 2005, 15:41:05
 Job time : 323.586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 693.631 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-5
Perfect score: 25
Sequence: 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_phi.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	I12898
2	14.6	58.4	21	6	E25007
3	14.4	57.6	30	6	A19073
4	14.4	57.6	30	6	AR059408
5	14.4	57.6	30	6	AR178489
6	14.4	57.6	37	6	CQ826719
7	14.4	57.6	37	6	CQ826720
8	14.2	56.8	47	6	A94788
9	14	56.0	29	6	BD258702
10	14	56.0	30	6	AX406739
11	14	56.0	40	6	BD180726
12	14	56.0	49	6	AR098688
13	14	56.0	49	6	AR098689
14	14	56.0	49	6	AR098690
15	14	56.0	49	6	AR098692
16	14	56.0	49	6	AR204762
17	14	56.0	49	6	AR204763
18	14	56.0	49	6	AR204764
19	14	56.0	49	6	AR204766

20	14	56.0	50	6	CQ008790	Sequence
21	13.8	55.2	29	6	BD138865	Secreted
22	13.8	55.2	38	6	AX573495	Sequence
23	13.8	55.2	48	6	BD081415	Sequence
24	13.8	55.2	50	6	AR107707	Fused pro
25	13.6	54.4	25	6	AR153673	Sequence
26	13.6	54.4	25	6	CQ862312	Sequence
27	13.6	54.4	29	6	BD197942	Method an
28	13.6	54.4	31	6	AX801708	Sequence
29	13.6	54.4	33	6	CQ867997	Sequence
30	13.6	54.4	36	6	AR366334	Sequence
31	13.6	54.4	36	6	AX030985	Sequence
32	13.6	54.4	42	6	AX767197	Sequence
33	13.6	54.4	50	6	AX157872	Sequence
34	13.4	53.6	19	6	AX671483	Sequence
35	13.4	53.6	19	6	AX675004	Sequence
36	13.4	53.6	25	6	AX043509	Sequence
37	13.4	53.6	27	6	AX817756	Sequence
38	13.4	53.6	30	6	AX115007	Sequence
39	13.4	53.6	36	6	AX026972	Sequence
40	13.4	53.6	36	6	AX035992	Sequence
41	13.4	53.6	36	6	AX093461	Sequence
42	13.4	53.6	38	6	BD137046	Method of
43	13.4	53.6	38	6	AX080051	Sequence
44	13.4	53.6	42	6	AR103109	Sequence
45	13.4	53.6	42	6	AR139725	Sequence

ALIGNMENTS

RESULT 1	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
VERSION	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
SOURCE	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ORGANISM	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
REFERENCE	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
AUTHORS	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
TITLE	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
JOURNAL	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
FEATURES	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ORIGIN	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Query Match	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Best Local Similarity	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Matches	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Qy	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Db	I12898	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
RESULT 2	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
VERSION	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
SOURCE	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ORGANISM	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
REFERENCE	E25007	Sequence 5 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 57.6%; Score 14.4; DB 6; Length 37;
Best Local Similarity 75.0%; Pred. No. 5.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGCTTCACCTCAGAGGAGAAA 25
||| ||||| ||||| ||||| |||||
Db 6 TGGCTTCACCTCAGAGGAGAAA 29

RESULT 7

CQ826720/c CQ826720 37 bp DNA linear PAT 29-JUN-2004
LOCUS Sequence 23 from Patent EPI431387.
DEFINITION CQ826720
ACCESSION CQ826720
VERSION CQ826720.1 GI:49455448
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Mueller, R., Kirschbaum, T., Suppmann, B., Schoen, H., Engh, R.,
Hoffmann, A., Thalhofer, J. P., Siedel, J., and Engel, W. D.
Heat-labile desoxyribonuclease I variants
Patent: EP 1431387-A 23 23-JUN-2004;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
JOURNAL
TITLE
AUTHORS
Muehler, R., Kirschbaum, T., Suppmann, B., Schoen, H., Engh, R.,
Hoffmann, A., Thalhofer, J. P., Siedel, J., and Engel, W. D.
DEFINITION CQ826720
ACCESSION CQ826720
VERSION CQ826720.1 GI:49455448
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

FEATURES

1. 37
Location/Qualifiers
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 57.6%; Score 14.4; DB 6; Length 37;
Best Local Similarity 75.0%; Pred. No. 5.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGCTTCACCTCAGAGGAGAAA 25
||| ||||| ||||| ||||| |||||
Db 32 TGGCTTCACCTCAGAGGAGAAA 9

RESULT 8

A94788 A94788 47 bp DNA linear PAT 26-JAN-2000
LOCUS Sequence 32 from Patent WO9932630.
DEFINITION A94788
ACCESSION A94788
VERSION A94788.1 GI:6779042
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE

1 (bases 1 to 47)
Jones, P. G. and Holt, D. C.
HERBICIDE BINDING PROTEINS AND TRANSGENIC PLANTS CONTAINING THEM
Patent: WO 9932630-A 32 01-JUL-1999;
JONES PAUL GLYN (GB); ZENECA LTD (GB)
JOURNAL
TITLE
AUTHORS
Jones, P. G. and Holt, D. C.
DEFINITION A94788
ACCESSION A94788
VERSION A94788.1 GI:6779042
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

FEATURES

1. 47
Location/Qualifiers
source
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/clone="VH3"

ORIGIN

Query Match 56.8%; Score 14.2; DB 6; Length 47;
Best Local Similarity 84.2%; Pred. No. 6.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGGCTTCACCTCAGAGGAGA 22
||| ||||| ||||| ||||| |||||
Db 20 GACTTACCTTCAGAGGAGA 38

RESULT 9

BD258702 BD258702 29 bp RNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
DEFINITION BD258702
ACCESSION BD258702
VERSION BD258702.1 GI:33068472
KEYWORDS JP 2002541795-A/6495.
SOURCE unidentified
ORGANISM unclassified

REFERENCE

1 (bases 1 to 29)
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6495 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
JOURNAL
TITLE
AUTHORS
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
DEFINITION BD258702
ACCESSION BD258702
VERSION BD258702.1 GI:33068472
KEYWORDS JP 2002541795-A/6495.
SOURCE unidentified
ORGANISM unclassified

COMMENT

OS Eukaryote
PN JP 2002541795-A/6495
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02, C12R1:91)
CC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..29
FT Location/Qualifiers
/organism="Eukaryote".

FEATURES
source
1..29
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 56.0%; Score 14; DB 6; Length 29;
Best Local Similarity 73.9%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAAA 25
||| ||||| ||||| ||||| |||||
Db 1 GGACTTCACCTGATGAGCGAAA 23

RESULT 10

AX406739/c AX406739 30 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 3 from Patent WO0227021.
DEFINITION AX406739
ACCESSION AX406739
VERSION AX406739.1 GI:21439664
KEYWORDS
SOURCE
ORGANISM
Candida albicans
Candida albicans

REFERENCE

1 Boettger, E. C., Rosenau, J., Kirschner, P. and Jack, T.
Method for detecting fungal infections
Patent: WO 0227021-A 3 04-APR-2002;
Cytonet GmbH & Co. KG (DE)
JOURNAL
TITLE
AUTHORS
Boettger, E. C., Rosenau, J., Kirschner, P. and Jack, T.
DEFINITION AX406739
ACCESSION AX406739
VERSION AX406739.1 GI:21439664
KEYWORDS
SOURCE
ORGANISM
Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

FEATURES

1..30
Location/Qualifiers
source
/organism="Candida albicans"

```

/mol_type="unassigned DNA"
/db_xref="taxon:5476"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 30;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  4 GGCCTCACTTCAGAGGAGAAA 25
    ||| ||||| ||||| |||
Db  29 GACTCCACTTCAGAGCGAGAA  8

RESULT 11
BD180726/c
LOCUS      BD180726          40 bp      DNA      linear      PAT 15-MAY-2003
DEFINITION Array of nucleic acid.
ACCESSION  BD180726
VERSION    BD180726.1 GI:30791644
KEYWORDS   JP 2002330767-A/18.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 40)
AUTHORS    Mineno,J., Rokushima,M., Sotozono,N., Asada,K. and Kato,I.
TITLE      Array of nucleic acid
JOURNAL    Patent: JP 2002330767-A 18 19-NOV-2002;
            TAKARA BIO INC
COMMENT     OS Artificial Sequence
            PN JP 2002330767-A/18
            PD 19-NOV-2002
            PF 11-MAY-2001 JP 2001142082
            PI JUNICHI MINENO,MASATOMO ROKUSHIMA,NARIKAZU SOTOZONO,KIYOZO PI
            ASADA,

PI IKUNOSHIN KATO
PC C12N15/09.C12M1/00,C12O1/68.G01N33/53.G01N37/00.C12N15/00 CC
Designed oligonucleotide probe for detecting in vitro CC
transcribed RNA of
CC Lamda DNA fragment 1
FH Key Location/Qualifiers
FT source 1..40
FT Location/Qualifiers
FEATURES
source 1..40
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 CTGGCTTCACCTTCAGAGGAGA 22
    ||| ||||| ||||| |||
Db  39 CTGGCATTCGCATCAAGAGGA 18

RESULT 12
AR098688/c
LOCUS      AR098688          49 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 46 from patent US 6077668.
ACCESSION  AR098688
VERSION    AR098688.1 GI:12808454
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 49)
AUTHORS    Kool,E.T.
TITLE      Highly sensitive multimeric nucleic acid probes
JOURNAL    Patent: US 6077668-A 46 20-JUN-2000;
            Location/Qualifiers
FEATURES
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 GGCCTTCACCTTCAGAGGAGAAA 24
    ||||| ||| ||||| |||
Db  11 GGCCTTTTCTGAAGAGCGGAAA 32

RESULT 15
```

```

source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 GGCCTTCACCTTCAGAGGAGAAA 24
    ||||| ||| ||||| |||
Db  43 GGCCTTTTCTGAAGAGCGGAAA 22

RESULT 13
AR098689
LOCUS      AR098689          49 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 47 from patent US 6077668.
ACCESSION  AR098689
VERSION    AR098689.1 GI:12808455
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 49)
AUTHORS    Kool,E.T.
TITLE      Highly sensitive multimeric nucleic acid probes
JOURNAL    Patent: US 6077668-A 47 20-JUN-2000;
            Location/Qualifiers
FEATURES
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 GGCCTTCACCTTCAGAGGAGAAA 24
    ||||| ||| ||||| |||
Db  3 GGCCTTTTCTGAAGAGCGGAAA 24

RESULT 14
AR098690
LOCUS      AR098690          49 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 48 from patent US 6077668.
ACCESSION  AR098690
VERSION    AR098690.1 GI:12808456
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 49)
AUTHORS    Kool,E.T.
TITLE      Highly sensitive multimeric nucleic acid probes
JOURNAL    Patent: US 6077668-A 48 20-JUN-2000;
            Location/Qualifiers
FEATURES
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 GGCCTTCACCTTCAGAGGAGAAA 24
    ||||| ||| ||||| |||
Db  3 GGCCTTTTCTGAAGAGCGGAAA 24
```

```
AR098692
LOCUS AR098692 49 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 50 from patent US 6077668.
ACCESSION AR098692
VERSION AR098692.1 GI:12808458
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 50 20-JUN-2000;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 16
AR204762/c
LOCUS AR204762 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 46 from patent US 6368802.
ACCESSION AR204762
VERSION AR204762.1 GI:21502171
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 46 09-APR-2002;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 17
AR204763
LOCUS AR204763 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 47 from patent US 6368802.
ACCESSION AR204763
VERSION AR204763.1 GI:21502172
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 47 09-APR-2002;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 43 GGGCTTTTCTGAAGAGCGGAAA 22

RESULT 18
AR204764
LOCUS AR204764 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 48 from patent US 6368802.
ACCESSION AR204764
VERSION AR204764.1 GI:21502174
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 48 09-APR-2002;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 3 GGGCTTTTCTGAAGAGCGGAAA 24

RESULT 19
AR204766
LOCUS AR204766 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 50 from patent US 6368802.
ACCESSION AR204766
VERSION AR204766.1 GI:21502176
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 50 09-APR-2002;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32

RESULT 20
CQ008790
LOCUS CQ008790 49 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6368802.
ACCESSION CQ008790
VERSION CQ008790.1 GI:21502177
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 49)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 49 09-APR-2002;
FEATURES
source
location/Qualifiers
1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 49;
Best Local Similarity 77.3%; Pred. No. 8.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| ||| ||||| |||||
Db 11 GGGCTTTTCTGAAGAGCGGAAA 32
```

LOCUS CQ008790 50 bp DNA linear PAT 16-JAN-2004
 DEFINITION Sequence 7430 from Patent WO0147944.
 ACCESSION CQ008790
 VERSION CQ008790.1 GI:41015507
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL Shimkets,R.A. and Leach,M.
 Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 PATENT: WO 0147944-A 7430 05-JUL-2001;
 Curagen Corporation (US)
 LOCATION/Qualifiers

FEATURES
 source
 1. .50
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 misc_feature
 25. .26
 /note="Nucleotide deleted between bases 25 and 26"
 Accession number cg43994815"

ORIGIN
 Query Match 56.0%; Score 14; DB 6; Length 50;
 Best Local Similarity 77.3%; Pred. No. 8.5e+04;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
 |||||
 Db 18 GAGTTTCACTACAGGGGACA 39

RESULT 21
 BD138865/C
 LOCUS BD138865 29 bp DNA linear PAT 18-SEP-2002
 DEFINITION Secreted proteins and polynucleotides encoding them.
 ACCESSION BD138865
 VERSION BD138865.1 GI:23233810
 KEYWORDS JP 2002505074-A/10.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (Bases 1 to 29)
 AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A.C., Evans,C.,
 Merberg,D., Treacy,M. and Spaulding,V.
 TITLE Secreted proteins and polynucleotides encoding them
 JOURNAL Patent: JP 2002505074-A 10 19-FEB-2002;
 GENETICS INSTITUTE INC

COMMENT OS Artificial Sequence
 PN JP 2002505074-A/10
 PD 19-FEB-2002
 PF 20-NOV-1998 JP 2000522221
 PR 21-NOV-1997 US 08/975936.26-OCT-1998 US 09/179034 PI
 KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI
 RACIE,
 PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY, VIKKI SPAULDING PC
 C12N15/09, C07K14/47, C12N15/10, C12N15/00, C12N5/00 CC
 oligonucleotide
 CC biotinylated phosphoramidite residue

FEATURES
 source
 1. .29
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 55.2%; Score 13.8; DB 6; Length 29;
 Best Local Similarity 88.2%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGA 17
 |||||
 Db 20 CTGGCTTCACTTCAGA 4

RESULT 22
 AX573495
 LOCUS AX573495 38 bp DNA linear PAT 07-JAN-2003
 DEFINITION Sequence 78 from Patent EP1249503.
 ACCESSION AX573495
 VERSION AX573495.1 GI:27551190
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Chen,J., Taylor,D.D., Weiner,M.P. and Ye,F.
 TITLE Multiplexed gene analysis on a mobile solid support
 JOURNAL Patent: EP 1249503-A 78 16-OCT-2002;
 SMITHKLINE BEECHAM CORPORATION (US)
 LOCATION/Qualifiers

FEATURES
 source
 1. .38
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 55.2%; Score 13.8; DB 6; Length 38;
 Best Local Similarity 88.2%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGA 17
 |||||
 Db 20 CTGGCTTCACTTCAGA 36

RESULT 23
 BD081415
 LOCUS BD081415 48 bp DNA linear PAT 27-AUG-2002
 DEFINITION Fused protein containing angiotensin component and utilization
 thereof in antitumor therapy.

ACCESSION BD081415
 VERSION BD081415.1 GI:22627018
 KEYWORDS JP 2001518304-A/58.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (Bases 1 to 48)
 AUTHORS Bolanowski,M.A., Caparon,M.H., Casperson,G.F., Gregory,S.A.,
 Klein,B.K. and McKearn,J.P.

TITLE Fused protein containing angiotensin component and utilization
 thereof in antitumor therapy
 JOURNAL Patent: JP 2001518304-A 58 16-OCT-2001;
 GD SEARLE AND CO

COMMENT OS Homo sapiens (human)
 PN JP 2001518304-A/58
 PD 16-OCT-2001
 PF 30-SEP-1998 JP 2000513958
 PR 01-OCT-1997 US 60/060609
 PI MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN A
 GREGORY,
 PI BARBARA K KLEIN, JOHN P MCKEARN
 PC C12N15/09, A61K38/00, A61K48/00, A61P9/10, A61P35/00, C07K14/52, PC
 C07K14/56,

FEATURES
 source
 1. .48
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 55.2%; Score 13.8; DB 6; Length 48;
 Best Local Similarity 88.2%; Pred. No. 1.1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
1. .29 /organism='Artificial Sequence'
```



```
DEFINITION Sequence 126 from Patent WO03042247.
ACCESSION AX767197
VERSION AX767197.1 GI:32260748
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 Macdonald,M.L., Goldberg,Y.P. and Hayden,M.R.
TITLE Methods for identifying therapeutic agents for treating diseases
        involving wnt polypeptides and wnt receptors
JOURNAL Patent: WO 03042247-A 126 22-MAY-2003;
        Merck Patent GmbH (DE)
FEATURES
source
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotides for Vh - OL 413"

ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAA 24
Db 12 GCTTCACCTTCGAGTGGACA 31

RESULT 33
AX671483/c
LOCUS AX157872
DEFINITION Sequence 1200 from Patent WO0140521.
ACCESSION AX157872
VERSION AX157872.1 GI:14539203
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0140521-A 1200 07-JUN-2001;
        Curagen Corporation (US)
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg27961578"
misc_feature 26
/note="2 of 2 allelic variants (1199 is other entry)"

ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CTTCACTTCAGAGGAGAAA 25
Db 50 CATCAATTCAGATGGAAA 31

RESULT 34
AX671483
LOCUS AX671483
DEFINITION Sequence 7 from Patent WO0304045.
ACCESSION AX671483
VERSION AX671483.1 GI:29329792
```

```
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 Macdonald,M.L., Goldberg,Y.P. and Hayden,M.R.
TITLE Methods for identifying therapeutic agents for treating diseases
        involving wnt polypeptides and wnt receptors
JOURNAL Patent: WO 0304045-A 7 16-JAN-2003;
        Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 53.6%; Score 13.4; DB 6; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAG 16
Db 4 TGGGCATCACTTCAG 18

RESULT 35
AX675004
LOCUS AX675004
DEFINITION Sequence 131 from Patent WO03005034.
ACCESSION AX675004
VERSION AX675004.1 GI:29333337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 Macdonald,M.L., Zeisler,J.M., Samuels,M., Goldberg,Y.P.,
        Robataille,J.M. and Hayden,M.R.
TITLE Processes for identifying therapeutic agents useful in treating
        diseases involving fz4 gene
JOURNAL Patent: WO 03005034-A 131 16-JAN-2003;
        Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 53.6%; Score 13.4; DB 6; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAG 16
Db 4 TGGGCATCACTTCAG 18

RESULT 36
AX043509/c
LOCUS AX043509
DEFINITION Sequence 1075 from Patent WO0065088.
ACCESSION AX043509
VERSION AX043509.1 GI:11342117
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
```


Qy 2 TGGGCTTCACTTCAGAGGAGAAA 24
| | | | |
Db 5 TAGAATTCATTAAAGAGGAGAAA 27

Search completed: November 18, 2005, 17:42:55
Job time : 695.731 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 172.148 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

Sequence: 1 CTGGCTTCACTTCAGAGGAGAAAA 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167236

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	2	AAQ91125
2	25	100.0	25	9	ACA63115
3	25	100.0	25	13	ADR05301
4	16	64.0	41	6	ABA02364
5	15.4	61.6	30	12	ADH43094
6	15.2	60.8	30	10	ACC58874
7	15.2	60.8	31	10	ACC58875
8	14.8	59.2	25	9	ACI46238
9	14.8	59.2	33	8	ABX12624
10	14.8	59.2	41	8	ABX12626
11	14.8	59.2	41	8	ABX12627
12	14.6	58.4	21	2	AAQ59982
13	14.6	58.4	34	12	ADQ28791
14	14.6	58.4	41	9	ACC42057
15	14.4	57.6	25	10	ABZ84436
16	14.4	57.6	37	12	ADP88540
17	14.4	57.6	37	12	ADP88541
18	14.4	57.6	41	6	ABA02365
19	14.2	56.8	25	9	ACI31972
20	14.2	56.8	25	12	ADP14058

c	21	14.2	56.8	25	12	ADP14057
c	22	14.2	56.8	33	2	AAT31079
c	23	14.2	56.8	39	10	ADF50502
c	24	14.2	56.8	41	6	ABZ24931
c	25	14.2	56.8	47	2	AAH78849
c	26	14.2	56.8	48	10	ADB73490
c	27	14.2	56.8	50	6	ABZ02803
c	28	14	56.0	29	3	AAF06504
c	29	14	56.0	30	6	ABA99901
c	30	14	56.0	40	10	ADH10991
c	31	14	56.0	49	2	AAV12937
c	32	14	56.0	49	2	AAV12941
c	33	14	56.0	49	2	AAV12938
c	34	14	56.0	49	2	AAV12939
c	35	14	56.0	49	2	AAV59251
c	36	14	56.0	49	2	AAV59252
c	37	14	56.0	49	2	AAV59253
c	38	14	56.0	49	2	AAV59253
c	39	14	56.0	49	10	ADC65914
c	40	14	56.0	49	10	ADC65915
c	41	14	56.0	49	10	ADC65913
c	42	14	56.0	49	10	ADC65917
c	43	14	56.0	50	4	AAI34222
c	44	13.8	55.2	24	8	ACC70890
c	45	13.8	55.2	25	9	ACI10278

ALIGNMENTS

RESULT 1

AAQ91125

ID AAQ91125 standard; cdna; 25 BP.

XX AAQ91125;

AC AAQ91125;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer C.

XX Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

KW diagnosis; primer; mutation; detection; ss.

XX Synthetic.

XX US5429923-A.

XX 04-JUL-1995.

XX 11-DEC-1992; 92US-00989160.

XX 11-DEC-1992; 92US-00989160.

XX (HARD) HARVARD COLLEGE.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

XX Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX useful for testing asymptomatic individual(s).

XX Example 1; Col 10; 22pp; English.

XX AAQ91121-Q91130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 CC
 CC Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 CC
 CC Query Match 100.0%; Score 25; DB 2; Length 25;
 CC Best Local Similarity 100.0%; Pred. NO. 0.11;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 CTGGGCTTCACTTCAGAGGAGAAA 25
 CC |||||
 CC 1 CTGGGCTTCACTTCAGAGGAGAAA 25
 CC
 CC RESULT 2
 CC ACA63115
 CC ID ACA63115 standard; DNA; 25 BP.
 CC AC ACA63115;
 CC
 CC 28-AUG-2003 (first entry)
 CC Human beta cardiac myosin heavy chain PCR primer C.
 CC
 CC Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
 CC familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
 CC sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
 CC Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
 CC phenylketonuria; cystic fibrosis.
 CC
 CC Homo sapiens.
 CC
 CC US2003054343-A1.
 CC
 CC 20-MAR-2003.
 CC
 CC 06-JUN-1995; 95US-00469172.
 CC
 CC 11-DEC-1992; 92US-00989160.
 CC
 CC (SEID/) SEIDMAN C.
 CC (SEID/) SEIDMAN J.
 CC (WATK/) WATKINS H.
 CC (ROSE/) ROSENZWEIG A.
 CC
 CC Seidman C, Seidman J, Watkins H, Rosenzweig A;
 CC WPI; 2003-512374/48.
 CC
 CC Detecting a presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
 CC hemophilia, by detecting a mutation in an amplified product of a beta
 CC cardiac myosin heavy-chain DNA.
 CC
 CC Example 1; Page 5; 22pp; English.
 CC
 CC The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
 CC and FHC) comprises detecting a mutation associated with hypertrophic
 CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
 CC chain DNA. The mutations associated with SHC/FHC are detected in the
 CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
 CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
 CC sample). FHC associated point mutation can be classified and used to
 CC determine life expectancy in affected individuals e.g. using a Kaplan-
 CC Meier curve for the classified type of FHC causing point mutation. Also
 CC included are an RNA probe comprising ribonucleotides arranged in a
 CC sequence which is complementary to at least a portion of beta-cardiac
 CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
 CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain cDNA containing an FHC-associated mutation
 CC
 CC Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 CC
 CC Query Match 100.0%; Score 25; DB 9; Length 25;
 CC Best Local Similarity 100.0%; Pred. NO. 0.11;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 CTGGGCTTCACTTCAGAGGAGAAA 25
 CC |||||
 CC 1 CTGGGCTTCACTTCAGAGGAGAAA 25
 CC
 CC RESULT 3
 CC ADR05301
 CC ID ADR05301 standard; DNA; 25 BP.
 CC AC ADR05301;
 CC
 CC 21-OCT-2004 (first entry)
 CC Human beta cardiac myosin heavy chain mutation detection primer C.
 CC
 CC Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
 CC familial hypertrophic cardiomyopathy;
 CC sporadic hypertrophic cardiomyopathy.
 CC
 CC Homo sapiens.
 CC
 CC US2004152121-A1.
 CC
 CC 05-AUG-2004.
 CC
 CC 27-FEB-2004; 2004US-00788779.
 CC
 CC 11-DEC-1992; 92US-00989160.
 CC
 CC 06-JUN-1995; 95US-00469172.
 CC
 CC (SEID/) SEIDMAN C.
 CC (SEID/) SEIDMAN J.
 CC (WATK/) WATKINS H.
 CC (ROSE/) ROSENZWEIG A.
 CC
 CC Seidman C, Seidman J, Watkins H, Rosenzweig A;
 CC WPI; 2004-592586/57.
 CC
 CC Detecting mutations associated with hypertrophic cardiomyopathy to
 CC diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
 CC myosin heavy-chain DNA and detecting the mutation in the amplified
 CC product.
 CC
 CC Claim 18; SEQ ID NO 5; 22pp; English.
 CC
 CC The invention relates to detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
 CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
 CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
 CC amplified product, and detecting the presence or absence of a mutation
 CC associated with hypertrophic cardiomyopathy in the amplified product,
 CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
 CC included are a set of DNA oligonucleotide primers for amplifying beta-
 CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

SQ Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCTTCACCTTCAGAGGAGAAA 25
DB 1 CTGGCTTCACCTTCAGAGGAGAAA 25

RESULT 4
ABA02364
ID ABA02364 standard; DNA; 41 BP.

AC ABA02364;

DT 22-FEB-2002 (first entry)

DE Human nucleotide reductase 9 probe, SEQ ID NO:8.

XX Human; nucleotide reductase 9; recombinant production; malignant tumour;
KW cancer; blood disease; HIV infection; human immunodeficiency virus;
KW immune disorder; inflammatory condition; purine; pyrimidine;
KW metabolism-disorder; embryonic disorder; growth disorder; gene therapy;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.

OS Homo sapiens.

XX WO200181385-A1.

PN 01-NOV-2001.

XX 23-APR-2001; 2001WO-CN000591.

XX 27-APR-2000; 2000CN-00115483.

PA (BTOW-) BLOWNDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-026142/03.

PT Human reductase nucleotide 9 and encoded polynucleotide, used in
PT diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.

XX

Example 7; Page 15; 35pp; Chinese.

CC The invention relates to human nucleotide reductase 9 (AAM52683), nucleic
CC acids encoding it (ABA02359), and a method for the recombinant production
CC of nucleotide reductase 9. The protein has a molecular weight of 9 kD.
CC The present invention additionally discloses an antagonist of nucleotide
CC reductase 9 for therapeutic use, and an antibody which specifically binds
CC to nucleotide reductase 9. Nucleotide reductase 9, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders, inflammatory conditions, disorders of purine
CC and pyrimidine metabolism, and embryonic and growth disorders. The
CC protein may also be used to screen for modulators of its activity or for
CC peptide fingerprinting identification. The polynucleotide can be used as
CC a primer for nucleic acid amplification reactions or as a probe for
CC hybridisation reactions, or in producing gene chips or microarrays.
CC Sequences ABA02364-ABA02365 represent human nucleotide reductase 9 probes
CC used in an exemplification of the invention

SQ Sequence 41 BP; 10 A; 5 C; 9 G; 17 T; 0 U; 0 Other;

Query Match 64.0%; Score 16; DB 6; Length 41;
Best Local Similarity 79.2%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TGGGCTTCACCTTCAGAGGAGAAA 25

DB 15 TGGGCTTCACCTTCAGTTGAAACAA 38

RESULT 5

ADH43094

ID ADH43094 standard; DNA; 30 BP.

AC ADH43094;

DT 25-MAR-2004 (first entry)

DE CRAM protein related primer sequence #SEQ ID 6.

XX Neuroprotective; neutralisation; CRAM;
KW collapsing-response mediator protein-associated molecule; gene therapy;
KW mitochondria; drug development; neural disease; pathosis; PCR; primer;
KW ss.

OS Synthetic.

XX WO2004001038-A1.

XX 31-DEC-2003.

XX 19-JUN-2003; 2003WO-JP007766.

XX 19-JUN-2002; 2002JP-00179105.

XX (NEWI-) NEW IND RES ORG.

XX Yanagi S;

XX WPI; 2004-099123/10.

XX Genes and proteins participating in neutralization of cells or tissues,
XX useful in gene therapy and regeneration medicine, applicable in
XX diagnosis, drug development for neural diseases and study of mechanism of
XX pathosis.

XX Example 1; SEQ ID NO 6; 101pp; Japanese.

XX The invention relates to a method for inducing neutralisation of cells or
XX tissues by using a protein binding to CRAM (collapsing-response mediator
XX protein-associated molecule) protein or its encoded gene. The proteins
XX and their encoded genes are useful in gene therapy and regenerative

CC medicine, e.g. by inducing neutralisation of mitochondria. They are also
CC applicable in diagnosis, drug development for neural diseases and
CC studying the mechanism of pathosis. The current sequence represents CRAM
CC protein related PCR primer sequence.

XX SQ Sequence 30 BP; 5 A; 8 C; 7 G; 10 T; 0 U; 0 Other;
Query Match 61.6%; Score 15.4; DB 12; Length 30;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGG 18
| | | | | | | | | |
Db 8 TGGGCTTCCTCAGG 24

RESULT 6
ACC58874/c
ID ACC58874 standard; DNA; 30 BP.

XX AC ACC58874;
XX DT 08-SEP-2003 (first entry)
XX DE Doubly labelled DNA probe.

XX KW Probe; nucleic acid detection; ss.
XX OS Synthetic.
XX PN WO2003043402-A2.
XX FD 30-MAY-2003.

XX PF 21-OCT-2002; 2002WO-US033699.
XX PR 19-OCT-2001; 2001US-0336432P.
XX FA (PROL-) PROLIGO LLC.

XX PI Bruce I, Davies M, Wolter A;
XX DR WPI; 2003-505122/47.

XX PT Detection or quantification of nucleic acid analyte, by hybridizing a
PT nucleic acid probe having non-identical covalently attached dyes, with
PT nucleic acid analyte, and measuring change in fluorescence of the probes.
XX PS Example 9; Page 33; 110pp; English.

XX CC The present sequence is an example of nucleic acid probes of the
CC invention. The probe may be doubly labelled with non-identical covalently
CC attached dyes, i.e. thiazole orange and MDCC. A bifunctional branched
CC linker is used to attach the dyes to the oligonucleotide. The probe
CC generates a fluorescent signal upon hybridisation to a complementary
CC nucleic acid based on the interaction of an intercalator or DNA groove
CC binder with the formed double-stranded DNA. Nucleic acid probes of the
CC invention can be used in homogeneous assays, real-time PCR monitoring,
CC transcription assays, expression analysis on nucleic acid microarrays and
CC other microarray applications such as genotyping

XX SQ Sequence 30 BP; 7 A; 11 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 15.2; DB 10; Length 30;
Best Local Similarity 85.0%; Pred. No. 3.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGG 21
| | | | | | | | | |
Db 22 TGGGCTTACTGAAGAGG 3

RESULT 7

ACC58875/c
ID ACC58875 standard; DNA; 31 BP.
XX AC ACC58875;

XX DT 08-SEP-2003 (first entry)
XX DE Doubly labelled DNA probe.
XX KW Probe; nucleic acid detection; ss.
XX OS Synthetic.

XX PN WO2003043402-A2.
XX PD 30-MAY-2003.

XX PF 21-OCT-2002; 2002WO-US033699.
XX PR 19-OCT-2001; 2001US-0336432P.
XX PA (PROL-) PROLIGO LLC.

XX PI Bruce I, Davies M, Wolter A;
XX DR WPI; 2003-505122/47.

XX PT Detection or quantification of nucleic acid analyte, by hybridizing a
PT nucleic acid probe having non-identical covalently attached dyes, with
PT nucleic acid analyte, and measuring change in fluorescence of the probes.
XX PS Example 9; Page 33; 110pp; English.

XX CC The present sequence is an example of nucleic acid probes of the
CC invention. The probe may be doubly labelled with non-identical covalently
CC attached dyes, i.e. thiazole orange and MDCC. A bifunctional branched
CC linker is used to attach the dyes to the oligonucleotide. The probe
CC generates a fluorescent signal upon hybridisation to a complementary
CC nucleic acid based on the interaction of an intercalator or DNA groove
CC binder with the formed double-stranded DNA. Nucleic acid probes of the
CC invention can be used in homogeneous assays, real-time PCR monitoring,
CC transcription assays, expression analysis on nucleic acid microarrays and
CC other microarray applications such as genotyping

XX SQ Sequence 31 BP; 8 A; 11 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 15.2; DB 10; Length 31;
Best Local Similarity 85.0%; Pred. No. 3.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGG 21
| | | | | | | | | |
Db 23 TGGGCTTACTGAAGAGG 4

RESULT 8
ACI46238
ID ACI46238 standard; DNA; 25 BP.
XX AC ACI46238;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 46229.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.


```

Qy      7  TTCACCTTCAGAGGAGAAA 24
      |||||
Db      3  TACACTTCAGAAGAGAAA 20

RESULT 11
ABX12627
ID  ABX12627 standard; DNA; 41 BP.
XX
XX  AC  ABX12627;
XX
XX  DT  13-MAY-2003 (first entry)
XX
DE  Human zinc finger protein 33.22, probe #2.
XX
XX  KW  Human; zinc finger protein 33.22; probe; ss.
XX
XX  OS  Homo sapiens.
XX
XX  PN  CN1376683-A.
XX
XX  PD  30-OCT-2002.
XX
XX  PF  22-MAR-2001; 2001CN-00105731.
XX
XX  PR  22-MAR-2001; 2001CN-00105731.
XX
XX  PA  (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX  PI  Mao Y, Xie Y;
XX
XX  DR  WPI; 2003-176047/18.
XX
XX  PT  Human zinc finger protein 33.22, encoding polynucleotide, antagonist and
XX  recombinant preparation, useful for treating tumors and diabetes.
XX
XX  PS  Example 7; Page 20 (Disclosure); 32pp; Chinese.
XX
XX  CC  The invention describes a human zinc finger protein -33.22, encoding
XX  polynucleotide, antagonist, and recombinant preparation. This sequence
XX  CC  represents a probe used to detect DNA encoding the human zinc finger
XX  CC  protein 33.22
XX
XX  SQ  Sequence 41 BP; 20 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

      Query Match      59.2%; Score 14.8; DB 8; Length 41;
      Best Local Similarity 88.9%; Pred. No. 6.1e+03;
      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7  TTCACCTTCAGAGGAGAAA 24
      |||||
Db      3  TACACTTCAGAAGAGAAA 20

RESULT 12
AAX59982/C
ID  AAX59982 standard; DNA; 21 BP.
XX
XX  AC  AAX59982;
XX
XX  DT  04-AUG-1999 (first entry)
XX
XX  DE  Oligonucleotide probe specific for Porphyromonas gingivalis.
XX
XX  CC  Species-specific; Bacteroides; microbe; identification; Rikenella;
XX  KW  Porphyromonas; Prevotella; probe; ss.
XX
XX  OS  Synthetic.
XX
XX  PN  JP11127899-A.
XX
XX  PD  18-MAY-1999.
XX

PF  29-OCT-1997; 97JP-00297085.
XX
PR  29-OCT-1997; 97JP-00297085.
XX
PA  (YAKU-) ZH YAKULT BIOSCIENCE KENKYU ZAIDAN.
XX
XX  WI  WPI; 1999-350346/30.
XX
XX  PT  New oligonucleotide probe species-specific to a Bacteroides group microbe
XX  - useful for identification of the microbe.
XX
XX  PS  Claim 1; Page 7; 9pp; Japanese.
XX
XX  CC  AAX59976-93 represents oligonucleotide probes that are species-specific
XX  Bacteroides group microbes. The probes are useful for species-specific
XX  CC  identification of a Bacteroides group microbe
XX
XX  SQ  Sequence 21 BP; 5 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

      Query Match      58.4%; Score 14.6; DB 2; Length 21;
      Best Local Similarity 81.0%; Pred. No. 6.8e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  CTGGGCTTCACCTCAGAGGAG 21
      |||||
Db      21  CCGGGCTTGACTTCAGTGGCG 1

RESULT 13
ADQ28791
ID  ADQ28791 standard; DNA; 34 BP.
XX
XX  AC  ADQ28791;
XX
XX  DT  07-OCT-2004 (first entry)
XX
XX  DE  PCR primer SP-23 to amplify B-IV group phage bacteriolytic gene Seq 11.
XX
XX  KW  bacteriophage; infectious disease; pathogenic; bacteriolysis; ss;
XX  KW  antimicrobial; bacteriolytic; PCR; primer.
XX
XX  OS  Synthetic.
XX
XX  PN  JP2004194654-A.
XX
XX  PD  15-JUL-2004.
XX
XX  PF  03-DEC-2003; 2003JP-00404062.
XX
XX  PR  04-DEC-2002; 2002JP-00352523.
XX
XX  PA  (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
XX
XX  DR  WPI; 2004-503333/48.
XX
XX  PT  Pharmaceutical composition useful for treating infectious diseases,
XX  comprises gene construct containing bacteriolytic gene of bacteriophage,
XX  and carrier.
XX
XX  PS  Example 7; SEQ ID NO 11; 25pp; Japanese.
XX
XX  CC  This invention relates to a novel pharmaceutical composition that
XX  comprises a bacteriolytic gene derived from a bacteriophage.
XX  CC  Specifically, it refers to a bacteriophage chosen from a levi virus of
XX  the Leviviridae family, which is a small globular form RNA phage or a
XX  micro virus of the Microviridae family, which is a small globular form
XX  DNA phage. The bacteriolytic gene in the construct is under the control
XX  of a phage lambda lactose promoter, and further contains a gene encoding
XX  a coat protein as well as an inducer of gene expression i.e. isopropyl
XX  beta-D-1 thio-galactopyranoside (IPTG). The present invention describes a
XX  CC  composition useful for treating infectious disease through the
XX  bacteriolysis of bacteria such as Escherichia coli infections occurring
XX  in both humans and animals. Furthermore, it is a highly reliable, safe

```


CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 XX
 XX SQ Sequence 25 BP; 9 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 10; Length 25;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGGAGAAA 24
 Db 2 CAGCGTTGAACCTCAGAGGAGAAA 25

RESULT 16
 ADP88540
 ID ADP88540 standard; DNA; 37 BP.
 XX
 AC ADP88540;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX
 DE Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO: 22.

XX ss; PCR; cow; bovine pancreatic DNase I;
 KW bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
 KW mutagenic.
 XX
 OS Bos taurus.
 OS Synthetic.
 XX
 XX EPI431387-A1.

XX 23-JUN-2004.
 XX
 XX 16-DEC-2003; 2003EP-00028861.
 XX
 XX 20-DEC-2002; 2002EP-00028558.
 PR
 PR 20-JAN-2003; 2003EP-00001214.
 PR
 PR 21-JAN-2003; 2003US-0441550P.

XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 FA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX
 XX Mueller R, Kirschbaum T, Suppmann B, Schoen H, Engh R;
 PI Hoffmann A, Thalhofer J, Siedel J, Engel W;
 PI
 XX WPI; 2004-452511/43.

XX Variant of bovine pancreatic desoxyribonuclease I produced by specific
 PT amino acid substitutions in bovine pancreatic desoxyribonuclease I, has
 PT increased thermostability and is useful for hydrolyzing DNA.

XX Example 2; SEQ ID NO 22; 46pp; English.

XX The present invention relates to a variant of bovine pancreatic
 CC desoxyribonuclease I (pancreatic DNase I), by way of amino acid
 CC substitution, where at least one different amino acid substitutes for an
 CC amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185,
 CC Arg187, Ile3, Phe82, and Phe128. Bovine pancreatic DNase I is useful for
 CC hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease
 CC activity of the variant of the enzyme to approximately zero units per mg
 CC of protein. The present sequence is a mutagenic primer used to alter the
 CC wild-type bovine pancreatic DNase I coding sequence.

XX
 SQ Sequence 37 BP; 11 A; 10 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 57.6%; Score 14.4; DB 12; Length 37;
 Best Local Similarity 75.0%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGGAGAAA 25
 Db 6 TGGCTTCAATTCACCTTGAGACA 29

RESULT 17
 ADP88541/C
 ID ADP88541 standard; DNA; 37 BP.
 XX
 AC ADP88541;
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX
 DE Bovine pancreatic DNase I mutagenic PCR primer SEQ ID NO: 23.

XX ss; PCR; cow; bovine pancreatic DNase I;
 KW bovine pancreatic desoxyribonuclease I; DNA hydrolysis; primer;
 KW mutagenic.

XX Bos taurus.
 OS Synthetic.
 OS
 XX EPI431387-A1.

XX 23-JUN-2004.

XX 16-DEC-2003; 2003EP-00028861.
 XX
 XX 20-DEC-2002; 2002EP-00028558.
 PR
 PR 20-JAN-2003; 2003EP-00001214.
 PR
 PR 21-JAN-2003; 2003US-0441550P.

XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX
 XX Mueller R, Kirschbaum T, Suppmann B, Schoen H, Engh R;
 PI Hoffmann A, Thalhofer J, Siedel J, Engel W;
 PI
 XX WPI; 2004-452511/43.

XX Variant of bovine pancreatic desoxyribonuclease I produced by specific
 PT amino acid substitutions in bovine pancreatic desoxyribonuclease I, has
 PT increased thermostability and is useful for hydrolyzing DNA.

XX Example 2; SEQ ID NO 23; 46pp; English.

XX The present invention relates to a variant of bovine pancreatic
 CC desoxyribonuclease I (pancreatic DNase I), by way of amino acid
 CC substitution, where at least one different amino acid substitutes for an
 CC amino acid residue chosen from Cys173, Cys101, Cys104, Lys117, Arg185,
 CC Arg187, Ile3, Phe82, and Phe128. Bovine pancreatic DNase I is useful for
 CC hydrolyzing DNA and subsequently reducing the specific desoxyribonuclease
 CC activity of the variant of the enzyme to approximately zero units per mg
 CC of protein. The present sequence is a mutagenic primer used to alter the
 CC wild-type bovine pancreatic DNase I coding sequence.

XX Sequence 37 BP; 12 A; 4 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 12; Length 37;
 Best Local Similarity 75.0%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGGAGAAA 25
 Db 32 TGGCTTCAATTCACCTTGAGACA 9

```
RESULT 18
ABAO2365
ID ABAO2365 standard; DNA; 41 BP.
XX
XX ABAO2365;
AC ABAO2365;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Human nucleotide reductase 9 probe, SEQ ID NO:9.
DE
XX
XX Human; nucleotide reductase 9; recombinant production; malignant tumour;
KW cancer; blood disease; HIV infection; human immunodeficiency virus;
KW immune disorder; inflammatory condition; purine; pyrimidine;
KW metabolism disorder; embryonic disorder; growth disorder; gene therapy;
KW cytosolic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200181385-A1.
FN
XX
XX 01-NOV-2001.
PD
XX
XX 23-APR-2001; 2001WO-CN000591.
PF
XX
XX 27-APR-2000; 2000CN-00115483.
PR
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-026142/03.
DR
XX
XX Human reductase nucleotide 9 and encoded polynucleotide, used in
PT diagnosis and treatment of malignant tumors, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation.
XX
XX Example 7; Page 15; 35pp; Chinese.
PS
XX
XX The invention relates to human nucleotide reductase 9 (AAM52683), nucleic
CC acids encoding it (ABAO2359), and a method for the recombinant production
CC of nucleotide reductase 9. The protein has a molecular weight of 9 kD.
CC The present invention additionally discloses an antagonist of nucleotide
CC reductase 9 for therapeutic use, and an antibody which specifically binds
CC to nucleotide reductase 9. Nucleotide reductase 9, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders, inflammatory conditions, disorders of purine
CC and pyrimidine metabolism, and embryonic and growth disorders. The
CC protein may also be used to screen for modulators of its activity or for
CC peptide fingerprinting identification. The polynucleotide can be used as
CC a primer for nucleic acid amplification reactions or as a probe for
CC hybridisation reactions, or in producing gene chips or microarrays.
CC Sequences ABAO2364-ABAO2365 represent human nucleotide reductase 9 probes
CC used in an exemplification of the invention
XX
XX Sequence 41 BP; 10 A; 6 C; 9 G; 16 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 14.4; DB 6; Length 41;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 TGGGCTTCACCTCAGAGGAGAAA 25
DB 15 TGGGTTCCACTTCAGTTGAAACAA 38
RESULT 19
ACI31972/c
ID ACI31972 standard; DNA; 25 BP.
XX
XX ACI31972;
AC
```

```
13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 31963.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
FN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX
XX (APFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 31963; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 3 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 56.8%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGGCTTCACCTCAGAGGAG 21
DB 22 GGGTACACTACCGAGGAG 4
RESULT 20
ADP14058/c
ID ADP14058 standard; DNA; 25 BP.
XX
XX ADP14058;
AC
XX
XX 26-AUG-2004 (first entry)
DT
```

XX Renal cell carcinoma differentially expressed gene probe #463.
DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
OS
XX WO2004048933-A2.
FN 10-JUN-2004.
XX
PD
XX 21-NOV-2003; 2003WO-US037481.
PF 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
PR (AMHP) WYETH.
XX (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
FI Sloni DK;
PI
XX WPI; 2004-460799/43.
DR
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 794; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 4 A; 5 C; 6 G; 10 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GGCTTCACTTCAGAGGAGA 22
DB 19 GGCTTCACTTCAGAGGAGA 1
RESULT 21
ID ADP14057/c
XX ADP14057 standard; DNA; 25 BP.
XX
AC ADP14057;
XX
XX 26-AUG-2004 (first entry)
DT
XX

DE Renal cell carcinoma differentially expressed gene probe #462.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
OS
XX WO2004048933-A2.
FN 10-JUN-2004.
XX
PD
XX 21-NOV-2003; 2003WO-US037481.
PF 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
PR (AMHP) WYETH.
XX (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
FI Sloni DK;
PI
XX WPI; 2004-460799/43.
DR
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 793; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 3 A; 6 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GGCTTCACTTCAGAGGAGA 22
DB 21 GGCTTCACTTCAGAGGAGA 3
RESULT 22
ID AAT31079
XX AAT31079 standard; DNA; 33 BP.
XX
AC AAT31079;
XX
XX 08-JAN-1997 (first entry)
DT
XX
DE Probe for fungal saccharopine dehydrogenase gene.

XX Probe; primer; fungal pathogen; detection; screening; AIDS;
 KW acquired immune deficiency syndrome; Candida albicans;
 KW Cryptococcus neoformans; Yarrowia lipolytica; Aspergillus fumigatus;
 KW Histoplasma capsulatum; postoperative patients; immunocompromised;
 KW immunosuppressed; ss.
 XX Synthetic.
 OS
 XX
 XX WO9619588-A2.
 PN
 XX
 XX 27-JUN-1996.
 PD
 XX
 XX 20-DEC-1995; 95WO-US016684.
 PF
 XX
 XX 21-DEC-1994; 94US-00360606.
 PR
 XX
 XX (UYMI-) UNIV MIAMI.
 PA (ELIL) LILLY & CO ELI.
 PA
 XX
 XX Bhattacharjee JK, Garrad RC, Skatrud PL, Peery RB;
 PI
 XX
 XX WPI; 1996-309602/31.
 DR
 XX
 XX Detecting fungal infection by detection of saccharopine dehydrogenase
 PT gene - uses probe, primer or antibody specific to conserved Candida
 PT albicans sequences as detection agents.
 PT
 XX
 XX Claim 3; Page 54; 84pp; English.
 PS
 XX
 XX Nucleic acid sequences derived from polypeptide fragments of Candida
 CC albicans saccharopine dehydrogenase and which are conserved in fungi can
 CC be used as probes and primers in methods for detecting fungal pathogens.
 CC They may be used for the detection of C. albicans, Yarrowia lipolytica,
 CC and Cryptococcus neoformans. They may also be used for the detection of
 CC Aspergillus fumigatus and Histoplasma capsulatum, especially in patients
 CC suffering from AIDS, those under treatment with immunosuppressive drugs,
 CC postoperative patients and other immunocompromised patients. The nucleic
 CC acid sequences are described in AAT31079-T31093. The peptide epitopes
 CC from which they are derived are described in AAW00483-W00495
 CC
 XX
 XX Sequence 33 BP; 15 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 2; Length 33;
 Best Local Similarity 84.2%; Pred. No. 1.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 24
 DB 1 CTTCACTTCAGAGGAGAA 19

RESULT 23
 ADF50502/c
 ID ADF50502 standard; DNA; 39 BP.
 AC ADF50502;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX
 XX PCR primer used to amplify human GPR43 DNA (SeqID 182).
 DE
 XX
 XX human; PCR; primer; ss; transformation; endocrine cell line;
 KW expression cloning system; bioactive peptide; GPCR ligand.
 KW
 XX Homo sapiens.
 OS
 XX WO2003087366-A1.
 PN
 XX
 XX 23-OCT-2003.
 PD
 XX
 XX 16-APR-2003; 2003WO-JP004840.
 PF
 XX
 XX

PR 16-APR-2002; 2002JP-00113030.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;
 PI Nishi T, Obinata M;
 PI
 XX WPI; 2003-833737/77.
 DR
 XX
 XX Endocrine cell lines originated from mammalian hypothalamus and
 PT pancreatic islet, applicable in expression cloning systems of bioactive
 PT peptide precursor genes, and in screening G protein-coupled receptor
 PT ligands.
 PT
 XX
 XX Example 25; SEQ ID NO 182; 316pp; Japanese.
 PS
 XX
 XX This invention relates to a novel method for obtaining a DNA that encodes
 CC a peptide acting as agonist, antagonist or inverse agonist on a target
 CC receptor. Specifically, it comprises transformation of endocrine cell
 CC lines originating from mammalian hypothalamus and pancreatic islets,
 CC culturing the transformants and contacting with cells expressing the
 CC target receptor. The identification of those cells with a response
 CC reaction can be used for selecting a transformant cell line with the
 CC appropriate target activity that is expressing the novel transformed DNA.
 CC Accordingly, the present invention describes novel cell lines that are
 CC applicable in expression cloning systems of bioactive peptide precursor
 CC genes, and in screening GPCR ligands for use as drugs including agonists,
 CC antagonists and inverse agonists i.e. activators and inhibitors. Such
 CC cell lines can provide a highly sensitive and convenient GPCR ligand
 CC assay system. This oligonucleotide sequence is a PCR primer used to
 CC amplify human GPCR DNA of the invention.
 CC
 XX
 XX Sequence 39 BP; 7 A; 11 C; 12 G; 9 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 10; Length 39;
 Best Local Similarity 84.2%; Pred. No. 1.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTCAGAGGAG 21
 DB 33 GGACTTCACACAGAGTAG 15

RESULT 24
 ABZ24931/c
 ID ABZ24931 standard; DNA; 41 BP.
 XX
 XX AC ABZ24931;
 XX
 XX 25-MAR-2003 (first entry)
 DT
 XX
 XX Cell division cycle regulatory protein 137.17 probe #1.
 DE
 XX
 XX Cell division cycle regulatory protein 137.17; tumour; cytostatic;
 KW diabetes; cell division; probe; ss.
 KW
 XX Unidentified.
 OS
 XX CN1359915-A.
 PN
 XX 24-JUL-2002.
 PD
 XX
 XX 20-DEC-2000; 2000CN-00135176.
 PF
 XX 20-DEC-2000; 2000CN-00135176.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-733604/80.
 DR
 XX
 XX Polypeptide-cell division cycle regulatory protein 137.17 and
 PT

```
PT polynucleotide encoding it.
XX
XX Example 7; Page 21 (Disclosure); 38pp; Chinese.
XX
CC The present invention relates to cell division cycle regulatory protein
CC 137.17 (see ABP59091). The protein can be used for treating diseases such
CC as diabetes and tumours. The present sequence is a probe, which was used
CC in an example from the invention
XX
XX Sequence 41 BP; 13 A; 8 C; 8 G; 12 T; 0 U; 0 Other;
SQ
    Query Match          56.8%; Score 14.2; DB 6; Length 41;
    Best Local Similarity 84.2%; Pred. No. 1.2e+04;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CTTCACTTCAGAGGAGAA 24
Db      38 CTTCACTTCGGATGACAA 20

RESULT 25
AAX78849
ID AAX78849 standard; DNA; 47 BP.
XX
XX AAX78849;
AC
XX
XX 07-SEP-1999 (first entry)
DT
XX Paraquat binding antibody PQXB1/2 variable heavy chain PCR primer VH3.
DE
XX Paraquat; antibody; light chain; herbicide; resistant; crop plant;
KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;
KW free radical; lipid peroxidation; electron transport; photosystem II;
KW vacuole; cell surface; cytotoxic; sensitive; heavy chain; PQXB1/2;
KW variable region; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO9932630-A1.
FN
XX 01-JUL-1999.
PD
XX
XX 15-DEC-1998; 98WO-GB003760.
PF
XX 19-DEC-1997; 97GB-00026955.
PR
XX (ZENE ) ZENECA LTD.
PA
XX Holt DC, Jones PG;
PI
XX WPI; 1999-405173/34.
XX
XX Herbicide binding proteins and related polynucleotides.
XX
XX Disclosure; Page 42; 60pp; English.
XX
XX This invention describes a novel herbicide binding protein which can
XX confer herbicide resistance activity. Crop plants, such as soybean,
XX cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,
XX potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
XX barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice,
XX pine, poplar, apple, grape, citrus or nut plants, transformed with a
XX herbicide binding protein gene are resistant to the herbicide. Hence,
XX weeds can be selectively controlled in a field of the transformed crops.
XX The plants are substantially resistant or tolerant to herbicides, such as
XX paraquat or diquat, that inhibit photosynthesis by accepting electrons
XX from photosystem I thus generating free radicals which cause lipid
XX peroxidation or by blocking electron transport in photosystem II. The
XX herbicide binding proteins advantageously sequester the herbicide, e.g.
XX at the cell surface or in the vacuoles of a treated plant. Sequestration
XX at the cell surface prevents the entry of the herbicide into the cell so
XX that the herbicide cannot reach its intracellular target and exert any
XX significant cytotoxic effect. The herbicide binding protein inhibits the
```

```
CC mobility of the herbicide from the application site to the whole plant
CC preventing the herbicide reaching particularly sensitive organs.
CC Additionally, tolerant plants can be produced against herbicides that
CC have more than one target site
XX
XX Sequence 47 BP; 16 A; 11 C; 12 G; 8 T; 0 U; 0 Other;
SQ
    Query Match          56.8%; Score 14.2; DB 2; Length 47;
    Best Local Similarity 84.2%; Pred. No. 1.2e+04;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 GGCTTCACCTTCAGAGGAGA 22
Db      20 GACTTACCTTCAGAGGAGA 38

RESULT 26
ADB73490
ID ADB73490 standard; DNA; 48 BP.
XX
XX ADB73490;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX Human breakpoint region AF-4 #4.
DE
XX Human; ds; MLL; cancer; AF-4; CDK-6; SEPTIN6; ALL;
KW acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;
KW chromosomal break point; chromosome 11q23; ATF; BCR; B cell receptor.
XX
XX Homo sapiens.
OS
XX US2003096255-A1.
FN
XX 22-MAY-2003.
PD
XX
XX 09-APR-2002; 2002US-00118783.
PF
XX 19-FEB-1997; 97US-0038624P.
PR
XX 25-AUG-1997; 97US-0056938P.
PR
XX 17-NOV-1997; 97US-0065911P.
PR
XX 19-FEB-1998; 98US-00026033.
XX
XX (FELI/) FELIX C A.
PA (JONE/) JONES D H.
PA (RAPP/) RAPPAPORT E.
XX
XX Felix CA, Jones DH, Rappaport E;
PI
XX WPI; 2003-606415/57.
XX
XX Amplifying an unknown region that flanks a known region of a cancer-
XX associated DNA sequence by subjecting the panhandle structure to
XX extension and to PCR in the presence of a first primer homologous to the
XX second portion.
XX
XX Example 8; Fig 18; 80pp; English.
XX
XX The invention relates to amplifying an unknown region that flanks a known
XX region of a cancer-associated DNA sequence comprising providing a
XX template polynucleotide, ligating a loop-forming oligonucleotide to the
XX 3'-end of the sense strand, annealing the loop-forming oligonucleotide
XX with the first portion to generate a panhandle structure, subjecting the
XX panhandle structure to extension, and subjecting the panhandle structure
XX to PCR in the presence of a first primer homologous to the second
XX portion, where the unknown region is amplified. In the method of
XX amplifying an unknown region that flanks a known region of a cancer-
XX associated DNA sequence, the template polynucleotide comprises a sense
XX strand, comprising the known and unknown regions. The unknown region is
XX nearer the 3'-end of the sense strand than is the known region. The known
XX region is comprises a first or second portion. The first portion is
XX nearer the unknown region than is the second portion. The loop-forming
XX oligonucleotide is complementary to the first portion. The third region
```


CC complementary to the second portion is generated at the free end of the
CC loop-forming oligonucleotide. The cancer-associated DNA sequence
CC comprises ATF1 (not defined) or BCR (B cell receptor). The method is
CC useful for amplifying an unknown region that flanks a known region of a
CC cancer-associated DNA sequence. Also disclosed as new is the use of the
CC method in the analysis of the breakpoint region of the human MLL gene,
CC where the chromosomal breaks results in gene fusions with AP-4, CDK-6 and
CC SEPRIN6 and are associated with ALL and AML (acute lymphoblastic
CC leukaemia and acute myeloid leukaemia). MLL is located on chromosome
CC 11q23. The present sequence is an MLL breakpoint junction region.

XX SQ Sequence 48 BP; 18 A; 11 C; 8 G; 11 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 10; Length 48;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTTCACCTTCAGAGGAGAAA 24
||| ||||| ||||| |||||
Db 20 CTGCACCTTCAGAGGCCAAA 38

RESULT 27
ABZ02803
ID ABZ02803 standard; DNA; 50 BP.
XX AC ABZ02803;
XX DT 09-JAN-2003 (first entry)
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 2794.
XX KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX OS Homo sapiens.
XX PN WO200257414-A2.
XX PD 25-JUL-2002.
XX PF 22-OCT-2001; 2001WO-US047856.
XX PR 20-OCT-2000; 2000US-0241994P.
XX PS 08-JUN-2001; 2001US-0296764P.
XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX PI Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX PT New system for leukocyte expression profiling, diagnosing a disease, or
XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX PS Claim 1; Page 416; Opp; English.

CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX SQ Sequence 50 BP; 15 A; 12 C; 9 G; 14 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TTCACCTTCAGAGGAGAAA 25
||| ||||| ||||| |||||
Db 24 TCCACCTTCAGAGGATAAA 42

RESULT 28
AAF06504
ID AAF06504 standard; RNA; 29 BP.
XX AC AAF06504;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme #3301.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO2000061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PS Claim 59; Page 132; 164pp; English.

XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
XX CC consequently increases expression of) genes involved in the production of
XX CC erythropoietin, granulocyte colony stimulating factor protein and
XX CC interferon alpha

XX SQ Sequence 29 BP; 9 A; 5 C; 7 G; 0 T; 7 U; 1 Other;
Query Match 56.0%; Score 14; DB 3; Length 29;
Best Local Similarity 60.9%; Pred. No. 1.4e+04;
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAAA 25
||| ||||| ||||| |||||
Db 1 GGACUUCACUGAGCGCGAAA 23

RESULT 29
ABA99901/c
ID ABA99901 standard; DNA; 30 BP.
XX AC ABA99901;
XX

CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC multimer at the cleavage site to produce (I) having well defined ends.
CC The method is used for the large-scale synthesis of DNA and RNA oligomers
CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX

SQ Sequence 49 BP; 9 A; 14 C; 8 G; 18 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 77.3%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 43 GGGCTTTCGAGAGGCGGAA 22

RESULT 32

AAV12941

ID AAV12941 standard; RNA; 49 BP.

AC AAV12941;

DT 15-MAY-1998 (first entry)

DE Oligonucleotide SEQ ID NO:50 from US5174320 Example 25.

XX Synthesis; selection; amplification; circular oligonucleotide;
XX rolling circle synthesis; diagnosis; therapeutic agent; ss.

XX Synthetic.

OS Homo sapiens.

XX US5714320-A.

XX 03-FEB-1998.

XX 23-FEB-1995; 95US-00393439.

XX 15-APR-1993; 93US-00047860.

XX (UVRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1998-144278/13.

XX Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT template to produce oligonucleotide multimer for cleavage.

XX Example 25; Col 63; 38pp; English.

XX The present sequence represents an oligonucleotide used in an example of
CC the present invention. The present invention describes a method for
CC synthesising a selected oligonucleotide (I) having well defined ends. The
CC method comprises: (a) annealing a primer to a single-stranded (ss)
CC circular template to yield a primed circular template, where the template
CC comprises: (i) at least one nucleotide sequence complementary to (I); and
CC (ii) at least one nucleotide effective to produce a cleavage site in the
CC oligonucleotide multimer; (b) combining the primed circular template with
CC at least two types of nucleotide triphosphates and a polymerase enzyme
CC without the addition of auxiliary proteins to yield a ss oligonucleotide
CC multimer complementary to the circular oligonucleotide template,
CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC multimer at the cleavage site to produce (I) having well defined ends.
CC The method is used for the large-scale synthesis of DNA and RNA oligomers
CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX

SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 11 GGGCUUUCUGAAGAGCGGAA 32

RESULT 33

AAV12938

ID AAV12938 standard; RNA; 49 BP.

AC AAV12938;

DT 15-MAY-1998 (first entry)

DE Oligonucleotide SEQ ID NO:47 from US5174320 Example 25.

XX Synthesis; selection; amplification; circular oligonucleotide;
XX rolling circle synthesis; diagnosis; therapeutic agent; ss.

XX Synthetic.

OS Homo sapiens.

XX US5714320-A.

XX 03-FEB-1998.

XX 23-FEB-1995; 95US-00393439.

XX 15-APR-1993; 93US-00047860.

XX (UVRP) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1998-144278/13.

XX Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT template to produce oligonucleotide multimer for cleavage.

XX Example 25; Col 61; 38pp; English.

XX The present sequence represents an oligonucleotide used in an example of
CC the present invention. The present invention describes a method for
CC synthesising a selected oligonucleotide (I) having well defined ends. The
CC method comprises: (a) annealing a primer to a single-stranded (ss)
CC circular template to yield a primed circular template, where the template
CC comprises: (i) at least one nucleotide sequence complementary to (I); and
CC (ii) at least one nucleotide effective to produce a cleavage site in the
CC oligonucleotide multimer; (b) combining the primed circular template with
CC at least two types of nucleotide triphosphates and a polymerase enzyme
CC without the addition of auxiliary proteins to yield a ss oligonucleotide
CC multimer complementary to the circular oligonucleotide template,
CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC multimer at the cleavage site to produce (I) having well defined ends.
CC The method is used for the large-scale synthesis of DNA and RNA oligomers
CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX

SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGGAA 24

RESULT 34

AAV12939

ID AAV12939 standard; RNA; 49 BP.

AC AAV12939;

DT	15-MAY-1998	(first entry)	
XX	Oligonucleotide SEQ ID NO:48 from US5174320 Example 25.		
DE	Synthesis; selection; amplification; circular oligonucleotide; rolling circle synthesis; diagnosis; therapeutic agent; ss.		
KW	Synthetic.		
XX	Homo sapiens.		
OS	US5714320-A.		
XX	03-FEB-1998.		
PN	23-FEB-1995;	95US-00393439.	
XX	15-APR-1993;		
XX	(UYRP) UNIV ROCHESTER.		
PA	Kool ET;		
XX	WPI; 1998-144278/13.		
DR	Rolling circle synthesis of oligo:nucleotide(s) - using primed circular template to produce oligonucleotide multimer for cleavage.		
PT	Example 25; Col 61; 38pp; English.		
XX	The present sequence represents an oligonucleotide used in an example of the present invention. The present invention describes a method for synthesising a selected oligonucleotide (I) having well defined ends. The method comprises: (a) annealing a primer to a single-stranded (ss) circular template to yield a primed circular template, where the template comprises: (i) at least one nucleotide sequence complementary to (I); and (ii) at least one nucleotide effective to produce a cleavage site in the oligonucleotide multimer; (b) combining the primed circular template with at least two types of nucleotide triphosphates and a polymerase enzyme without the addition of auxiliary proteins to yield a ss oligonucleotide multimer complementary to the circular oligonucleotide template, comprising multiple copies of (I); and (c) cleaving the oligonucleotide multimer at the cleavage site to produce (I) having well defined ends. The method is used for the large-scale synthesis of DNA and RNA oligomers for use, e.g. as probes and diagnostic agents and/or therapeutic agents		
XX	SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;		
QY	Query Match 56.0%; Score 14; DB 2; Length 49; Best Local Similarity 63.6%; Pred. No. 1.5e+04; Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		
DB	3	GGGCTTCACCTTCAGAGGAGAAA 24	
	11	GGGCUUUCUGAAGAGGGGAAA 32	
RESULT 35			
AAV59251/c			
ID	AAV59251 standard; DNA; 49 BP.		
XX	AAV59251;		
AC	21-OCT-2004 (revised)		
XX	14-DEC-1998 (first entry)		
DT	Circular oligomer sequence ID No.46.		
DE	ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent; circular; cyclic.		
KW	Synthetic.		
XX	Key Location/Qualifiers		
OS			
XX			
PH			
FT	misc_binding	1. .4	
FT	/*tag= b		
FT	/bound_moiety= "Bound to positions 36 to 39"		
FT	misc_binding	1	
FT	/*tag= a		
FT	/bound_moiety= "Bound to position 49"		
FT	misc_binding	6. .9	
FT	/*tag= c		
FT	/bound_moiety= "Bound to positions 12 to 15"		
FT	misc_binding	12. .15	
FT	/*tag= d		
FT	/bound_moiety= "Bound to position 6 to 9"		
FT	misc_binding	19. .21	
FT	/*tag= e		
FT	/bound_moiety= "Bound to positions 26 to 28"		
FT	misc_binding	26. .28	
FT	/*tag= f		
FT	/bound_moiety= "Bound to positions 19 to 21"		
FT	misc_binding	36. .39	
FT	/*tag= g		
FT	/bound_moiety= "Bound to positions 1 to 4"		
FT	misc_binding	40	
FT	/*tag= h		
FT	/bound_moiety= "Bound to position 49"		
FT	misc_binding	49	
FT	/*tag= i		
FT	/bound_moiety= "Bound to positions 1 and 40"		
XX	W09838300-A1.		
PN	03-SEP-1998.		
XX	26-FEB-1998;		
XX	98WO-US003784.		
XX	26-FEB-1997;		
XX	97US-00805631.		
XX	(UYRP) UNIV ROCHESTER.		
XX	Kool ET;		
XX	WPI; 1998-481202/41.		
XX	Synthesis of oligo:nucleotide(s) - using a single-stranded circular oligo:nucleotide template ribonucleotide tri:phosphate(s) and a polymerase to form multimer(s) which can be cleaved.		
XX	Example 25; Page 67; 100pp; English.		
PS	The oligomer sequence ID No.46 was used in an example of the invention for synthesising an RNA oligonucleotide, comprising combining a single-stranded circular oligonucleotide template comprising at least one copy of a nucleotide sequence complementary to the sequence of the desired RNA oligonucleotide with at least 2 types of ribonucleotide triphosphate and a polymerase enzyme to yield a single-stranded RNA oligonucleotide multimer complementary to the circular oligonucleotide template, where the RNA oligonucleotide multimer comprises multiple copies of the desired RNA oligonucleotide. The methods can be used for producing RNA oligonucleotides having a specific sequence and well defined ends. The RNA oligonucleotides produced can be used as probes, standards and diagnostic or therapeutic agents. They can be used for modifying the structure or function of a target molecule. They can also be used to cleave disease-associated RNA, DNA or protein		
CC	Revised record issued on 21-OCT-2004 : Correction to feature table key		
XX	SQ Sequence 49 BP; 9 A; 14 C; 8 G; 18 T; 0 U; 0 Other;		
QY	Query Match 56.0%; Score 14; DB 2; Length 49; Best Local Similarity 77.3%; Pred. No. 1.5e+04; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
	3	GGGCTTCACCTTCAGAGGAGAAA 24	
	11	GGGCUUUCUGAAGAGGGGAAA 32	

CC structure or function of a target molecule. They can also be used to
 CC cleave disease-associated RNA, DNA or protein
 CC Revised record issued on 21-OCT-2004 : Correction to feature table key
 XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
 SQ

Query Match 56.0%; Score 14; DB 2; Length 49;
 Best Local Similarity 63.6%; Pred. No. 1.5e+04;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTCAGAGGAGAAA 24
 ||||:|:|||||||
 Db 3 GGGCUUUUCUGAAGAGCGGAAA 24

RESULT 37
 AAV59253
 ID AAV59253 standard; RNA; 49 BP.
 XX
 AC AAV59253;
 XX
 DT 14-DEC-1998 (first entry)
 XX
 DE Monomeric ribozyme sequence ID No.48.
 XX
 KW ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 11..18
 FT /tag= a
 FT /bound_moiety= "K28 junction in chronic myeloid leukemia"
 FT /note= "Forms double stranded region with bases 8 to 15
 FT of AAV59254"
 FT misc_structure 19..38
 FT /tag= b
 FT /function= "Catalytic_domain"
 FT stem_loop 26..35
 FT /tag= c
 FT misc_binding 39..44
 FT /tag= d
 FT /bound_moiety= "K28 junction in chronic myeloid leukemia"
 FT /note= "Forms double stranded region with bases 1 to 6 of
 XX AAV59254"
 PN WO9838300-A1.
 PD 03-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-US003784.
 XX
 PR 26-FEB-1997; 97US-00805631.
 XX
 XX (UYRP) UNIV ROCHESTER.
 XX
 XX Kool ET;
 XX
 DR WPI; 1998-481202/41.
 XX
 XX
 PT Synthesis of oligo:nucleotide(s) - using a single-stranded circular
 PT oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
 PT polymerase to form multimer(s) which can be cleaved.
 XX
 PS Example 25; Page 67; 100pp; English.
 XX
 CC The oligomer sequence ID No.48 was used in an example of the invention
 CC for synthesising an RNA oligonucleotide, comprising combining a single-
 CC stranded circular oligonucleotide template comprising at least one copy
 CC of a nucleotide sequence complementary to the sequence of the desired RNA
 CC oligonucleotide with at least 2 types of ribonucleotide triphosphate and
 CC a polymerase enzyme to yield a single-stranded RNA oligonucleotide
 CC the RNA oligonucleotide multimer comprises multiple copies of the desired
 CC RNA oligonucleotide. The methods can be used for producing RNA
 CC oligonucleotides having a specific sequence and well defined ends. The
 CC RNA oligonucleotides produced can be used as probes, standards and
 CC diagnostic or therapeutic agents. They can be used for modifying the

43 GGGCTTTCTGAAGAGCGGAAA 22

RESULT 36
 AAV59252
 ID AAV59252 standard; RNA; 49 BP.
 XX
 AC AAV59252;
 XX
 DT 21-OCT-2004 (revised)
 DT 14-DEC-1998 (first entry)
 XX
 DE multimeric RNA transcript sequence ID No.47.
 XX
 KW ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 6..10
 FT /tag= a
 FT /bound_moiety= "Bound to positions 42 to 46"
 FT misc_binding 18..20
 FT /tag= b
 FT /bound_moiety= "Bound to positions 25 to 27"
 FT misc_binding 25..27
 FT /tag= c
 FT /bound_moiety= "Bound to positions 18 to 20"
 FT misc_binding 31..34
 FT /tag= d
 FT /bound_moiety= "Bound to positions 37 to 40"
 FT misc_binding 37..40
 FT /tag= e
 FT /bound_moiety= "Bound to positions 31 to 34"
 FT misc_feature 41..42
 FT /tag= f
 FT /note= "Cleavage site"
 FT misc_binding 42..46
 FT /tag= g
 FT /bound_moiety= "Bound to positions 6 to 10"
 PN WO9838300-A1.
 PD 03-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-US003784.
 XX
 PR 26-FEB-1997; 97US-00805631.
 XX
 XX (UYRP) UNIV ROCHESTER.
 XX
 XX Kool ET;
 XX
 DR WPI; 1998-481202/41.
 XX
 XX
 PT Synthesis of oligo:nucleotide(s) - using a single-stranded circular
 PT oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
 PT polymerase to form multimer(s) which can be cleaved.
 XX
 PS Example 25; Page 67; 100pp; English.
 XX
 CC The oligomer sequence ID No.47 was used in an example of the invention
 CC for synthesising an RNA oligonucleotide, comprising combining a single-
 CC stranded circular oligonucleotide template comprising at least one copy
 CC of a nucleotide sequence complementary to the sequence of the desired RNA
 CC oligonucleotide with at least 2 types of ribonucleotide triphosphate and
 CC a polymerase enzyme to yield a single-stranded RNA oligonucleotide
 CC the RNA oligonucleotide multimer comprises multiple copies of the desired
 CC RNA oligonucleotide. The methods can be used for producing RNA
 CC oligonucleotides having a specific sequence and well defined ends. The
 CC RNA oligonucleotides produced can be used as probes, standards and
 CC diagnostic or therapeutic agents. They can be used for modifying the

CC multimer complementary to the circular oligonucleotide template, where
CC the RNA oligonucleotide multimer comprises multiple copies of the desired
CC RNA oligonucleotide. The methods can be used for producing RNA
CC oligonucleotides having a specific sequence and well defined ends. The
CC RNA oligonucleotides produced can be used as probes, standards and
CC diagnostic or therapeutic agents. They can be used for modifying the
CC structure or function of a target molecule. They can also be used to
CC cleave disease-associated RNA, DNA or protein
XX
XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 11 GGGCUUUUCUGAAGAGCGGAA 32

RESULT 38
AAX30039
ID AAX30039 standard; RNA; 49 BP.
AC AAX30039;
XX
XX 16-JUN-1999 (first entry)
XX
XX RNA oligonucleotide SEQ ID NO:50.

XX Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX Synthetic.
XX WO9909216-A2.
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-US016776.
XX
XX 13-AUG-1997; 97US-00910632.
XX (UYRP) UNIV ROCHESTER.
XX
XX Kool ET;
XX
XX WPI; 1999-181062/15.

XX New detectably labelled oligonucleotide multimer, comprising multiple
XX contiguous copies of a repeated oligonucleotide - useful for detecting
XX target molecules in diagnosis and medicinal applications.
XX
XX Example 25; Page 70; 103pp; English.
XX
XX The present invention describes a detectably labelled oligonucleotide
XX multimer, comprising multiple contiguous copies of a repeated
XX oligonucleotides. The detectably labelled oligonucleotide multimer is
XX useful for detecting a target molecule. Oligonucleotide multimers may be
XX produced in sufficient quantity to be useful for diagnostic and medical
XX applications. The multimers are useful for affinity labelling of
XX proteins, and for signal amplification in highly sensitive affinity
XX capture and sequence identification applications. The method provides a
XX faster, cheaper and simpler way for large-scale production of DNA and RNA
XX oligomers and multimers. The incorporation of labels enables the
XX oligonucleotide multimers to be useful in diagnostics and medicine. The
XX present sequence represents an oligonucleotide used in an example from
XX the present invention

XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
XX
XX Query Match 56.0%; Score 14; DB 2; Length 49;
XX Best Local Similarity 63.6%; Pred. No. 1.5e+04;
XX Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 11 GGGCUUUUCUGAAGAGCGGAA 32

RESULT 39
ADC65914
ID ADC65914 standard; RNA; 49 BP.
XX
XX AC ADC65914;
XX
XX 18-DEC-2003 (first entry)
XX
XX RNA oligonucleotide #4.

XX RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
XX electroporation; calcium phosphate treatment; lipid-mediated delivery;
XX cation-mediated delivery; bacterial infection; viral infection;
XX drug resistant infection; double stranded DNA oligomer; ss.
XX Synthetic.
XX OS
XX US2003087241-A1.
XX
XX 08-MAY-2003.
XX
XX 30-NOV-2001; 2001US-00997931.
XX
XX 15-APR-1993; 93US-00047860.
XX 23-FEB-1995; 95US-00393439.
XX 26-FEB-1997; 97US-00805631.
XX 11-MAY-2000; 2000US-00569344.
XX
XX (UYRP) UNIV ROCHESTER.
XX
XX Kool ET;
XX
XX WPI; 2003-755141/71.

XX Synthesizing RNA oligonucleotide involves combining single-stranded
XX circular oligonucleotide, ribonucleotide triphosphate and polymerase
XX enzyme to yield desired RNA complementary to circular oligonucleotide
XX template.
XX
XX Example 25; SEQ ID NO 47; 78pp; English.
XX
XX The invention relates to a method for synthesising an RNA
XX oligonucleotide, comprising combining a single-stranded circular
XX oligonucleotide template with at least two types of ribonucleotide
XX triphosphate and a polymerase enzyme to yield a single-stranded RNA
XX oligonucleotide multimer complementary to the circular oligonucleotide
XX template, where the RNA oligonucleotide multimer comprises multiple
XX copies of the desired RNA oligonucleotide. The method is useful for
XX synthesising an RNA oligonucleotide with well-defined ends. The circular
XX oligonucleotide is introduced into the cell using direct injection,
XX electroporation, calcium phosphate treatment, lipid-mediated delivery, or
XX cation-mediated delivery. The method is useful for treating bacterial
XX and/or viral infections in mammals, particularly drug resistant
XX infections, and for producing double stranded DNA oligomers. The method
XX is performed in the absence of an oligonucleotide primer, or without the
XX addition of auxiliary proteins. This sequence represents an
XX oligonucleotide used in the method of the invention.
XX
XX Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;

Query Match 56.0%; Score 14; DB 10; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 3 GGGCUUUUCUGAAGAGCGGAA 24

Query Match 56.0%; Score 14; DB 10; Length 49;
Best Local Similarity 63.6%; Pred. No. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
||||: |: ||||| ||||
Db 3 GGGCUUUUCUGAAGAGCGGAA 24

```
RESULT 40
ADC65915
ID ADC65915 standard; RNA; 49 BP.
XX
AC ADC65915;
XX
DT 18-DEC-2003 (first entry)
XX
DE RNA oligonucleotide #5.
XX
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX
OS Synthetic.
XX
PN US2003087241-A1.
XX
PD 08-MAY-2003.
XX
PF 30-NOV-2001; 2001US-00997931.
XX
PR 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX
PA (UYRP ) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 2003-755141/71.
XX
PT Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX
PS Example 25; SEQ ID NO 48; 78pp; English.
XX
CC The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX
SQ Sequence 49 BP; 18 A; 8 C; 14 G; 0 T; 9 U; 0 Other;
Query Match 56.0%; Score 14; DB 10; Length 49;
Best Local Similarity 63.6%; Pred. NO. 1.5e+04;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGGCTTCACTTCAGAGGAGAAA 24
||||| : ||||| |||||
DB 11 GGGCUUUUCUAGAGGCGAAA 32
```

Search completed: November 18, 2005, 11:52:27
Job time : 174.148 secs

This Page Blank (uspio)

No.	Score	Match	Length	DB	ID	Description
1	15.4	61.6	50	8	AF039758	AF039758 AF
C 2	14.6	58.4	40	8	BH853060	BH853060 SA
C 3	14.4	57.6	49	9	CL656736	CL656736 PR
4	14	56.0	43	1	AA074188	AA074188 zf
C 5	13.8	55.2	35	2	AW246497	AW246497 28
C 6	13.8	55.2	46	1	AA908626	AA908626 OG
C 7	13.8	55.2	46	8	BZ379892	BZ379892 SA
C 8	13.8	55.2	49	2	BF322803	BF322803 ma
9	13.6	54.4	31	1	AA479970	AA479970 zv
C 10	13.6	54.4	38	8	BH809976	BH809976 KG
C 11	13.4	53.6	29	8	BH840479	BH840479 KJ
C 12	13.4	53.6	50	1	AU105696	AU105696 AU
C 13	13	52.0	40	7	W89034	W89034 mf68
14	13	52.0	47	9	CL214736	CL214736 M0
C 15	13	52.0	48	8	BZ289408	BZ289408 SA
C 16	13	52.0	50	1	AU107432	AU107432 AU
C 17	13	52.0	50	1	AU107433	AU107433 AU
C 18	13	52.0	50	1	AU107434	AU107434 AU
C 19	13	52.0	50	7	CN488991	CN488991 Md
C 20	12.8	51.2	35	4	BI388654	BI388654 ES
21	12.8	51.2	41	8	BZ288847	BZ288847 SA
22	12.8	51.2	41	8	BZ660542	BZ660542 SA
23	12.8	51.2	44	1	AU247370	AU247370 AU
24	12.8	51.2	47	8	BZ353192	BZ353192 SA

```

RESULT 2
BH853060/c          BH853060          40 bp      DNA      linear      GSS 13-JUN-2002
LOCUS               SALUK_075945.23.15.x Arabidopsis thaliana TDNA insertion lines
DEFINITION          Arabidopsis thaliana genomic clone SALUK_075945.23.15.x, genomic
                    survey sequence.
ACCESSION            BH853060
VERSION              BH853060.1      GI:21423931
KEYWORDS              GSS.
SOURCE               Arabidopsis thaliana (thale cress)
ORGANISM             Arabidopsis thaliana
                    Arabidopsis thaliana
                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE            1 (bases 1 to 40)
AUTHORS              Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                    Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                    Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE                A Sequence-Indexed Library of Insertion Mutations in the
                    Arabidopsis Genome
JOURNAL              Unpublished (2001)
COMMENT              Contact: Joseph R. Ecker
                    Salk Institute Genomic Analysis Laboratory (SIGNAL)
                    The Salk Institute for Biological Studies
                    10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                    Tel: 858 453 4100 x1752
                    Fax: 858 558 6379
                    Email: ecker@salk.edu
                    This is single pass sequence recovered from the left border of
                    TDNA. This sequence lies within an annotated exon of Atg30890.
                    Class: TDNA tagged.
FEATURES             location/Qualifiers
                    1..40
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /ecotype="Col-0"
                        /db_xref="taxon:3702"
                        /clone="SALUK_075945.23.15.x"
                        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                        /note="PCR was performed on Arabidopsis thaliana lines
                        each of which contained one or more TDNA insertion
                        elements. The resultant fragment for each line was
                        directly sequenced to determine the genomic sequence at
                        the site of insertion. Details of the protocols used can
                        be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match          58.4%; Score 14.6; DB 8; Length 40;
Best Local Similarity 81.0%; Pred.No. 6.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAAA 25
|||||
Db 23 GTTTCATTTTCAGAGGCCAA 3

RESULT 3
CL656736/c          CL656736          49 bp      DNA      linear      GSS 09-JUL-2004
LOCUS               PR10127b_G02 - PR10127b.B21 (49) Mixed stage fosmid library of P.
DEFINITION          pacificus var. California Pristionchus pacificus genomic, genomic
                    survey sequence.
ACCESSION            CL656736
VERSION              CL656736.1      GI:50137472
KEYWORDS              GSS.
SOURCE               Pristionchus pacificus
                    Pristionchus pacificus
                    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                    Neodiplogasteridae; Pristionchus.
REFERENCE            1 (bases 1 to 49)
AUTHORS              Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE                AppaDB: an AcedB database for the nematode satellite organism

```

```

Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
                    location/Qualifiers
                    1..49
                        /organism="Pristionchus pacificus"
                        /mol_type="genomic DNA"
                        /strain="California"
                        /db_xref="taxon:54126"
                        /clone_lib="Mixed stage fosmid library of P. pacificus
                        var. California"
                        /note="vector: pBpifos-5 Fosmid vector"
ORIGIN
Query Match          57.6%; Score 14.4; DB 9; Length 49;
Best Local Similarity 75.0%; Pred.No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAAAA 25
|||||
Db 30 TGGGCTGCTCTTTGGAGGAGATAA 7

RESULT 4
AA074188
LOCUS               zF82G02.r1 Soares pineal gland N3HPG Homo sapiens cDNA clone
DEFINITION          IMAGE:383474.5, similar to SW:NB7M_BOVIN_Q02367 NADH-UBIQUINONE
                    OXIDOREDUCTASE B17 SUBUNIT ;, mRNA sequence.
ACCESSION            AA074188
VERSION              AA074188.1      GI:1614251
KEYWORDS              EST.
SOURCE               Homo sapiens (human)
ORGANISM             Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            1 (bases 1 to 43)
AUTHORS              Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                    Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
                    Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                    Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
                    Wilson,R.
                    The WashU-Merck EST Project
                    Unpublished (1995)
                    Contact: Wilson RK
                    Washington University School of Medicine
                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                    Tel: 314 286 1800
                    Fax: 314 286 1810
                    Email: est@watson.wustl.edu
                    This clone is available royalty-free through LLNL ; contact the
                    IMAGE Consortium (info@image.llnl.gov) for further information.
                    Possible reversed clone: similarity on wrong strand
                    Seq primer: -28M13 rev2 from Amersham
                    High quality sequence stop: 1.
FEATURES             location/Qualifiers
                    1..43
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="GDB:1291731"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:383474"
                        /lab_host="DH10B (ampicillin resistant)"

```



```

SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS 1 (bases 1 to 46)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At2g2970.
Class: TDNA tagged.
FEATURES
source
1..46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_114176.40.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 55.2%; Score 13.8; DB 8; Length 46;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 TTCCTTCAGGAGGAA 23
Db 44 TTCTCTTCAGTGGAGAA 28
RESULT 8
BF322803/c 49 bp mRNA linear EST 21-NOV-2000
LOCUS maa33h03.x1 NCI_CGAP_L110 Mus musculus cDNA clone IMAGE:3812980 3',
DEFINITION mRNA sequence.
ACCESSION BF322803
VERSION BF322803.1 GI:11272264
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: maa33h03.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
MGI:1455092
Seq primer: -40UP from Gibco.
FEATURES
source
1..49
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3812980"
/sex="female"
/dev_stage="10 weeks"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_L110"
/note="Organ: liver; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 55.2%; Score 13.8; DB 2; Length 49;
Best Local Similarity 72.0%; Pred. No. 1.5e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCATCTCAGAGGAGAAAA 25
Db 25 CTGTGCCTTACTTCACAAAAA 1
RESULT 9
AA479970
LOCUS zvi18b11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:753981 3',
DEFINITION Similar to SW:CA1H_HUMAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN ;,
mRNA sequence.
ACCESSION AA479970
VERSION AA479970.1 GI:2208121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WaahU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5976854"
/db_xref="taxon:9606"
/clone="IMAGE:753981"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"

```

/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalised libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Query Match 54.4%; Score 13.6; DB 1; Length 31;
Best Local Similarity 80.0%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAAAA 25
DB 8 CTTGCGTGCAAGGAGAAAA 27

RESULT 10
BH809976/c

LOCUS BH809976 38 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK 036880 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_036880, genomic survey sequence.

ACCESSION BH809976
VERSION BH809976
KEYWORDS GSS.
SOURCE BH809976.1 GI:20387793

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..38

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_036880"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAAAA 25

DB 34 CTTAACTTAAGACACAAA 15

RESULT 11
BH840479
LOCUS

DEFINITION

KEYWORDS

ACCESSION

VERSION

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 29)

Levis,R., Hoskins,R., Liao,G., Mozden,N., Tsang,G., He,Y.,

Karpen,G., Bellen,H., Rubin,G. and Spradling,A.

The Berkeley Drosophila Genome Project Gene Disruption Project

Unpublished (2001)

Contact: Gerald Rubin

Berkeley Drosophila Genome Project

University of California, Berkeley

LSA Building, Berkeley, CA 94720-3200, USA

Fax: 5106439947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P

element

The P element insertion position is base 1 in the 29 bases. This

insertion position refers to the first base of the 8 base target

recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1..29

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster P(SUPOR-P) P element

insertion lines"

/note="Inverse PCR was performed on Drosophila

melanogaster strains each of which contains one or more

P(SUPOR-P) P-element transposon insertion. The resultant

fragment for each strain was directly sequenced to

determine the genomic sequence at the site of insertion.

Details of the protocols used can be found at

<http://www.fruitfly.org/about/methods/inverse.pcr.html>."

ORIGIN

Query Match 53.6%; Score 13.4; DB 8; Length 29;
Best Local Similarity 73.9%; Pred. No. 2.1e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAAA 25

DB 6 GCGCATCGTTTCAGCCGAGAAA 28

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUI05696 50 bp mRNA linear EST 28-JAN-2004
AUI05696 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL05574, mRNA sequence.

ACCESSION AUI05696

VERSION AUI05696.1

KEYWORDS EST.

SOURCE AUI05696.1

ORGANISM Homo sapiens (human)

```

REFERENCE
AUTHORS   1 (bases 1 to 50)
           Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
           Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
           Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE      Diverse transcriptional initiation revealed by fine, large-scale
           mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE    21270072
PUBMED
COMMENT    Contact: Yutaka Suzuki
           Department of Virology
           Institute of Medical Science, University of Tokyo
           4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
           Email: yusuzuki@ms.u-tokyo.ac.jp
           Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
           Sugano, S. Construction and characterization of a full
           length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
           149-156 (1997).
FEATURES   Location/Qualifiers
           source
             1..50
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="COL05574"
               /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.6%; Score 13.4; DB 1; Length 50;
Best Local Similarity 93.3%; Pred. No. 2.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 TCACCTTCAGAGGAGA 22
        ||||| |||||
Db      31 TCACCTCCGAGGAGA 45

RESULT 13
W88034/c
LOCUS      W88034
DEFINITION m668d04.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
           clone IMAGE:419431 5' similar to SW:AGRI_RAT P25304 AGRIN
           PRECURSOR. [1] ;, mRNA sequence.
ACCESSION  W88034
VERSION     W88034.1 GI:1402164
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
           Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
           Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
           Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
           Waterston, R.
TITLE       The WashU-HMMI Mouse EST Project
JOURNAL     Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
           WashU-HMMI Mouse EST Project
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LInL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:253983
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
           Location/Qualifiers
             1..40
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 Sv"
               /db_xref="taxon:10090"
               /clone="M073D06"
               /sex="Male"

```

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:419431"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. "
ORIGIN
Query Match      52.0%; Score 13; DB 7; Length 40;
Best Local Similarity 76.2%; Pred. No. 3.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CTGGGCTTCACTTCAGAGGAG 21
        ||||| ||||| |||||
Db      36 CTGGCATCCACTTCACAGCAG 16

RESULT 14
CL214736
LOCUS      CL214736
DEFINITION CL214736
           M073D06 GGTC Gene Trap Library GV04C04 Mus musculus cDNA clone
           M073D06, mRNA sequence.
ACCESSION  CL214736
VERSION     CL214736.2 GI:49489678
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 47)
AUTHORS     Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
           Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
TITLE       A large-scale, gene-driven mutagenesis approach for the functional
           analysis of the mouse genome
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE    22810117
PUBMED     12904583
COMMENT     On Jun 30, 2004 this sequence version replaced gi:40731637.
           Contact: GGTC
           German Genetrap Consortium (GGTC)
           Email: info@genetrap.de
           Rosabeteago gene trap. Sequence tag generated by 5'RACE. Additional
           sequence information can be found at:
           'http://genetrap.gsf.de/project/web/new/database/result_clone.html?
           clone_id=M073D06'. ES cell line harboring insertion mutation of
           target gene is available at:
           'http://genetrap.gsf.de/project/web/new/order_clones/howtoorder.htm
           1' Inhouse Sequence Identifier: 09460
           Class: Gene Trap.
           Location/Qualifiers
             1..47
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="129 Sv"
               /db_xref="taxon:10090"
               /clone="M073D06"
               /sex="Male"

```

/cell type="Embryonic stem cell"
 /cell_line="ES cells 12952 (formerly 129/SvPas)"
 /clone_lib="GGTC Gene Trap Library GV04C04"
 /note="Vector: ROSNbtagos"

ORIGIN

Query Match 52.0%; Score 13; DB 9; Length 47;
 Best Local Similarity 76.2%; Pred. No. 3.5e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTCAGGAG 21
 ||||| ||||| ||||| |||||
 Db 9 CTGAGCTGTACTGCAGAGGG 29

RESULT 15

BZ289408/c

LOCUS

DEFINITION BZ289408 48 bp DNA linear GSS 24-OCT-2002
 Arabidopsis thaliana genomic clone SALK_022805.55.00.x, genomic
 survey sequence.

ACCESSION

BZ289408

VERSION

BZ289408.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

1 (bases 1 to 48)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

Arabidopsis Genome

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

FEATURES

Class: TDNA tagged.

Location/Qualifiers

1..48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_022805.55.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

Best Local Similarity

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GCTTCACCTCAGGAGGAAA 25

||||| ||||| ||||| |||||

Db 47 GCTTCTTAGAGAGGAAA 27

RESULT 16

AU107432/c

LOCUS

DEFINITION

AU107432 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION

LNG11157, mRNA sequence.

VERSION

AU107432.1

KEYWORDS

GI:13556953

SOURCE

EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL

mapping of mRNA start sites

MEDLINE

EMBO Rep. 2 (5), 388-393 (2001)

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="LNG11157"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match

Best Local Similarity

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAA 23

||||| ||||| ||||| |||||

Db 35 GGGCTTCCTCGTGGGAGAA 15

RESULT 17

AU107433/c

LOCUS

AU107433 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION

LNG14512, mRNA sequence.

ACCESSION

AU107433

VERSION

AU107433.1

KEYWORDS

GI:13556954

SOURCE

EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL

mapping of mRNA start sites

MEDLINE

EMBO Rep. 2 (5), 388-393 (2001)

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG14512"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GGGCTTCACCTTCAGAGGAGAA 23
|||||
Db 46 GGGCTTCCTCGTGGCGAGAA 26
|||||

RESULT 18

AUI07434/c
LOCUS AUI07434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION AUI07434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNIG15774, mRNA sequence.

ACCESSION

AUI07434
VERSION AUI07434.1 GI:13556955
KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL

EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE

PUBMED

11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG15774"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.0%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GGGCTTCACCTTCAGAGGAGAA 23
|||||
Db 46 GGGCTTCCTCGTGGCGAGAA 26
|||||

RESULT 19

CN488991/c
LOCUS CN488991 Malus x domestica cDNA clone Mdfw2018i03 5',
DEFINITION Mdfw2018i03.y1 Mdfw Malus x domestica cDNA clone Mdfw2018i03 5',

mRNA sequence.

CN488991 GI:46602340
EST.
KEYWORDS
SOURCE
ORGANISM

Malus x domestica (cultivated apple)

Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

1 (bases 1 to 50)

Korban, S., Vodkin, L., Liu, L., Gasic, K., Gonzales, O., Hernandez, A.,
Aldwinckle, H., Malnoy, M., Carroll, N., Goldsbrough, P., Orvis, K.,
Clifton, S., Pape, D., Marta, M., Hillier, L., Martin, J., Wylie, T.,
Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Ronko, I.,
Teagareishvili, R., Kennedy, S., Waterston, R. and Wilson, R.
Apple Functional Genomics grant - NSF 0321702
Unpublished (2004)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

Library materials provided by: Schuyler S. Korban Library

constructed by: A. Hernandez / K. Gasic Library sequenced by:

Washington University Genome Sequencing Center

WashU EST name: aaf69e02.y1

High quality sequence stop: 50.

FEATURES

source

1..50
/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="Mdfw2018i03"

/lab_host="DH10B ampicillin resistant"

/clone_lib="Mdfw"

/note="Vector: DH10B ampicillin resistant; Site 1: NotI;
Site 2: EcoRI; Total RNA was extracted separately from
each stage (bud, balloon, open and after pollination),
using the 'pine tree' method. Poly(A)+mRNA was isolated
twice from total RNA from each stage using the Oligotex
Direct mRNA kit (Qiagen). mRNA was reverse transcribed
into double stranded cDNA using a modified oligo18(dT)
primer with an identifying tag sequence (see table below).
cDNAs from different stages were pooled in equal amounts
before adaptor ligation. Tag identification when
sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA;
Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert
18(A)TCGCT; Stage 4 (after pollination) insert 18(A)TCGGT.
Tag identification when sequencing from 3' end: Stage 1
(bud) TCCGAl8(T) insert; Stage 2 (balloon) TCGCAl8(T)
insert; Stage 3 (open) ACGCAl8(T) insert; Stage 4 (after
pollination) ACCGAl8(T) insert. Double stranded cDNAs were
size selected (more than 450 bp), adapted with EcoRI
adapters at both ends and then digested with NotI. The
cDNAs were then directionally cloned into EcoRI-NotI
digested pBS II SK(+) phagemid vector (Stratagene).

Identification of adaptors and tags in 5'-end sequenced
clones: <Vector>...TAAGCTT<End Vector><Start
EcoRI adaptor>GATATCGAATTCATTTGTTGGG<End
EcoRI adaptor><Start Insert>...AAAAAAAAAAAAAAAAAA-End
Insert><Start tag>GCGGCCCGCCCGCGG... The total number of
white colony forming units (cfu) in the primary library
before amplification was 1.1x10⁶ cfu (colony forming
units). The background of empty clones was less than 1%.

Inserts ranged from 0.5kb to 3 kb, as determined by PCR.

Purified plasmid DNA from the primary library was
converted to single-stranded circles and used as a
template for PCR amplification using the T7 and T3 priming
sites flanking the cloned cDNA inserts. The purified PCR
products, representing the entire cloned cDNA population,

were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated and hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10⁶ cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 52.0%; Score 13; DB 7; Length 50;
Best Local Similarity 76.2%; Pred. No. 3.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAAA 25
||||| - ||||| - |||||
Db 36 GCTTCCTCCAGATGTGATAA 16
||||| - ||||| - |||||

RESULT 20
B1388654/c
LOCUS
DEFINITION EST-CD34NN-022 cDNA Library from human CD34+ stem/progenitor cells
ACCESSION Homo sapiens cDNA 3', mRNA sequence.
VERSION B1388654
KEYWORDS EST.
SOURCE B1388654.1 GI:17737237
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 35)
AUTHORS Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J.D. and Wang, S.M.
TITLE The pattern of gene expression in human hematopoietic CD34+ stem/progenitor cells
JOURNAL Unpublished (2001)
COMMENT Contact: Wang SM
Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002

Email: swang@midway.uchicago.edu
This EST fragment was amplified from cDNA Library of human CD34+ stem/progenitor cells with GLGI technique (Generation of Longer cDNA fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the first CATG site of the targeted cDNA sequence.
Seq primer: M13 Forward.

FEATURES

source

1..35
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Bone marrow"
/cell_type="CD34+ stem/progenitor cells"
/clone_lib="cDNA Library from human CD34+ stem/progenitor cells"
/note="3'ESTs converted from the SAGE tag sequences using GLGI method"

ORIGIN

Query Match 51.2%; Score 12.8; DB 4; Length 35;
Best Local Similarity 70.8%; Pred. No. 4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAAAA 25
||||| - ||||| - |||||
Db 33 TGGCGTGGTCCACAGAGGAGAAAA 10
||||| - ||||| - |||||

RESULT 21
B2288847

LOCUS

DEFINITION BZ288847 41 bp DNA linear GSS 24-OCT-2002
SALK_022237.36.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_022237.36.30.x, genomic survey sequence.

ACCESSION BZ288847
VERSION BZ288847.1 GI:24329575
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 41)

REFERENCE

AUTHORS

Alonso, J.M., Leisese, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE

A sequence-indexed library of insertion mutations in the

JOURNAL

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10310 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of Atg16100 and 300 bases of the 5' end of Atg16110.
Class: TDNA tagged.

FEATURES

source

1..41
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_022237.36.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 41;
Best Local Similarity 70.8%; Pred. No. 4.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAAAA 25
||||| - ||||| - |||||
Db 15 TGGAGTTGACTTTTGATGATAAAA 38
||||| - ||||| - |||||

RESULT 22

BZ660542

LOCUS

DEFINITION BZ660542 41 bp DNA linear GSS 31-JAN-2003
SALK_023993.41.95.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_023993.41.95.x, genomic survey sequence.

ACCESSION BZ660542
VERSION BZ660542.1 GI:28173689
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 41)

REFERENCE

AUTHORS

Alonso, J.M., Leisese, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of Atlg16100 and 300 bases of the 5' end of Atlg16110.
Class: TDNA tagged.

FEATURES source Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_023993.41.95.x"
/notes="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 51.2%; Score 12.8; DB 8; Length 41;
Best Local Similarity 70.8%; Pred.No. 4.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TGGCCTTCACCTTCAGAGGAAAA 25
||| ||| ||| ||| ||| |||
Db 15 TGGAGTTGACTTTTGTATGATAAAA 38

RESULT 23
AU247370 FL Lolium multiflorum cDNA clone FLO31A04-5, mRNA
LOCUS AU247370 44 bp mRNA linear EST 22-APR-2004
DEFINITION sequence.
VERSION AU247370 GI:46504639
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Lolium multiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooidae; Poae; Lolium.
1 (bases 1 to 44)

REFERENCE Ikeda,S.
AUTHORS Lolium multiflorum EST Project
TITLE Unpublished (2004)
JOURNAL
COMMENT Contact: Seishi Ikeda
Japan Grassland Farming Forage Seed Association(JFSA)
Forage Crop Research Institute(FCRI)
Higashitakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: siked@ifsass.or.jp
contact:radaashi.takamizo@takamizoaffrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.
Location/Qualifiers
1..44
/organism="Lolium multiflorum"
/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="FLO31A04-5"
/tissue type="Inflorescence"

```

ACCESSION      AZ818575
VERSION        AZ818575.1  GI:12988483
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 48)
                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                Niederhausern, A. and Wright, D., Weiss, R.
                Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
                Unpublished (2000)
TITLE          Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: dunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0088 row: M column: 10
                Seq primer: CACACAGGAAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 48.
                Location/Qualifiers
                1..48
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0088M10"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Query Match      51.2%; Score 12.8; DB 8; Length 48;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGCTTCACCTTCAG 16
    ||||| |||||
Db 43 CTGGGATTGACTTCAG 28

RESULT 26
CN488991
LOCUS
DEFINITION      CN488991
                  Mdfw2018i03.y1 Mdfw Malus x domestica cDNA clone Mdfw2018i03 5',
                  mRNA sequence.

ACCESSION      CN488991
VERSION        CN488991.1  GI:46602340
KEYWORDS
SOURCE         Malus x domestica (cultivated apple)
ORGANISM       Malus x domestica

REFERENCE
AUTHORS        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                1 (bases 1 to 50)
                Korban, S., Vodkin, L., Liu, L., Gasic, K., Gonzales, O., Hernandez, A.,
                Alwinckle, H., Malnoy, M., Carroll, N., Goldsbrough, P., Orvis, K.,
                Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T.,
                Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Ronko, I.,
                Tsagaris, V., Kennedy, S., Waterston, R. and Wilson, R.
                Apple Functional Genomics grant - NSF 0321702
                Unpublished (2004)
TITLE          Contact: Schuyler S. Korban
                Apple Functional Genomics grant - NSF 0321702
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                Library materials provided by: Schuyler S. Korban Library
                constructed by: A. Hernandez / K. Gasic Library sequenced by:
                Washington University Genome Sequencing Center
                WashU EST name: aaf69e02.y1
                High quality sequence stop: 50.
                Location/Qualifiers
                1..50
                /organism="Malus x domestica"
                /mol_type="mRNA"
                /db_xref="taxon:3750"
                /clone="Mdfw2018i03"
                /lab_host="DH10B ampicillin resistant"
                /clone_lib="Mdfw"
                /note="Vector: DH10B ampicillin resistant; Site 1: NotI;
                Site 2: EcoRII; Total RNA was extracted separately from
                each stage (bud, balloon, open and after pollination),
                using the 'pine tree' method. Poly(A)+mRNA was isolated
                twice from total RNA from each stage using the Oligotex
                Direct mRNA kit (Qiagen). mRNA was reverse transcribed
                into double stranded cDNA using a modified oligo18(dT)
                primer with an identifying tag sequence (see table below).
                cDNAs from different stages were pooled in equal amounts
                before adaptor ligation. Tag identification when
                sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA;
                Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert
                18(A)TCGGT; Stage 4 (after pollination) insert 18(A)TCGGT.
                Tag identification when sequencing from 3' end: Stage 1
                (bud) TCCGAl8(T) insert; Stage 2 (balloon) TCCGAl8(T)
                insert; Stage 3 (open) ACCGAl8(T) insert; Stage 4 (after
                pollination) ACCGAl8(T) insert. Double stranded cDNAs were
                size selected (more than 450 bp), adaptor with EcoRI
                adapters at both ends and then digested with NotI. The
                cDNAs were then directionally cloned into EcoRI-NotI
                digested pBS II SK(+) phagemid vector (Stratagene).
                Identification of adaptors and tags in 5'-end sequenced
                clones: <Vector>...TAAGCTT<End Vector><Start
                EcoRI adaptor>GATATCGAATTCATTGTGTGGG <End
                EcoRI adaptor><Start Inset>...AAAAAAAAAAAAAAAAAA-End
                Inset> <Start tag>TCGCA<End Tag><Start
                NotI site>Vector>GCGGCCGCACCGG... The total number of
                white colony forming units (cfu) in the primary library
                before amplification was 1.1x10^6 cfu (colony forming
                units). The background of empty clones was less than 1%.
                Inserts ranged from 0.5kb to 3 kb, as determined by PCR.
                Purified plasmid DNA from the primary library was
                converted to single-stranded circles and used as a
                template for PCR amplification using the T7 and T3 priming
                sites flanking the cloned cDNA inserts. The purified PCR
                products, representing the entire cloned cDNA population,
                were used as a driver for normalization. Hybridization

```

between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10⁶ cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 51.2%; Score 12.8; DB 7; Length 50;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCTCAGAGGAGAA 23

Db 19 TCACATCTGAGGAGAA 34

RESULT 27
CR449386/c
LOCUS
DEFINITION CR449386 50 bp mRNA linear EST 19-JUN-2004
mRNA sequence.
ACCESSION CR449386
VERSION CR449386
KEYWORDS CR449386.1 GI:48974973
SOURCE EST.
ORGANISM Xenopus tropicalis (western clawed frog)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLES Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
JOURNAL Xenopodinae; Xenopus; Silurana.
COMMENT 1 (bases 1 to 50)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk

TR0PICALIS SEQUENCE ID: TTbA045116.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
Location/Qualifiers
1..50
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTbA045116"
/dev_stages="tailbud (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGC-tailbud"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5' of poly A+ RNA from tailbud. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match 51.2%; Score 12.8; DB 7; Length 50;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGGAGAAA 25

Db 39 TCGGCCGACATCAGAGCAGAACA 16

RESULT 28
AZ792764
LOCUS
DEFINITION AZ792764 24 bp plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045N21 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

AZ792764
AZ792764.1 GI:12937031
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: N column: 21
Seq primer: CGTTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number ligated
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source

ORIGIN

Query Match 50.4%; Score 12.6; DB 8; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGG 19

Db 3 CTGGGTATCATCTGGGAGG 21

RESULT 29
CG723173
LOCUS
DEFINITION CG723173 33 bp DNA linear GSS 20-OCT-2003
1119075A10.1EL x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.

```

ACCESSION CG7231173
VERSION CG7231173.1 GI:37758756
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 33)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119075 row: A column: 10
Class: transposon-tagged
FEATURES
    source
        1..33
            Location/Qualifiers
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/A188/B73/K55"
                /db_xref="taxon:4577"
                /tissue_type="leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="1119 - RescueMu Grid AA"
                /note="Organ: leaf; Vector: RescueMu (engineered from
                pBluescript backbone); Site_1: BamHI; Site_2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescueMu, go to the web
                site 'www.zmdb.iastate.edu' and follow the links for
                'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
                was extracted from leaf strips, double digested using
                BamHI and BglII, and ligated to form circular plasmids.
                DH10B cells were transformed and then screened on LB
                plates with ampicillin."
ORIGIN
    Query Match 50.4%; Score 12.6; DB 9; Length 33;
    Best Local Similarity 78.9%; Pred. No. 4.9e+05;
    Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GCTTCACCTCAGAGGAA 23
Db 6 GATCCAAATTCAGAGAGAA 24

RESULT 30
BX569109/c
LOCUS BX569109 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse97e10_glc, mRNA sequence.
ACCESSION BX569109
VERSION BX569109.1 GI:33437048
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 34)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
    Location/Qualifiers
        1..34
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse97e10_glc"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"
ORIGIN
    Query Match 50.4%; Score 12.6; DB 5; Length 34;
    Best Local Similarity 78.9%; Pred. No. 5e+05;
    Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TTCACCTCAGAGAGAAAA 25
Db 28 TTCACCTTAGAAGAGAAAA 10

RESULT 31
A1597737
A1597737/c
LOCUS A1597737.1 GI:4606785
DEFINITION EST.
ACCESSION A1597737
VERSION A1597737.1 GI:4606785
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
    Location/Qualifiers

```

•

GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES source

```
Location/Qualifiers
1..39
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-598D09-021211"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
```

ORIGIN

```
Query Match      50.4%; Score 12.6; DB 9; Length 39;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 7 TTCACCTTCAGAGGAGAAAA 25
    |||||
DB 28 TTCTCTTTAGCGTAAAA 10
```

RESULT 34

```
AZ776620
LOCUS      AZ776620          40 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION  ZM0010823F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0010823 F, genomic survey sequence.
```

```
ACCESSION  AZ776620
VERSION    AZ776620.1  GI:12904354
```

```
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
```

```
REFERENCE   1 (bases 1 to 40)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
```

```
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
JOURNAL     Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
```

```
Tel: 801 585 5606
Fax: 801 585 7177
```

```
Email: dund@genetics.utah.edu
```

```
Insert Length: 10000 Std Error: 0.00
```

```
Plate: 0010 row: E column: 23
```

```
Seq primer: CGTTGTAACGACGCGCAGT
```

```
Class: plasmid ends
```

```
High quality sequence stop: 40.
```

```
Location/Qualifiers
```

```
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0010E23"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
```

FEATURES source

```
Query Match      50.4%; Score 12.6; DB 9; Length 44;
Best Local Similarity 78.9%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
Query Match      50.4%; Score 12.6; DB 8; Length 40;
Best Local Similarity 78.9%; Pred. No. 5.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 7 TTCACCTTCAGAGGAGAAAA 25
    |||||
DB 3  TTCTTTCAAGGAGAAAA 21
```

RESULT 35

```
CG784583/c
LOCUS      CG784583          44 bp      mRNA      linear      GSS 16-JUN-2004
DEFINITION  RRR727 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
mRNA sequence.
```

```
ACCESSION  CG784583
VERSION    CG784583.2  GI:40647596
```

```
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
```

```
REFERENCE   1 (bases 1 to 44)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            BayGenomics.
```

```
1 (bases 1 to 44)
http://baygenomics.ucsf.edu/
```

```
Unpublished (2001)
```

```
On Mar 1, 2004 this sequence version replaced gi:38157143.
```

```
Contact: BayGenomics
```

```
Bay Area Functional Genomics Consortium (BayGenomics)
```

```
Email: info@baygenomics.ucsf.edu
```

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from

http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RRR727

Class: Gene Trap.

Location/Qualifiers

```
1..44
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"
```

FEATURES

source

```
Query Match      50.4%; Score 12.6; DB 9; Length 44;
Best Local Similarity 78.9%; Pred. No. 5.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

Qy      6  CTTCACTTCAGAGGAGAA 24
Db      40 CTTCCCATCTGAGGAGAA 22

RESULT 36
AI446300
LOCUS   AI446300               46 bp  mRNA  linear  EST 09-MAR-1999
DEFINITION t3j3ig05.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2143160 3'
similar to gb:MS9371 TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION AI446300
VERSION   AI446300.1 GI:4294243
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 46)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL  Unpublished (1997)
COMMENT  Contact: Robert Strausberg, Ph.D.
Email: cgaps-romail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source
1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2143160"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panl"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 50.4%; Score 12.6; DB 1; Length 46;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6  CTTCACTTCAGAGGAGAA 24
Db      15 CTTTATTCAGAGGAGAA 33

RESULT 37
BH629703
LOCUS   BH629703               46 bp  DNA  linear  GSS 30-JAN-2002
DEFINITION 1007075E03.2EL_x1 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
ACCESSION BH629703
VERSION   BH629703.1 GI:18442954
KEYWORDS GSS.
SOURCE   Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 46)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
AUTHORS Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007075 column: 36
Class: transposon-tagged.
Location/Qualifiers
1. .46
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.lastate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 50.4%; Score 12.6; DB 8; Length 46;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  TGGGCTTCACATTCAGAGGA 20
Db      7  TGGGCTTCGATTCGTGGA 25

RESULT 38
BH911440
LOCUS   BH911440               47 bp  DNA  linear  GSS 04-SEP-2002
DEFINITION SALK 068707.30.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_068707.30.80.x, genomic
survey sequence.
ACCESSION BH911440.1 GI:22724373
VERSION   BH911440
KEYWORDS GSS.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 47)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

```


Email: ecker@ealk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SAUK_068707.30.80.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.ealk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.4%; Score 12.6; DB 8; Length 47;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TTCACTTCAGAGGAGAAA 25

Db 19 TTCTTTTACAGAGAGAAA 37

RESULT 39

AU105888/c

LOCUS

DEFINITION AU105888 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS03170, mRNA sequence.

ACCESSION AU105888

VERSION AU105888.1

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS03170"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES

source

ORIGIN

Query Match 50.4%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 5.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAG 21

Db

RESULT 40

AZ992198/c

LOCUS

DEFINITION

2M0276E17R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
clone UUCG2M0276E17 R, genomic survey sequence.

ACCESSION AZ992198

VERSION AZ992198.1

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: E column: 17
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0276E17"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 49.6%; Score 12.4; DB 8; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTC 14

Db | ||||| |||||
 16 CAGGCTTCACTTC 3

Search completed: November 18, 2005, 21:12:46
Job time : 1198.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

Sequence: 1 CTGGGCTTCACTTCAGAGGAGAAAA 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	1	US-07-989-160-5
2	16.8	67.2	25	4	US-09-396-196G-113292
3	14.6	58.4	25	4	US-09-396-196G-90079
4	14.4	57.6	30	2	US-08-353-372A-28
5	14.4	57.6	30	3	US-08-057-430A-19
6	14.2	56.8	33	2	US-08-360-606B-14
7	14	56.0	49	3	US-08-910-632-46
8	14	56.0	49	3	US-08-910-632-47
9	14	56.0	49	3	US-08-910-632-48
10	14	56.0	49	3	US-08-910-632-50
11	14	56.0	49	3	US-08-805-631A-46
12	14	56.0	49	3	US-08-805-631A-47
13	14	56.0	49	3	US-08-805-631A-48
14	14	56.0	49	3	US-08-805-631A-50
15	14	56.0	49	3	US-09-569-344-46
16	14	56.0	49	3	US-09-569-344-47
17	14	56.0	49	3	US-09-569-344-48
18	14	56.0	49	3	US-09-569-344-50
19	13.8	55.2	25	4	US-09-396-196G-113293
20	13.8	55.2	25	4	US-08-388-029A-60
21	13.6	54.4	25	2	US-08-659-251-19
22	13.6	54.4	25	3	US-09-256-490-19
23	13.6	54.4	25	4	US-09-396-196G-50968
24	13.6	54.4	25	4	US-09-396-196G-50969
25	13.6	54.4	25	4	US-09-396-196G-52946
26	13.6	54.4	25	4	US-09-396-196G-117350
27	13.6	54.4	25	5	PCT-US96-11445-19

c	28	13.6	54.4	36	3	US-09-230-288-5	Sequence 5, Appli
	29	13.4	53.6	22	3	US-08-943-731-239	Sequence 239, App
c	30	13.4	53.6	25	4	US-09-396-196G-13674	Sequence 13674, A
c	31	13.4	53.6	25	4	US-09-396-196G-56218	Sequence 56218, A
	32	13.4	53.6	25	4	US-09-396-196G-64443	Sequence 64443, A
	33	13.4	53.6	25	4	US-09-396-196G-64567	Sequence 64567, A
c	34	13.4	53.6	34	1	US-08-160-670A-19	Sequence 19, Appl
	35	13.4	53.6	42	3	US-08-660-645A-36	Sequence 36, Appl
c	36	13.4	53.6	42	3	US-09-298-718-36	Sequence 36, Appl
c	37	13.4	53.6	42	3	US-09-546-969-36	Sequence 36, Appl
c	38	13.4	53.6	42	3	US-08-980-832-15	Sequence 15, Appl
c	39	13.4	53.6	42	4	US-09-547-267-36	Sequence 36, Appl
c	40	13.4	53.6	42	4	US-09-920-923B-15	Sequence 15, Appl
c	41	13.4	53.6	47	3	US-09-336-643A-66	Sequence 66, Appl
	42	13.2	52.8	20	3	US-09-331-260-5	Sequence 5, Appl
	43	13.2	52.8	20	3	US-09-142-138-3	Sequence 3, Appl
	44	13.2	52.8	20	3	US-09-582-660-3	Sequence 3, Appl
	45	13.2	52.8	20	4	US-09-142-141A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-5
; Sequence 5, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-989-160-5

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACTTCAGAGGAGAAAA 25
|||||

```
Db      1 CTGGGCTTCACTTCAGAGAGAAA 25

RESULT 2
US-09-396-196G-113292
; Sequence 113292, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-113292

Query Match      67.2%; Score 16.8; DB 4; Length 25;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CTGGGCTTCACTTCAGAGGA 20
        |||||
Db      4 CTGGGCTTCACTTCGGAGGA 23

RESULT 3
US-09-396-196G-90079
; Sequence 90079, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-90079

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 TGGGCTTCACTTCAGAGAGA 22
        |||||
Db      1 TGGGCTACACGTCGGATGAGA 21

RESULT 4
US-08-353-372A-28
; Sequence 28, Application US/08353372A
; Patent No. 5840479
; GENERAL INFORMATION:
; APPLICANT: Little, Melvyn
; APPLICANT: Breitling, Frank B.
; APPLICANT: Seehaus, Thomas
; APPLICANT: Dubel, Stefan

; APPLICANT: Breitling, Frank B
; APPLICANT: Seehaus, Thomas
; APPLICANT: Dubel, Stefan
; TITLE OF INVENTION: Preparation and Use of Gene Banks of
; TITLE OF INVENTION: Synthetic Human Antibodies ("Synthetic Human-Antibody
; LIBRARIES")
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,372A
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/654,207
; FILING DATE: 30-JAN-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 02 897.6
; FILING DATE: 01-FEB-1990
; APPLICATION NUMBER: DE P 40 03 880.7
; FILING DATE: 09-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1032-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-353-372A-28

Query Match      57.6%; Score 14.4; DB 2; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CTGGGCTTCACTTCAGAGAGAAA 24
        |||||
Db      7 CTTGATTCATTAAAGAGAGAAA 30

RESULT 5
US-08-057-430A-19
; Sequence 19, Application US/08057430A
; Patent No. 6319690
; GENERAL INFORMATION:
; APPLICANT: Little, Melvyn
; APPLICANT: Breitling, Frank B.
; APPLICANT: Seehaus, Thomas
; APPLICANT: Dubel, Stefan
```

```

; APPLICANT: Kiewinghaus, Iris
; TITLE OF INVENTION: PREPARATION AND USE OF GENE BANKS OF
; TITLE OF INVENTION: HUMAN ANTIBODIES ("HUMAN-ANTIBODY LIBRARIES")
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/057,430A
; FILING DATE: 06-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,522
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 02 898.4
; FILING DATE: 01-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 03 881.5
; FILING DATE: 09-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1033-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-057-430A-19

Query Match 57.6%; Score 14.4; DB 3; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGGAGAAA 24
Db 7 CTGGAATTCATTAAAGAGGAGAAA 30

RESULT 6
US-08-360-606B-14
; Sequence 14, Application US/08360606B
; Patent No. 5919617
; GENERAL INFORMATION:
; APPLICANT: Jnanendra K. Bhattacharjee
; APPLICANT: Richard C. Garrad
; APPLICANT: Paul L. Skatrud
; APPLICANT: Robert P. Peery
; TITLE OF INVENTION: Methods and Reagents for
; TITLE OF INVENTION: Detecting Fungal Pathogens in a
; TITLE OF INVENTION: Biological Sample
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.

```

```

; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,606B
; FILING DATE: December 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berghoff, Paul H.
; REGISTRATION NUMBER: 30,243
; REFERENCE/DOCKET NUMBER: 94,319
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-360-606B-14

Query Match 56.8%; Score 14.2; DB 2; Length 33;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTCACCTTCAGAGGAGAAA 24
Db 1 CTCATTTAAGAGCAGAAA 19

RESULT 7
US-08-910-632-46/c
; Sequence 46, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220,00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; CURRENT FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: coding DNA circle
US-08-910-632-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAAA 24
Db 43 GGGCTTTCTGAGAGGCGAAA 22

RESULT 8

```

```
US-08-910-632-47
; Sequence 47, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multimeric RNA transcript
US-08-910-632-47
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 3 GGGCUUUCUGAGAGGCGAA 24

RESULT 9
US-08-910-632-48
; Sequence 48, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: monomeric ribozyme
US-08-910-632-48
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCUUUCUGAGAGGCGAA 32

RESULT 10
US-08-910-632-50
; Sequence 50, Application US/08910632B
; Patent No. 6077668
```

```
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 49
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: monomeric ribozyme
US-08-910-632-50
Query Match          56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCUUUCUGAGAGGCGAA 32

RESULT 11
US-08-805-631A-46/c
; Sequence 46, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; TITLE OF INVENTION: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING RAASCH & GERHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; City: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
```

STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-805-631A-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 43 GGGCTTTCTGAAGAGCGAAA 22

RESULT 12
US-08-805-631A-47
; Sequence 47, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-805-631A-47

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 3 GGGCUUUCUGAAGAGCGAAA 24

RESULT 13
US-08-805-631A-48
; Sequence 48, Application US/08805631A

Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-805-631A-48

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACTTCAGAGGAGAA 24
||||| : ||||| |||||
Db 11 GGGCUUUCUGAAGAGCGAAA 32

RESULT 14
US-08-805-631A-50
; Sequence 50, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-805-631A-50

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAA 24
|||||:|:|||||
Db 11 GGGCUUUCUGAGAGCGGAA 32

RESULT 15
US-09-569-344-46/c
; Sequence 46, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-569-344-46

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAA 24
|||||:|:|||||
Db 43 GGGCTTTCTGAGAGCGGAA 22

RESULT 16
US-09-569-344-47
; Sequence 47, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-569-344-47

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 3 GGGCUUUCUGAAGAGCGGAA 24

RESULT 17

US-09-569-344-48
; Sequence 48, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MURTING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-569-344-48

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 11 GGGCUUUCUGAAGAGCGGAA 32

RESULT 18
US-09-569-344-50
; Sequence 50, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MURTING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-569-344-50

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

CORRESPONDENCE ADDRESS:
; ADDRESSEE: MURTING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-569-344-50

Query Match 56.0%; Score 14; DB 3; Length 49;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGGCTTCACCTTCAGAGGAGAA 24
||||:|:|||||
Db 11 GGGCUUUCUGAAGAGCGGAA 32

RESULT 19
US-09-396-196G-113293
; Sequence 113293, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCES: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-113293

Query Match 55.2%; Score 13.8; DB 4; Length 25;

```
Best Local Similarity 88.2%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTTCAGAGGA 20
Db 1 GGCTTCACCTCGGAGGA 17

RESULT 20
US-08-388-029A-60
; Sequence 60, Application US/08388029A
; Patent No. 6110665
; GENERAL INFORMATION:
; APPLICANT: FENGER, CLARA K.
; APPLICANT: GRANSTROM, DAVID R.
; APPLICANT: GAJADHAR, ALVIN A.
; TITLE OF INVENTION: SARCOCYSTIS NEURONA DIAGNOSTIC PRIMER
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 CANAL CENTER PLAZA, SUITE 300
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,029A
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PRICE, ROBERT L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 434-046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; TELEX: AMERPAT
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-388-029A-60

Query Match 55.2%; Score 13.8; DB 3; Length 50;
Best Local Similarity 78.9%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TTCACCTTCAGAGGAAAA 25
Db 3 TTAACNNAGAGGTGAAAA 21

RESULT 21
US-08-659-251-19
; Sequence 19, Application US/08659251
; Patent No. 5883081
; GENERAL INFORMATION:
; APPLICANT: Kraus, Guenter
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Talbott, Randy
; APPLICANT: Poeschla, Eric
; TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,251
; FILING DATE: No. 5883081 yet assigned
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,441
; FILING DATE: 26-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 02307E-056410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..25
; OTHER INFORMATION: /note= "GR72 (outside, left) primer for
; OTHER INFORMATION: HIV-2KR env"
; US-08-659-251-19

Query Match 54.4%; Score 13.6; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTTCAGAGGAA 23
Db 5 GGACTAACTCGAGAGGAA 24

RESULT 22
US-09-256-490-19
; Sequence 19, Application US/09256490
; Patent No. 6235881
; GENERAL INFORMATION:
; APPLICANT: Kraus, Guenter
; APPLICANT: Wong-Staal, Flossie
; APPLICANT: Talbott, Randy
; APPLICANT: Poeschla, Eric
; TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/256,490
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,251
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..25
OTHER INFORMATION: /note= "GR72 (outside, left) primer for
OTHER INFORMATION: HIV-2KR env"
US-09-256-490-19

Query Match 54.4%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGCCTTCACTTCAGAGGAGAA 23
||| ||| ||| ||| ||| ||| |||
DB 5 CGACTAACTGCAGAGGAGAA 24

RESULT 23
US-09-396-196G-50968
Sequence 50968, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50968
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-50968

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 25
||| ||| ||| ||| ||| ||| |||
DB 6 CTTACAGCCGAGGAGAGA 25

RESULT 24
US-09-396-196G-50969
Sequence 50969, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:

APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50969
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-50969

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 25
||| ||| ||| ||| ||| ||| |||
DB 4 CTTACAGCCGAGGAGAGA 23

RESULT 25
US-09-396-196G-52946/c
Sequence 52946, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52946
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-52946

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTTCACTTCAGAGGAGAA 25
||| ||| ||| ||| ||| ||| |||
DB 22 CTTCACTTCAGATGCAACA 3

RESULT 26
US-09-396-196G-117350/c
Sequence 117350, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678

```

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-117350

```

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

Qy 2 TGGGCTTCACTTCAGAGGAG 21
Db 25 TGGGATACACTTCTGTGGAG 6

RESULT 27

```

PCT-US96-11445-19
; Sequence 19, Application PC/TUS9611445
; GENERAL INFORMATION:
;
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11445

```

FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berliner, Robert
 REGISTRATION NUMBER: 20,121
 REFERENCE/DOCKET NUMBER: 5555-399C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 977-1001
 TELEFAX: (213) 977-1003
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:

```

; NAME/KEY: - 1.25 /note= "GR72 (outside, left) primer for
; LOCATION: 1..25 HIV-2KR env"
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US96-11445-19

```

Query Match 54.4%; Score 13.6; DB 5; Length 25;
Best Local Similarity 80.0%; Pred. NO. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

Qy 4 GGCTTCACTTCAGAGGAGAA 23
|||
Db 5 GGACTAACTGCAGAGGAGAA 24
|||

RESULT 28

US-09-230-288-5/c

```

1 Sequence 5, Application US/09230288
2 Patent No. 6329160
3 GENERAL INFORMATION:
4 APPLICANT: SCHNEIDER, Rene
5 VANCOR, Tony
6 JURY, Karen
7 TITLE OF INVENTION: BIOSENSORS
8 NUMBER OF SEQUENCES: 18
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
11 STREET: 624 Ninth Street, N.W., Suite 300
12 CITY: Washington
13 STATE: D.C.
14 COUNTRY: USA
15 ZIP: 20001
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patentin Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 FILING DATE: 07-Sep-1999
23 APPLICATION NUMBER: US/09/230,288
24 CLASSIFICATION: <Unknown>
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/AU97/00473
27 FILING DATE: 25-JUL-1997
28 APPLICATION NUMBER: AU P01280
29 FILING DATE: 29-JUL-1996
30 ATTORNEY/AGENT INFORMATION:
31 NAME: NEWMARK, Sheridan
32 REGISTRATION NUMBER: 20,520
33 REFERENCE/DOCKET NUMBER: SCHNEIDER-2
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 202-628-5197
36 TELEFAX: 202-737-5288
37 INFORMATION FOR SEQ ID NO: 5:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 36 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: cDNA
44 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
45 US-09-230-288-5

```

Query Match 54.4%; Score 13.6; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels

Qy 1 CTGGGCTTCACTTCAGAGGA 20
Db 34 CGGCGTTTCACTTCTGAGGA 15

RESULT 29

```

US-08-343-731-239
? Sequence 239, Application US/08943731
? Patent No. 6265157
? GENERAL INFORMATION:
?
? APPLICANT: PROCKOP, DARWIN J.
?
? APPLICANT: SPOTILA, LORETTA D.
?
? APPLICANT: DELTAS, CONSTANTINOS D.
?
? APPLICANT: SEREDA, LARISA
?
? APPLICANT: LARSON, ANDREA W.
?
? APPLICANT: PACK, MICHAEL
?
? APPLICANT: COLIGE, ALAIN
?
? APPLICANT: EARLY, JAMES
?
? APPLICANT: KORKKO, JARMO
?
? APPLICANT: ALA-KOKKO, LEENA, et al.
?
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
?
? TYPE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE
?
? NUMBER OF SEQUENCES: 666

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
;; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;; STREET: FLR.
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-7086
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/943,731
;; FILING DATE: 03-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,322
;; FILING DATE: 14-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/803,628
;; FILING DATE: 03-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOYLE LEARY Ph.D., KATHRYN
;; REGISTRATION NUMBER: 36,317
;; REFERENCE/DOCKET NUMBER: 9598-27
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-965-1284
;; TELEFAX: 215-567-2991
;; TELEX: 831-494
;; INFORMATION FOR SEQ ID NO: 239:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-943-731-239

Query Match 53.6%; Score 13.4; DB 3; Length 22;
Best Local Similarity 93.3%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCA 15
Db 7 CTGGGCTTCACGTCA 21

RESULT 30

US-09-396-196G-13674/C
; Sequence 13674, Application US/09396196G
; Patent No. 6821724

;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 13674

;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-396-196G-13674

Query Match 53.6%; Score 13.4; DB 4; Length 25;

Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGGAGAA 24
Db 25 TGGCATTGCTGAGATGGGAAA 3

RESULT 31

US-09-396-196G-56218/C
; Sequence 56218, Application US/09396196G
; Patent No. 6821724

;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 56218
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-56218

Query Match 53.6%; Score 13.4; DB 4; Length 25;

Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGGAGAA 23
Db 23 CTGGTATTGCTCCAGGGGAGAA 1

RESULT 32

US-09-396-196G-64443
; Sequence 64443, Application US/09396196G
; Patent No. 6821724

;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 64443
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-64443

Query Match 53.6%; Score 13.4; DB 4; Length 25;

Best Local Similarity 73.9%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGGCTTCACCTCAGAGGAGAAA 25
Db 2 GAGCATCTGCTGTGGAGAAA 24

RESULT 33

```

? FILING DATE: 12/7/93
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Esmond, Robert W.
? REGISTRATION NUMBER: 32,893
? REFERENCE/DOCKET NUMBER: 0942.2580000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 371-2600
? TELEFAX: (202) 371-2540
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 34 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: both
?
? US-08-160-670A-19
?
? Query Match 53.6%; Score 13.4; DB 1; Length 34;
? Best Local Similarity 69.6%; Pred. No. 3.8e+03;
? Matches 16; Conservative 1; Mismatches 6; Indels

```

```

Query Match      53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACTTCAGAGGAA 23
    ||||| ||||| ||||| |||||
Db 32 CTGGCCGTCGCTTCAAGAGGA 10

```

RESULT 36
US-09-298-718-36/c
; Sequence 36, Application US/03298718
; Patent No. 6124113
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Pasaamontes, Luis
; APPLICANT: Tessier, Michel
; APPLICANT: van Loon, Adolphus
; TITLE OF INVENTION: FERMENTATIVE

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-298-718-36

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTCAGAGGAGAA 23
|||||
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 37
US-09-546-969-36/c
Sequence 36, Application US/09546969
Patent No. 6207409
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-546-969-36

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTCAGAGGAGAA 23
|||||
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 38
US-08-980-832-15/c
Sequence 15, Application US/08980832B
Patent No. 6291204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer MUT6
US-08-980-832-15

Query Match 53.6%; Score 13.4; DB 3; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTCAGAGGAGAA 23
|||||
Db 32 CTGGCCGTCGCTTGAAGAGGA 10

RESULT 39
US-09-547-267-36/c
Sequence 36, Application US/09547267
Patent No. 6613543
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-547-267-36

Query Match 53.6%; Score 13.4; DB 4; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGCGTTCCTTCAGAGGAGAA 23
|||||
DB 32 CTGGCGTTCCTTCAGAGGAGAA 10

RESULT 40
US-09-920-923B-15/c
Sequence 15, Application US/09920923B
Patent No. 6677134
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent In version 3.1
SEQ ID NO 15
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Primer MUT6
US-09-920-923B-15

Query Match 53.6%; Score 13.4; DB 4; Length 42;
Best Local Similarity 73.9%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGCGTTCCTTCAGAGGAGAA 23

Db 32 CTGGCGTTCCTTCAGAGGAGAA 10
|||||

Search completed: November 18, 2005, 11:22:00
Job time : 49.5741 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-5

Perfect score: 25

Sequence: 1 CTGGGCTTCACTTCAGAGGAGAAA 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20:	/cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21:	/cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22:	/cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
24:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
25:	/cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	US-08-469-172-5	Sequence 5, Appli
2	25	100.0	25	US-10-788-779-5	Sequence 5, Appli
3	17.2	68.8	25	US-10-719-900-593102	Sequence 593102,
C 4	17	68.0	25	US-10-719-900-978129	Sequence 978129,
C 5	16.8	67.2	25	US-10-719-900-424739	Sequence 424739,

6	16.8	67.2	25	22	US-10-809-189-113292	Sequence 113292,
C 7	16.8	67.2	25	26	US-11-036-317-100259	Sequence 100259,
C 8	16.8	67.2	25	26	US-11-036-317-633439	Sequence 633439,
C 9	16.8	67.2	25	26	US-11-036-317-764997	Sequence 764997,
C 10	16.6	66.4	25	22	US-10-719-900-970185	Sequence 970185,
C 11	16.6	66.4	25	22	US-10-719-900-970186	Sequence 970186,
C 12	16.4	65.6	25	24	US-10-719-956-261669	Sequence 261669,
C 13	16.2	64.8	25	22	US-10-719-900-482864	Sequence 482864,
C 14	16.2	64.8	25	24	US-10-719-956-243899	Sequence 243899,
C 15	16.2	64.8	25	24	US-10-719-956-419311	Sequence 419311,
C 16	16	64.0	25	22	US-10-956-157-311797	Sequence 311797,
C 17	16	64.0	25	26	US-11-036-317-209513	Sequence 209513,
C 18	16	64.0	25	26	US-11-036-317-366428	Sequence 366428,
C 19	16	64.0	25	26	US-11-036-317-823362	Sequence 823362,
C 20	16	64.0	25	26	US-11-036-317-823363	Sequence 823363,
C 21	15.8	63.2	25	22	US-10-719-900-383306	Sequence 383306,
C 22	15.8	63.2	25	22	US-10-719-900-430473	Sequence 430473,
C 23	15.8	63.2	25	22	US-10-719-900-866704	Sequence 866704,
C 24	15.8	63.2	25	26	US-11-036-317-788701	Sequence 788701,
C 25	15.6	62.4	25	22	US-10-719-900-248480	Sequence 248480,
C 26	15.6	62.4	25	22	US-10-719-900-387762	Sequence 387762,
C 27	15.6	62.4	25	22	US-10-719-900-593103	Sequence 593103,
C 28	15.6	62.4	25	22	US-10-956-157-279510	Sequence 279510,
C 29	15.6	62.4	25	22	US-10-956-157-315928	Sequence 315928,
C 30	15.6	62.4	25	26	US-11-036-317-270365	Sequence 270365,
C 31	15.6	62.4	25	26	US-11-036-317-366190	Sequence 366190,
C 32	15.6	62.4	25	26	US-11-036-317-423606	Sequence 423606,
C 33	15.4	61.6	25	22	US-10-719-900-978130	Sequence 978130,
C 34	15.4	61.6	25	24	US-10-719-956-62957	Sequence 62957, A
C 35	15.4	61.6	25	24	US-10-719-956-439125	Sequence 439125,
C 36	15.4	61.6	25	26	US-11-036-317-430286	Sequence 430286,
C 37	15.4	61.6	25	26	US-11-036-317-828946	Sequence 828946,
C 38	15.4	61.6	25	26	US-11-060-756-182301	Sequence 182301,
C 39	15.2	60.8	25	22	US-10-719-900-424738	Sequence 424738,
C 40	15.2	60.8	25	22	US-10-719-900-823433	Sequence 823433,
C 41	15.2	60.8	25	24	US-10-719-956-626249	Sequence 626249,
C 42	15.2	60.8	25	26	US-11-036-317-9865	Sequence 9865, Ap
C 43	15.2	60.8	25	26	US-11-036-317-629374	Sequence 629374,
C 44	15.2	60.8	25	26	US-11-036-317-633436	Sequence 633436,
C 45	15.2	60.8	25	26	US-11-036-317-764996	Sequence 764996,

ALIGNMENTS

RESULT 1
US-08-469-172-5
; Sequence 5, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

RESULT 5

US-10-719-900-424739/c
; Sequence 424739, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424739
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-424739

Query Match 67.2%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGGAGAAA 24
||||| |||||||
DB 25 GCTTCACCTGGAGAGGAGAAA 6

RESULT 6

US-10-809-189-113292
; Sequence 113292, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-113292

Query Match 67.2%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCTTCACCTTCAGAGA 20
||||| |||||||
DB 4 CTGGGCTTCACCTCCGGAGA 23

RESULT 7

US-11-036-317-100259/c
; Sequence 100259, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-100259

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGGAGAAA 24
||||| |||||||
DB 25 GCTTCACCTGGAGAGGAGAAA 6

RESULT 8

US-11-036-317-633439/c
; Sequence 633439, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 633439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-633439

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCTTCACCTTCAGAGGAGAAA 24
||||| |||||||
DB 25 GCTTCACCTGGAGAGGAGAAA 6

RESULT 9

US-11-036-317-764997/c
; Sequence 764997, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 764997
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-764997

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      6 CTTCACTTCAGAGGAGAAA 25
      |||||||
Db     24 CCTCACTTCGGAGGAGAAA 5
      |||||||

RESULT 10
US-10-719-900-970185/c
; Sequence 970185, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970185

Query Match      66.4%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 TGGGCTTCACATTCAGAGGAGAA 24
      |||||||
Db     23 TGGGCTTCACGCTCGAGAGAA 1
      |||||||

RESULT 11
US-10-719-900-970186/c
; Sequence 970186, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970186
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970186

Query Match      66.4%; Score 16.6; DB 22; Length 25;
Best Local Similarity 82.6%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 TGGGCTTCACATTCAGAGGAGAA 24
      |||||||
Db     23 TGGGCTTCACCTCGGCTGAGAAA 1
      |||||||

RESULT 12
US-10-719-956-261669/c
; Sequence 261669, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

Qy      2 TGGGCTTCACATTCAGAGGAGAA 24
      |||||||
Db     23 TGGGCTTCACCTCGGCTGAGAAA 1
      |||||||

RESULT 13
US-10-719-900-482864/c
; Sequence 482864, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 482864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-482864

Query Match      64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TGGGCTTCATTCAGAGGAGA 22
      |||||||
Db     25 TGGCTTCACATCAGAGAAGA 5
      |||||||

RESULT 14
US-10-719-956-243899/c
; Sequence 243899, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 243899
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-243899

Query Match      64.8%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 CTGGGCTTCACCTTCAGAGAG 21
Db 22 CTGGGCTTCACCTTCAGAGGTG 2

RESULT 15

US-10-719-956-419911/c
; Sequence 419911, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 419911
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-419911

Query Match 64.8%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGAGA 22
Db 25 TGGTCTTCACCTTCAGAGACA 5

RESULT 16

US-10-956-157-311797/c
; Sequence 311797, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 311797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-311797

Query Match 64.0%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGAGAAA 25
Db 24 TGGGTTTATCTACAGAGACAAA 1

RESULT 17

US-11-036-317-209513/c
; Sequence 209513, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 209513
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-209513

Query Match 64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CTGGGCTTCACCTTCAGAGAGAAA 24
Db 25 CAGGGCTAGCCTTCAGAGAGAGA 2

RESULT 18

US-11-036-317-366428/c
; Sequence 366428, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-366428

Query Match 64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGAGAAA 24
Db 24 CAGGGCTAGCCTTCAGAGAGAGA 1

RESULT 19

US-11-036-317-823362
; Sequence 823362, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 823362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-823362

Query Match 64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;

```
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAAAA 25
   ||| ||||| || |||||
Db 1 TGGTCTTCACCTCAGGATGAGAAAA 24
   ||| ||||| || |||||

RESULT 20
US-11-036-317-823363
; Sequence 823363, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 823363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-823363

Query Match 64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAAAA 25
   ||| ||||| || |||||
Db 1 TGGTCTTCACCTGATGAGAAAA 24
   ||| ||||| || |||||

RESULT 21
US-10-719-900-383306/c
; Sequence 383306, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 383306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-383306

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGG 19
   ||| ||||| ||||| ||
Db 23 CTGGCTTCACCTCAGTGG 5
   ||| ||||| ||||| ||

RESULT 22
US-10-719-900-430473
; Sequence 430473, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430473
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-430473

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGG 19
   ||| ||||| ||||| ||
Db 23 CTGGCTTCACCTCAGTGG 5
   ||| ||||| ||||| ||

RESULT 23
US-10-719-900-866704/c
; Sequence 866704, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 866704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-866704

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTCAGAGGAGA 22
   ||||| ||||| ||||| ||
Db 4 GGCTTAACCTCAGAGGAGA 22
   ||||| ||||| ||||| ||

RESULT 24
US-11-036-317-788701
; Sequence 788701, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 788701
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-788701

Query Match 63.2%; Score 15.8; DB 26; Length 25;
```

```
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430473
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-430473

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTCAGAGGAGA 22
   ||||| ||||| ||||| ||
Db 4 GGCTTAACCTCAGAGGAGA 22
   ||||| ||||| ||||| ||

RESULT 23
US-10-719-900-866704/c
; Sequence 866704, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 866704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-866704

Query Match 63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGG 19
   ||| ||||| ||||| ||
Db 22 CTGGCTTCACCTCAGTGG 4
   ||| ||||| ||||| ||

RESULT 24
US-11-036-317-788701
; Sequence 788701, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 788701
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-788701

Query Match 63.2%; Score 15.8; DB 26; Length 25;
```

Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTTCAGAGGAGA 22
Db 4 GGATTCACCTTCAGAGGAGA 22

RESULT 25

US-10-719-900-248480/c
; Sequence 248480, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248480

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 23 CTCGCTTCACCTGCCGAGGAGA 2

RESULT 26

US-10-719-900-387762
; Sequence 387762, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 387762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-387762

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 1 CTGGGCTACACGTGGATGAGA 22

RESULT 27

US-10-719-900-593103
; Sequence 593103, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-593103

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTTCAGAGGAGA 22
Db 4 CTAGGCTTCCTCAGAGGAGA 25

RESULT 28

US-10-956-157-279510
; Sequence 279510, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 279510
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-279510

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTTCAGAGGAGAA 23
Db 3 TGGACATCCCTTCACAGGAGAA 24

RESULT 29

US-10-956-157-315928/c
; Sequence 315928, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 315928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-315928

Query Match 62.4%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;

```
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAGAGAA 23
Db 22 TAGTCTTCATTCAGGGAGAA 1

RESULT 30
US-11-036-317-270365/c
; Sequence 270365, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 270365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-270365

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 23 CAGGCGTAGCCTTCAGAGAGAA 2

RESULT 31
US-11-036-317-366190/c
; Sequence 366190, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-366190

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 22 CAGGCGTAGCCTTCAGAGAGAA 1

RESULT 32
US-11-036-317-423606
; Sequence 423606, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
```

```
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 423606
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-423606

Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAA 22
Db 2 CTGGGCTACACGTCGGATGAGA 23

RESULT 33
US-10-719-900-978130/c
; Sequence 978130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 978130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-978130

Query Match 61.6%; Score 15.4; DB 22; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGAGAAA 25
Db 25 CTGGGCTTTATAACGGAGGTGAAAA 1

RESULT 34
US-10-719-956-62957
; Sequence 62957, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 62957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-62957
```


Query Match 61.6%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCTTCACCTCAGAGGA 20
| | | | | | | | | |
Db 7 GGCTTCACCTCAGAGGA 23

RESULT 35
US-10-719-956-439125/c
; Sequence 439125, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439125
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-439125

Query Match 61.6%; Score 15.4; DB 24; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACTTCAGAGGAGAAA 25
| | | | | | | | | |
Db 21 CACTTCATAGGAGAAA 5

RESULT 36
US-11-036-317-430286/c
; Sequence 430286, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-430286

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGGCTTCACCTCAGAG 18
| | | | | | | | | |
Db 20 TGGGCTTCACCTCAGAG 4

RESULT 37
US-11-036-317-828846/c
; Sequence 828846, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 828846
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-828846

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGA 17
| | | | | | | | | |
Db 19 CTGGGCTTCACCTCAGA 3

RESULT 38
US-11-060-756-182301
; Sequence 182301, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182301
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-182301

Query Match 61.6%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CTGGGCTTCACCTCAGAGGAGAAA 25
| | | | | | | | | |
Db 1 CTGGGCTCCAGCTCTGAGGAGGACA 25

RESULT 39
US-10-719-900-424738/c
; Sequence 424738, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-424738

Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GCTTCACCTTCAGAGGAGAAA 24
||||| ||| ||| ||| |||
Db 25 GCTTCACCTGGAGTGGAGAAA 6

RESULT 40
US-10-719-900-823343
; Sequence 823343, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 823343
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-823343

Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTTCACTTCAGAGGAGAAA 25
||||| ||| ||| ||| |||
Db 6 CTTCACTATCAGAGAAGCAAA 25

Search completed: November 18, 2005, 15:41:06
Job time : 337.027 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCCGCGCTTGAGAA 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_by.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	I12899 Sequence 6
2	18.2	60.7	26	6	AR256113 Sequence
3	18.2	60.7	26	6	AR410127 Sequence
4	16.6	55.3	48	6	A42996 Sequence 11
5	16.6	55.3	48	6	A72867 Sequence 11
6	16.6	55.3	48	6	AR023759 Sequence 11
7	16.6	55.3	48	6	I91791 Sequence 11
8	16.4	54.7	30	6	I85833 Sequence 1
9	16.2	54.0	28	6	AR256115 Sequence
10	16.2	54.0	28	6	AR256117 Sequence
11	16.2	54.0	28	6	AR410129 Sequence
12	16.2	54.0	28	6	AR410131 Sequence
13	16.2	54.0	33	6	A06417 Sequence
14	16.2	54.0	33	6	A10235 oligonucleo
15	16	53.3	50	6	AX157316 Sequence
16	15.8	52.7	50	6	CQ008354 Sequence
17	15.6	52.0	32	6	A37857 Sequence 27
18	15.6	52.0	32	6	AR069895 Sequence
19	15.6	52.0	32	6	AR099292 Sequence

C 20	15.6	52.0	32	6	AR124176	AR124176 Sequence
C 21	15.6	52.0	32	6	AR442783	AR442783 Sequence
C 22	15.6	52.0	43	6	AR036016	AR036016 Sequence
C 23	15.6	52.0	43	6	AR161840	AR161840 Sequence
C 24	15.6	52.0	43	6	I85694	I85694 Sequence 43
C 25	15.4	51.3	27	6	BD000197	BD000197 Viral vec
C 26	15.4	51.3	40	6	AR035911	AR035911 Sequence
C 27	15.4	51.3	40	6	AR035913	AR035913 Sequence
C 28	15.4	51.3	40	6	I20147	I20147 Sequence 10
C 29	15.4	51.3	40	6	I20149	I20149 Sequence 10
C 30	15.4	51.3	40	6	AR340325	AR340325 Sequence
C 31	15.4	51.3	40	6	AR340327	AR340327 Sequence
C 32	15.4	51.3	42	9	HS4010898	AJ010898 Homo sapi
C 33	15.4	51.3	43	6	A59897	A59897 Sequence 15
C 34	15.4	51.3	50	6	CQ006450	CQ006450 Sequence
C 35	15.2	50.7	40	6	A58595	A58595 Sequence 1
C 36	15.2	50.7	44	6	A58596	A58596 Sequence 2
C 37	15.2	50.7	44	6	A58603	A58603 Sequence 9
C 38	14.8	49.3	28	6	BD016942	BD016942 Plant pro
C 39	14.8	49.3	30	6	AX069192	AX069192 Sequence
C 40	14.8	49.3	32	6	E59198	E59198 Method for
C 41	14.8	49.3	32	6	E64379	E64379 Process of
C 42	14.8	49.3	33	6	AX781258	AX781258 Sequence
C 43	14.6	48.7	30	6	AX697914	AX697914 Sequence
C 44	14.6	48.7	44	6	I90211	I90211 Sequence 37
C 45	14.6	48.7	48	6	I90209	I90209 Sequence 35

ALIGNMENTS

RESULT 1

LOCUS I12899 30 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 6 from patent US 5429923.
ACCESSION I12899
VERSION I12899.1 GI:910876
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 6 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGCTTGAGAA 30

Db 1 GCGGTACCCAGCAGCCCGCGCTTGAGAA 30

RESULT 2

LOCUS AR256113 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 9 from patent US 6482923.
ACCESSION AR256113
VERSION AR256113.1 GI:27305503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Shi,Y. and Ruben,S.M.

TITLE	Interleukin 17-like receptor protein									
JOURNAL	Patent: US 6482923-A 9 19-NOV-2002;									
FEATURES	Location/Qualifiers									
source	1..26									
	/organism="unknown"									
	/mol_type="genomic DNA"									
ORIGIN										
Query Match	60.7%; Score 18.2; DB 6; Length 26;									
Best Local Similarity	87.0%; Pred. No. 1.2e+04;									
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	1 GCGGTACCCAGCAGCCCGGCTT 23									
Dd	2 GCGGTACCCAGCAGCCCGGCTT 24									
RESULT 3										
LOCUS	AR410127 26 bp DNA linear PAT 18-DEC-2003									
DEFINITION	Sequence 9 from patent US 6635443.									
ACCESSION	AR410127									
VERSION	AR410127.1 GI:40161304									
KEYWORDS	.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Shi, Y. and Ruben, S. M.									
TITLE	Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein									
JOURNAL	Patent: US 6635443-A 9 21-OCT-2003;									
FEATURES	Location/Qualifiers									
source	1..26									
	/organism="unknown"									
	/mol_type="genomic DNA"									
ORIGIN										
Query Match	60.7%; Score 18.2; DB 6; Length 26;									
Best Local Similarity	87.0%; Pred. No. 1.2e+04;									
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	1 GCGGTACCCAGCAGCCCGGCTT 23									
Dd	2 GCGGTACCCAGCAGCCCGGCTT 24									
RESULT 4										
LOCUS	A42996 48 bp DNA linear PAT 06-MAR-1997									
DEFINITION	Sequence 11 from Patent WO9504149.									
ACCESSION	A42996									
VERSION	A42996.1 GI:2298440									
KEYWORDS	.									
SOURCE	unidentified									
ORGANISM	unclassified.									
REFERENCE	1 (bases 1 to 48)									
AUTHORS	Bovenberg, R. A., Koekman, B. P., Hoekema, A., Van, D. L. and Verweij, J. J.									
TITLE	PROCESS FOR THE EFFICIENT PRODUCTION OF 7-ADCA VIA 3-(CARBOXYETHYLTHIO)PROPYONYL-7-ADCA									
JOURNAL	Patent: WO 9504149-A 11 09-FEB-1995;									
COMMENT	GIST BROCADES NV (NL)									
FEATURES	Other publication PL 312747 960513									
	Other publication CA 2168004 950209.									
source	Location/Qualifiers									
	1..48									
	/organism="unidentified"									
	/mol_type="unassigned DNA"									
	/db_xref="taxon:32644"									
ORIGIN										
Query Match	55.3%; Score 16.6; DB 6; Length 48;									

RESULT 7
LOCUS 191791
DEFINITION Sequence 11 from patent US 5726032.
ACCESSION 191791
VERSION 191791.1 GI:3936261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Bovenberg,R.Ary.Jans., Koekman,B.Pieter., Hoekema,A., Van Der Laan,J.Metske., Verweij,J. and De Vroom,E.
TITLE Process for the efficient production of 7-ADCA via 2-(carboxyethylthio)acetyl-7-ADCA and 3-(carboxymethylthio)propionyl-7-ADCA
JOURNAL Patent: US 5726032-A 11 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..48
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 55.3%; Score 16.6; DB 6; Length 48;
Best Local Similarity 82.6%; Pred. No. 5e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 ACCCCAGCAGCCGGCCTTGAG 28
|||||
Db 18 ACCGCCGCGCCGGCTTGAG 40
|||||
RESULT 8
LOCUS 185833/c
DEFINITION Sequence 1 from patent US 5698763.
ACCESSION 185833
VERSION 185833.1 GI:3205551
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Weissmann,C., Bueler,H., Aguet,M., Fischer,M. and Sailer,A.
TITLE Transgenic animals lacking prion proteins
JOURNAL Patent: US 5698763-A 1 16-DEC-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 54.7%; Score 16.4; DB 6; Length 30;
Best Local Similarity 76.9%; Pred. No. 6.2e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 5 TACCCAGCAGCCGGCCTTGAGAA 30
|||||
Db 29 TACAGCAGCAGCAGGACTTGAGAA 4
|||||
RESULT 9
LOCUS AR256115
DEFINITION Sequence 11 from patent US 6482923.
ACCESSION AR256115
VERSION AR256115.1 GI:27305505
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.
TITLE Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
JOURNAL Patent: US 6635443-A 11 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGGCTT 23
|||||
Db 6 GGTACCCAGCAGCTCCCGGCTT 26
|||||

Interleukin 17-like receptor protein
Patent: US 6482923-A 11 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGGCTT 23
|||||
Db 6 GGTACCCAGCAGCTCCCGGCTT 26
|||||
RESULT 10
LOCUS AR256117
DEFINITION Sequence 13 from patent US 6482923.
ACCESSION AR256117
VERSION AR256117.1 GI:27305507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.
TITLE Interleukin 17-like receptor protein
JOURNAL Patent: US 6482923-A 13 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGGCTT 23
|||||
Db 6 GGTACCCAGCAGCTCCCGGCTT 26
|||||
RESULT 11
LOCUS AR410129
DEFINITION Sequence 11 from patent US 6635443.
ACCESSION AR410129
VERSION AR410129.1 GI:40161306
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi,Y. and Ruben,S.M.
TITLE Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
JOURNAL Patent: US 6635443-A 11 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGGCTT 23
|||||
Db 6 GGTACCCAGCAGCTCCCGGCTT 26
|||||

Db 6 GGTACCCAGCCTCCCGGCTT 26

RESULT 12
LOCUS AR410131 28 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 13 from patent US 6635443.
ACCESSION AR410131
VERSION AR410131.1 GI:40161308
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Shi, Y. and Ruben, S.M.
TITLE Polynucleotides encoding a novel interleukin receptor termed interleukin-17 receptor-like protein
JOURNAL Patent: US 6635443-A 13 21-OCT-2003;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCGCT 23
|||||
Db 6 GGTACCCAGCCTCCCGGCTT 26

RESULT 13
LOCUS A06417/c 33 bp DNA linear PAT 22-JUN-1993
DEFINITION Oligonucleotide primer.
ACCESSION A06417
VERSION A06417.1 GI:412865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS
TITLE NOVEL GLUCOSE ISOMERASE ENZYMES AND THEIR USE
JOURNAL Patent: WO 9000601-A 7 25-JAN-1990;
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 33;
Best Local Similarity 72.4%; Pred. No. 7.4e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCTTGAAGAA 30
|||||
Db 32 CGCGACTCCATCATCTCGACCTTCAGAA 4

RESULT 14
LOCUS A10235/c 33 bp DNA linear PAT 25-JAN-1994
DEFINITION oligonucleotide primer.
ACCESSION A10235
VERSION A10235.1 GI:490665
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 33)
AUTHORS Luiten, R.G.M., Quax, W.J., Schuurhuizen, P.W. and Mrabet, N.
TITLE Novel glucose isomerase enzymes and their use
JOURNAL Patent: EP 0351029-A 8 17-JAN-1990;
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 33;
Best Local Similarity 72.4%; Pred. No. 7.4e+04;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCTTGAAGAA 30
|||||
Db 32 CGCGACTCCATCATCTCGACCTTCAGAA 4

RESULT 15
LOCUS AX157316/c 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 644 from Patent WO0140521.
ACCESSION AX157316
VERSION AX157316.1 GI:14538647
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 644 07-JUN-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg20705188"
misc_feature 26
/note="2 of 2 allelic variants (643 is other entry)"

ORIGIN
Query Match 53.3%; Score 16; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 8.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTTGA 26
|||||
Db 38 GGCCCCCAACAGCCAGGCGCTTGA 15

RESULT 16
LOCUS CQ008354/c 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 6994 from Patent WO0147944.
ACCESSION CQ008354
VERSION CQ008354.1 GI:41015052
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof
Patent: WO 0147944-A 6994 05-JUL-2001;
Curagen Corporation (US)
JOURNAL
FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
25..26
misc_feature
/note="Nucleotide deleted between bases 25 and 26"
Accession number CG41501665"
ORIGIN
Query Match 52.7%; Score 15.8; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 CCCAGCAGCCGCGCCTTG 25
|||||:|||||:|||||:
Db 21 CCCAGCAGCGCGCCTTG 3
RESULT 17
A37857/c
LOCUS A37857 32 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 27 from Patent WO9408014.
ACCESSION A37857
VERSION A37857.1 GI:2294537
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D. and Zagorec,M.
TITLE POLYPEPTIDES INVOLVED IN STREPTOGRAMIN BIOSYNTHESIS, NUCLEOTIDE
SEQUENCES CODING FOR SAID POLYPEPTIDES AND USE THEREOF
JOURNAL Patent: WO 9408014-A 27 14-APR-1994;
COMMENT RHONE-POULENC RORER SA (FR)
Other publication AU 482393 940426
Other publication CA 2145523 940414
Other publication ZA 9307102 940422
Other publication FI 951403 950324
Other publication FR 2696189 940401
Other publication JP 8501696T 960227.
FEATURES
source
1..32
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
|||||:|||||:|||||:
Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 18
AR069895/c
LOCUS AR069895 32 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 43 from patent US 5891695.
ACCESSION AR069895
VERSION AR069895.1 GI:7220783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., DeBussche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins, use
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 5891695-A 43 06-APR-1999;
FEATURES
source
1..32
Location/Qualifiers
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Thibaut,D., Zagorec,M., DeBussche,L. and De Crecy-Lagard,V.
Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
Patent: US 5891695-A 43 06-APR-1999;
JOURNAL
FEATURES
source
1..32
Location/Qualifiers
/organism="unassigned DNA"
/mol_type="unassigned DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
|||||:|||||:|||||:
Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 19
AR099292/c
LOCUS AR099292 32 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 45 from patent US 6077699.
ACCESSION AR099292
VERSION AR099292.1 GI:12809058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., DeBussche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6077699-A 45 20-JUN-2000;
FEATURES
source
1..32
Location/Qualifiers
/organism="unassigned DNA"
/mol_type="unassigned DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 2 CGGTACCCAGCAGCCGCGCCTTG 25
|||||:|||||:|||||:
Db 32 CGGTACCASAGSGSGGCTTS 9
RESULT 20
AR124176/c
LOCUS AR124176 32 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 43 from patent US 6171846.
ACCESSION AR124176
VERSION AR124176.1 GI:14109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., LaCroix,P.,
Thibaut,D., Zagorec,M., DeBussche,L. and De Crecy-Lagard,V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6171846-A 43 09-JAN-2001;
FEATURES
source
1..32
Location/Qualifiers
/organism="unassigned DNA"
/mol_type="unassigned DNA"
ORIGIN
Query Match 52.0%; Score 15.6; DB 6; Length 32;

```
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCGCTTG 25
Db 32 CGGTACCASAGSGSGGCTTS 9

RESULT 21
AR442783/c
LOCUS AR442783 32 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 43 from patent US 6670157.
ACCESSION AR442783
VERSION AR442783.1 GI:42670187
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Blanc,V., Blanche,F., Crouzet,J., Jacques,N., Lacroix,P.,
Thibaut,D., Zagorec,M., Debussche,L. and De Crecy-Lagard,V.
TITLE polypeptides involved in the biosynthesis of streptogramins,
nucleotide sequences coding for these polypeptides and their use
JOURNAL Patent: US 6670157-A 43 30-DEC-2003;
FEATURES
source
Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 52.0%; Score 15.6; DB 6; Length 32;
Best Local Similarity 62.5%; Pred. No. 1.3e+05;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCCGGCGCTTG 25
Db 32 CGGTACCASAGSGSGGCTTS 9

RESULT 22
AR036016/c
LOCUS AR036016 43 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 43 from patent US 5871974.
ACCESSION AR036016
VERSION AR036016.1 GI:5952684
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Huse,W.D.
TITLE Surface expression libraries of heteromeric receptors
JOURNAL Patent: US 5871974-A 43 16-FEB-1999;
FEATURES
source
Location/Qualifiers
1..43
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CGGTACCCAGCAGCCCGGCGCTTGAGAA 30
Db 42 CGGTACCCAGCTTAATCGCCTTGCGAGAA 13

RESULT 23
AR161840/c
LOCUS AR161840 43 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 42 from patent US 6258530.
ACCESSION AR161840
```

```
VERSION ARI161840.1 GI:16228821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Huse,W.D.
TITLE Surface expression libraries of randomized peptides
JOURNAL Patent: US 6258530-A 42 10-JUL-2001;
FEATURES
source
Location/Qualifiers
1..43
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGGCGCTTGAGAA 30
Db 42 GCGGTACCCAGCTTAATCGCCTTGCGAGAA 13

RESULT 24
I85694/c
LOCUS I85694 43 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 43 from patent US 5698426.
ACCESSION I85694
VERSION I85694.1 GI:3205412
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Huse,W.D.
TITLE Surface expression libraries of heteromeric receptors
JOURNAL Patent: US 5698426-A 43 16-DEC-1997;
FEATURES
source
Location/Qualifiers
1..43
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 52.0%; Score 15.6; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.3e+05;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGGCGCTTGAGAA 30
Db 42 GCGGTACCCAGCTTAATCGCCTTGCGAGAA 13

RESULT 25
BD000197
LOCUS BD000197 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Viral vector.
ACCESSION BD000197
VERSION BD000197.1 GI:18623276
KEYWORDS JP 2000279178-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Hamada,H.
TITLE Viral vector
JOURNAL Patent: JP 2000279178-A 10 10-OCT-2000;
COMMENT JAPANESE FOUNDATION FOR CANCER RESEARCH
OS Artificial Sequence
PN JP 2000279178-A/10
PD 10-OCT-2000
PR 24-FEB-1999 JP 1999093263
PR
```


PI HIROFUMI HAMADA
PC C12N15/09,A61K31/00,A61K38/00,A61K39/235,A61K48/00,
PC C07K14/075,
PC C07K14/52,C07K14/68,C07K14/72,C12N7/00,C12N9/12,C12N9/80, PC
G01N33/574,
PC C12N15/00,A61K37/02
CC
FH Key Location/Qualifiers
FT source 1..27
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 27;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCGGTACCCAGCAGCCCGCCTTG 25
|||||
Db 3 GCGGTACCCAGCAGCATCGTGACCTG 27
RESULT 26
AR035911/c
LOCUS AR035911 40 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 104 from patent US 5871962.
ACCESSION AR035911
VERSION AR035911.1 GI:5952579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods
JOURNAL Patent: US 5871962-A 104 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..40
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGCCTTGAA 27
|||||
Db 40 GGCACATCAATAGCAGCGCCTTGAA 16
RESULT 27
AR035913/c
LOCUS AR035913 40 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 106 from patent US 5871962.
ACCESSION AR035913
VERSION AR035913.1 GI:5952581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods
JOURNAL Patent: US 5871962-A 106 16-FEB-1999;

FEATURES
source Location/Qualifiers
1..40
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGCCTTGAA 27
|||||
Db 27 GGCACATCAATAGCAGCGCCTTGAA 3
RESULT 28
I20147/c
LOCUS I20147 40 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 104 from patent US 5514539.
ACCESSION I20147
VERSION I20147.1 GI:1600502
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines
JOURNAL Patent: US 5514539-A 104 07-MAY-1996;
FEATURES
source Location/Qualifiers
1..40
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGCCTTGAA 27
|||||
Db 40 GGCACATCAATAGCAGCGCCTTGAA 16
RESULT 29
I20149/c
LOCUS I20149 40 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 106 from patent US 5514539.
ACCESSION I20149
VERSION I20149.1 GI:1600504
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Bukh,J., Miller,R.H. and Purcell,R.H.
TITLE Nucleotide and deduced amino acid sequences of the envelope 1 gene of 51 isolates of hepatitis C virus and the use of reagents derived from these sequences in diagnostic methods and vaccines
JOURNAL Patent: US 5514539-A 106 07-MAY-1996;
FEATURES
source Location/Qualifiers
1..40
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 51.3%; Score 15.4; DB 6; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 GGTACCCAGCAGCCCGCCTTGAA 27
|||||
Db 3 GGTACCCAGCAGCCCGCCTTGAA 27

[illegible][illegible]

JOURNAL Patent: JP 2001258558-A 4 25-SEP-2001;
MITSUI CHEM INC
COMMENT OS Artificial Sequence
PN JP 2001258558-A/4
PD 25-SEP-2001
PF 17-MAR-2000 JP 2000075781
PI MASANORI YOSHIDA, YUKIHIRO YANAI, SHIGERU TAKAHASHI PC
C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Description of
Artificial Sequence: oligo nucleotide primer FH Key
Location/Qualifiers
Location/Qualifiers
1. .28
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Query Match 49.3%; Score 14.8; DB 6; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 2 CGGTACCCAGCAGCCGCGCTTGAA 27
|||||
Db 1 CGGGATCCTAATAGCAGCGCTTGAA 26
|||||

RESULT 39
AX069192
LOCUS AX069192 30 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 3 from Patent WO0102594.
ACCESSION AX069192
VERSION AX069192.1 GI:12579073
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Greaves, D.R., Thomsen, L., Catchpole, I.R. and Ford, M.J.
TITLE Dna constructs based on the elf4a gene promoter
JOURNAL Patent: WO 0102594-A 3 11-JAN-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
source
Location/Qualifiers
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 3 GGTACCCAGCAGCCGCGCTTGAA 28
|||||
Db 5 GGTACCATGGCTGCCAGCGCTCGAG 30
|||||

RESULT 40
E59198
LOCUS E59198 32 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for searching antibacterial or herbicidally active compound.
ACCESSION E59198
VERSION E59198.1 GI:18622469
KEYWORDS JP 2000300257-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 32)
AUTHORS Miyake, K., Hashimoto, S., Motoyama, H., Ozaki, A., Set, H., Kuzuyama, T.
and Takahashi, S.
TITLE Method for searching antibacterial or herbicidally active compound
JOURNAL Patent: JP 2000300257-A 18 31-OCT-2000;

JOURNAL Patent: JP 2001258558-A 4 25-SEP-2001;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000300257-A/18
PD 31-OCT-2000
PF 12-APR-1999 JP 1999104590
PR
PI KOICHIRO MIYAKE, SHINICHI HASHIMOTO, HIROAKI MOTOYAMA, AKIO
OZAKI, HARUO SETO,
PI TOMOHIISA KUZUYAMA, SHUNJI TAKAHASHI
PC C12N15/09, A01N57/12, C12N1/21, C12N9/00, C12P23/00, C12Q1/18// PC
(C12N1/21, C12R1:18), (C12P23/00, C12R1:19), (C12P23/00, C12R1:18), PC
C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .32
/organism="Artificial Sequence".

FEATURES
source
Location/Qualifiers
1. .32
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 32;
Best Local Similarity 73.1%; Pred. No. 2.7e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 1 GCGGTACCCAGCAGCCGCGCTTGAA 26
|||||
Db 1 GGGGATCCTGCCAGCGCGCTTGAA 26
|||||

Search completed: November 18, 2005, 17:42:57
Job time : 834.457 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCGCCCTTGAAGAA 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	2	AAQ91126
2	30	100.0	30	9	ACA63116
3	30	100.0	30	13	ADR05302
4	18.2	60.7	26	3	AZ35752 Human IL1
5	18.2	60.7	26	3	AZ52041 3' primer
6	18.2	60.7	26	3	AA75767
7	18.2	60.7	26	13	ADT93849
8	17.2	57.3	24	12	ACF36917
9	17.2	57.3	37	12	ACF36933
10	16.6	55.3	48	2	AAQ84993
11	16.6	55.3	48	2	AAQ82717
12	16.2	54.0	25	9	ACI28074
13	16.2	54.0	25	9	ACI41032
14	16.2	54.0	28	3	AZ35754
15	16.2	54.0	28	3	AZ35756
16	16.2	54.0	28	3	AZ52043
17	16.2	54.0	28	3	AA75769
18	16.2	54.0	28	3	AA75771
19	16.2	54.0	28	13	ADT93853
20	16.2	54.0	28	13	ADT93851

21	16.2	54.0	38	10	ADF72771
22	16.2	54.0	38	12	ADH34521
23	16	53.3	29	6	ABK49653
24	16	53.3	50	4	AAI73703
25	15.8	52.7	19	9	ACD82439
26	15.8	52.7	19	9	ACD82353
27	15.8	52.7	39	10	ACF79913
28	15.8	52.7	41	6	ABN86094
29	15.8	52.7	50	4	AAI33786
30	15.6	52.0	43	2	AAI16927
31	15.6	52.0	43	3	AAZ91566
32	15.4	51.3	20	9	ACD82542
33	15.4	51.3	27	3	AAA93835
34	15.4	51.3	40	2	AAQ83899
35	15.4	51.3	40	2	AAQ83897
36	15.4	51.3	40	2	AAI16692
37	15.4	51.3	40	2	AAI16690
38	15.4	51.3	40	10	ADF08491
39	15.4	51.3	50	4	AAI31882
40	15.2	50.7	25	11	ADL96717
41	15.2	50.7	33	10	ADJ72409
42	15.2	50.7	40	2	AAI58818
43	15.2	50.7	44	2	AAI58825
44	15.2	50.7	44	2	AAI58819
45	15	50.0	25	9	ACK29080

ALIGNMENTS

RESULT 1

AAQ91126
ID AAQ91126 standard; cDNA; 30 BP.

AC AAQ91126;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer D.

XX Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.

OS Synthetic.

FN US5429923-A.

PD 04-JUL-1995.

PF 11-DEC-1992; 92US-00989160.

PR 11-DEC-1992; 92US-00989160.

XX (HARD) HARVARD COLLEGE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

WPI; 1995-245715/32.

DR Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

PT Example 1; Col 10; 22pp; English.

XX AAQ91121-091130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
CC a broad applicability and may be used to detect mutations responsible for
CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 2

ACA63116

ID ACA63116 standard; DNA; 30 BP.

AC ACA63116;

28-AUG-2003 (first entry)

Human beta cardiac myosin heavy chain PCR primer D.

Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
phenylketonuria; cystic fibrosis.

Homo sapiens.

US2003054343-A1.

20-MAR-2003.

06-JUN-1995; 95US-00469172.

11-DEC-1992; 92US-00989160.

(SEID/) SEIDMAN C.

(SEID/) SEIDMAN J.

(WATK/) WATKINS H.

(ROSE/) ROSENZWEIG A.

Seidman C, Seidman J, Watkins H, Rosenzweig A;

WPI; 2003-512374/48.

Detecting a presence or absence of a mutation associated with
hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
hemophilia, by detecting a mutation in an amplified product of a beta
cardiac myosin heavy-chain DNA.

Example 1; Page 5; 22pp; English.

The invention relates to detecting the presence or absence of a mutation
associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
and FHC) comprises detecting a mutation associated with hypertrophic
cardiomyopathy in an amplified product of a beta cardiac myosin heavy
chain DNA. The mutations associated with SHC/FHC are detected in the
myosin gene isolated from blood, by detecting mis-matched areas in RNA-
DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
sample). FHC associated point mutation can be classified and used to
determine life expectancy in affected individuals e.g. using a Kaplan-
Meier curve for the classified type of FHC causing point mutation. Also
included are an RNA probe comprising ribonucleotides arranged in a
sequence which is complementary to at least a portion of beta-cardiac
myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
CC DNA. The method is useful for detecting the presence or absence of a
CC mutation associated with hypertrophic cardiomyopathy. This method is
CC especially useful for diagnosing SHC and FHC, as well as for determining
CC the estimated life expectancy of a person with familial hypertrophic
CC cardiomyopathy. In particular, the method is useful for determining an
CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
CC chain cDNA containing an FHC-associated mutation

XX Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 3

ADR05302

ID ADR05302 standard; DNA; 30 BP.

XX ADR05302;

21-OCT-2004 (first entry)

Human beta cardiac myosin heavy chain mutation detection primer D.

Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
familial hypertrophic cardiomyopathy;
sporadic hypertrophic cardiomyopathy.

Homo sapiens.

US2004152121-A1.

05-AUG-2004.

27-FEB-2004; 2004US-00788779.

11-DEC-1992; 92US-00989160.

06-JUN-1995; 95US-00469172.

(SEID/) SEIDMAN C.

(SEID/) SEIDMAN J.

(WATK/) WATKINS H.

(ROSE/) ROSENZWEIG A.

Seidman C, Seidman J, Watkins H, Rosenzweig A;

WPI; 2004-592586/57.

Detecting mutations associated with hypertrophic cardiomyopathy to
diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
myosin heavy-chain DNA and detecting the mutation in the amplified
product.

Claim 18; SEQ ID NO 6; 22pp; English.

The invention relates to detecting the presence or absence of a mutation
associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
amplified product, and detecting the presence or absence of a mutation
associated with hypertrophic cardiomyopathy in the amplified product,
thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
included are a set of DNA oligonucleotide primers for amplifying beta-
cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 30 BP; 7 A; 11 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
|||
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 4

AAZ35752
ID AAZ35752 standard; DNA; 26 BP.

XX AAZ35752;

XX 01-FEB-2000 (first entry)

XX Human IL17RLP PCR 3' primer SEQ ID NO:9.

XX Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
KW detection; immune system related disorder; haemostasis;
KW cellular activation; angiogenesis; tumour metastasis; ovulation;
KW cellular migration; neurogenesis; infection; T-cell proliferation;
KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;
KW immunosuppression; immunity; inflammatory bowel disease;
KW myelo suppression; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9914240-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019121.

XX 17-SEP-1997; 97US-0059133P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Shi Y, Ruben SM;

XX WPI; 2000-061918/05.

XX

PT New human interleukin-17 receptor like protein, e.g. to treat disorders
PT relating to cellular activation.

PS Example 2; Page 95; 133pp; English.

XX The present invention describes human interleukin 17 receptor like
CC protein (IL17RLP), isolated from a cDNA library of human adult pulmonary
CC tissue. The present sequence represents a PCR primer for human IL17RLP.
CC IL17RLP and its agonists can be used to treat disorders relating to
CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
CC cellular migration and ovulation, and neurogenesis. They can also be used
CC to enhance host defences against resistant chronic and acute infections,
CC e.g. mycobacterial infections via the attraction and activation of
CC microbial leukocytes. IL17RLP may also be used to increase T-cell
CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
CC regulate haematopoiesis by regulating the activation and differentiation
CC of various haematopoietic progenitor cells, e.g. to release mature
CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
CC mobilisation or to treat sepsis. The products can also be used for the
CC diagnosis or treatment of immune system related disorders e.g. tumours,
CC cancers, interstitial lung disease, and any dysregulation of immune cell
CC function including autoimmunity, arthritis, leukaemias, lymphomas,
CC immunosuppression, immunity, humoral immunity, inflammatory bowel
CC disease, or myelo suppression

XX Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 60.7%; Score 18.2; DB 3; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGCGCT 23
|||
Db 2 GCGGTACCCAGCAGCTCCGCGCTT 24

RESULT 5

AAZ52041
ID AAZ52041 standard; DNA; 26 BP.

XX AAZ52041;

XX 09-AUG-2000 (first entry)

XX 3'primer for amplification of IL-17RLP leader sequence.

XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
KW resistant chronic infection; acute infection; mycobacterial infection;
KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hyridoma;
KW IL-6 expression; myeloma; plasmacytoma; Lennert's Lymphoma;
KW immunoprotective; cytostatic; hematopoietic; proliferative;
KW antibacterial; PCR primer; ss.

XX Homo sapiens.

XX WO200015759-A1.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021048.

XX 16-SEP-1998; 98US-00154219.

XX 16-SEP-1998; 98WO-US019121.

XX 16-MAR-1999; 99US-00268311.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y;

XX WPI; 2000-271403/23.

XX

PT Novel polynucleotides encoding interleukin-17-like receptor protein,
PT useful for diagnosis and treatment of immune system-related disorders,
XX e.g. sepsis and cancers.

PS Example 2; Page 98; 147pp; English.

XX The patent relates to novel interleukin-17-like receptor protein (IL-
CC 17RLP). IL-17RLP is a homologue of the IL-17 receptor and has a wide
CC range of cytokine receptor-like activities. IL-17RLP or its agonists may
CC be used to enhance host defenses against resistant chronic and acute
CC infections, e.g. mycobacterial infections, via the attraction and
CC activation of microbicidal leukocytes. It may also be used to increase T-
CC cell proliferation by stimulating IL-2 biosynthesis, for the treatment of
CC T-cell mediated autoimmune diseases and lymphocytic leukaemias. IL-17RLP
CC may also be used to regulate hematopoiesis and to treat sepsis.
CC Extracellular IL-17RLP domains may be used as antagonists of IL-17RLP. IL
CC -17RLP agonists and antagonists can also be used to modulate IL-6
CC expression, useful in treatment of cancers such as myelomas.
CC plasmacytomas and hybridomas and Lennert's Lymphoma. The present sequence
CC is the 3' PCR primer used for the amplification of IL-17RLP leader
CC sequence. This is used in the cloning and expression of IL-17RLP protein
CC in a baculovirus expression system

XX SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 60.7%; Score 18.2; DB 3; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCCT 23
Db 2 GCGGTACCCAGCAGCCGGCCT 24

RESULT 6

AAAT5767
ID AAAT5767 standard; DNA; 26 BP.

XX AC AAAT5767;

XX DT 22-JAN-2001 (first entry)

XX DE PCR primer for a human interleukin 17 receptor-like cDNA fragment.

XX KW Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
KW cellular migration; ovulation; neurogenesis; arthritis;
KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.

XX OS Homo sapiens.

XX FN WO200055204-A1.

XX PD 21-SEP-2000.

XX PF 06-MAR-2000; 2000WO-US005759.

XX PR 16-MAR-1999; 99US-00268311.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Shi Y, Ruben SM;

XX DR WPI; 2000-647065/62.

XX PT Novel gene encoding a polypeptide of the interleukin-17 receptor family,
PT and an antagonist and agonist of the polypeptide, useful for treating,
PT diagnosing, detecting and/or preventing immune system related disorders.

XX PS Example 2; Page 179; 247pp; English.

XX PCR primers AAAT5766-67 were used to amplify a fragment of cDNA encoding
CC a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP

CC polypeptide is useful for screening for agonists and antagonists. These
CC antagonists and agonists are useful for treating, diagnosing, detecting
CC and or preventing disorders related to cellular activation, haemostasis,
CC angiogenesis, tumour metastasis, cellular migration, ovulation or
CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
CC e.g. systemic lupus erythromatosus

XX SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 60.7%; Score 18.2; DB 3; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCCT 23
Db 2 GCGGTACCCAGCAGCCGGCCT 24

RESULT 7

ADT93849
ID ADT93849 standard; DNA; 26 BP.

XX AC ADT93849;

XX DT 16-DEC-2004 (first entry)

XX KW Human interleukin 17 receptor-like protein cDNA expression 3' primer.
XX ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;
KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
KW hemostasis; angiogenesis; tumour metastasis; cellular migration;
KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
KW graft versus host disease; chromosomal identification; primer; PCR.

XX OS Homo sapiens.

XX FN AU2004200961-A1.

XX PD 01-APR-2004.

XX PF 09-MAR-2004; 2004AU-00200961.

XX PR 09-MAR-2004; 2004AU-00200961.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Shi Y, Ruben SM;

XX DR WPI; 2004-662639/65.

XX PT Novel isolated interleukin 17-receptor-like protein useful for treating
PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
PT disease.

XX PS Example 2; SEQ ID NO 9; 145pp; English.

XX The invention relates to an isolated interleukin 17-receptor-like protein
CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
CC identical to a sequence e.g., sequence having amino acids from positions
CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
CC the specification, sequence having amino acids from positions 18-407 of
CC (S1) that comprises N-terminal methionine or sequence having amino acids
CC from positions 1-407 of (S1). (I) is useful for treating disorders
CC related to cellular activation, hemostasis, angiogenesis, tumor
CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
CC for treating immune-related disorders e.g., Crohn's disease, tumor,
CC inflammatory bowel disease, autoimmune diseases, lymphocytic leukemias,
CC or graft versus host disease. (II) is useful for chromosomal
CC identification. (I) exhibits enhanced activity, solubility and stability,
CC and is produced in large quantities. This sequence corresponds to a PCR
CC primer to amplify the extracellular region DNA from the human IL17RLP


```

CC cDNA sequence (AD793841) for expression in a baculovirus expression
CC system.
XX
SQ Sequence 26 BP; 2 A; 13 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match      60.7%; Score 18.2; DB 13; Length 26;
  Best Local Similarity 87.0%; Pred. No. 1.1e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 23
   |||||
Db 2 GCGGTACCCAGCCTCCCGGCTT 24

RESULT 8
ACF36917
ID ACF36917 standard; DNA; 24 BP.
XX
AC ACF36917;
XX
DT 15-APR-2004 (first entry)
XX
DE Human alpha1,3 fucosyltransferase VII plasmid PCR primer #1.
XX
KW Alpha1,3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
XX enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FN WO2003093448-A2.
XX
PD 13-NOV-2003.
XX
PF 05-MAY-2003; 2003WO-US014235.
XX
PR 03-MAY-2002; 2002US-0377730P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Bayer RJ, Mendoza G;
XX
DR WPI; 2004-053043/05.
XX
CC New fusion protein comprising a stem region of fucosyltransferase VI and
CC a catalytic domain of fucosyltransferase VII, useful for enzymatically
CC synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
XX
PS Example 1; Page 72; Opp; English.
XX
CC The present invention relates to a fusion protein comprising a stem
CC region of human fucosyltransferase VI and a catalytic domain of
CC fucosyltransferase VII, where the fusion protein has high enzymatic
CC activity, and catalyses the transfer of fucose residue from a donor
CC substrate to an acceptor substrate. The fusion protein is useful for
CC enzymatically synthesizing glycoproteins, glycolipids, and
CC oligosaccharide moieties. The present sequence is a PCR primer used to
CC isolate a coding sequence in the exemplification of the invention
XX
SQ Sequence 24 BP; 4 A; 13 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match      57.3%; Score 17.2; DB 12; Length 24;
  Best Local Similarity 86.4%; Pred. No. 2.7e+03;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 22
   |||||
Db 1 GCGGTACCCAGCAGCCCGGCTT 22

RESULT 9
ACF36933
ID ACF36933 standard; DNA; 37 BP.
XX

```

```

AC ACF36933;
XX
DT 15-APR-2004 (first entry)
XX
DE Human alpha1,3 fucosyltransferase VII plasmid PCR primer #9.
XX
KW Alpha1,3 fucosyltransferase; FT; glycosyltransferase; fusion protein;
XX enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FN WO2003093448-A2.
XX
PD 13-NOV-2003.
XX
PF 05-MAY-2003; 2003WO-US014235.
XX
PR 03-MAY-2002; 2002US-0377730P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI Bayer RJ, Mendoza G;
XX
DR WPI; 2004-053043/05.
XX
CC New fusion protein comprising a stem region of fucosyltransferase VI and
CC a catalytic domain of fucosyltransferase VII, useful for enzymatically
CC synthesizing glycoproteins, glycolipids, and oligosaccharide moieties.
XX
PS Example 3; Page 81; Opp; English.
XX
CC The present invention relates to a fusion protein comprising a stem
CC region of human fucosyltransferase VI and a catalytic domain of
CC fucosyltransferase VII, where the fusion protein has high enzymatic
CC activity, and catalyses the transfer of fucose residue from a donor
CC substrate to an acceptor substrate. The fusion protein is useful for
CC enzymatically synthesizing glycoproteins, glycolipids, and
CC oligosaccharide moieties. The present sequence is a PCR primer used to
CC isolate a coding sequence in the exemplification of the invention
XX
SQ Sequence 37 BP; 7 A; 18 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match      57.3%; Score 17.2; DB 12; Length 37;
  Best Local Similarity 86.4%; Pred. No. 2.8e+03;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGTACCCAGCAGCCCGGCTT 22
   |||||
Db 14 GCGGTACCCAGCAGCCCGGCTT 35

RESULT 10
AAQ84993
ID AAQ84993 standard; DNA; 48 BP.
XX
AC AAQ84993;
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
DE Expandase gene amplification primer #11 for expression cassette.
XX
KW Primer; amplify; PCR; expandase gene; cefE; Nicotiana lactamurans;
XX Streptomyces clavuligerus; expression cassette; acyltransferase; fungus;
XX Penicillin chrysoeum; hybrid promoter; Aspergillus nidulans; 7-ADCA;
XX 7-amino-desacetoxycapthalosporanic acid; cephalosporin; antibiotic; ss.
XX
OS Synthetic.
XX
FN WO9504148-A1.
XX
PD 09-FEB-1995.
XX

```

```
PF 29-JUL-1994; 94WO-EP002543.
XX
PR 30-JUL-1993; 93EP-00202259.
PR 24-DEC-1993; 93EP-00203696.
XX
PA (KONN ) GIST-BROCADES NV.
XX
FI Bovenberg RAL, Koekman BP, Hoekema A, Van Der Laan JM, Verweij J;
XX
DR WPI; 1995-082231/11.
XX
XX 7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum
PT - by simultaneous expression of expandase and acyl-transferase.
XX
XX Example 1; Page 14; 37pp; English.
XX
XX Primers (AAQ84983-95) were used to amplify the expandase gene (cefE) from
CC either Nicotidia lactamurans or Streptomyces clavuligerus. The resultant
CC sequences were placed in an expression cassette for simultaneous
CC expression of the cefE gene and the gene encoding an acyltransferase. The
CC expression cassette is placed in the fungus Penicillium chrysogenum.
CC Expression of the genes in the cassette is driven either by a trp-lac
CC hybrid promoter or the promoter from the Aspergillus nidulans gpdA gene.
CC The terminator is the 3'-end of the P.chrysogenum penDE gene. The primers
CC AAQ84991-3 were used to amplify a 0.5 kb region containing the
CC P.chrysogenum penDE (acyltransferase gene) terminator sequence. This
CC sequence was linked by PCR to the 3' end of the N.lactamurans cefE gene.
CC The cassette is used in the production of 7-amino-
CC desacetoxyccephalosporanic acid (7-ADCA), an intermediate in the
CC production of cephalosporin antibiotics. Note: the sequences shown in
CC this patent are identical to those in patent WO 95/04149. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 55.3%; Score 16.6; DB 2; Length 48;
Best Local Similarity 82.6%; Pred. No. 5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 ACCCGCAGCAGCCGCGCTTGAAG 28
||| ||| ||| ||| ||| ||| ||| |||
DB 18 ACCGCGCGCGCGCGCTTGAAG 40
||| ||| ||| ||| ||| ||| ||| |||
RESULT 11
AAQ82717
ID AAQ82717 standard; DNA; 48 BP.
XX
AC AAQ82717;
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
DE P. chrysogenum cefE gene expression cassette construction oligo.
XX
KW N. lactamurans; S. clavuligerus; P. chrysogenum; cefE gene;
KW expression cassette; 7-amino-desacetoxy-cephalosporanic acid;
KW expandase gene; cephalosporin antibiotics; ss.
XX
OS Synthetic.
XX
FN WO9504149-A1.
XX
PD 09-FEB-1995.
XX
PF 29-JUL-1994; 94WO-EP002544.
XX
PR 30-JUL-1993; 93EP-00202260.
PR 24-DEC-1993; 93EP-00203695.
XX
PA (KONN ) GIST-BROCADES NV.
XX
PI Bovenberg RAL, Koekman BP, Hoekema A, Van Der Laan JM, Verweij J;
XX
XX WPI; 1995-082232/11.
XX
XX 7-amino-desacetoxy-cephalosporanic acid prodn. in Penicillium chrysogenum
PT - transformed with expandase gene, using 3,3'-thiodi:propionic acid as
PT side chain precursor and deacylation of intermediate.
XX
XX Example 1; Page 14; 37pp; English.
XX
XX AAQ82707-Q82719 are oligonucleotides used in the construction of P.
CC chrysogenum expression cassettes for the N. lactamurans and S.
CC clavuligerus cefE (expandase) gene. The transformed P. chrysogenum can
CC now be used for 7-amino-desacetoxy-cephalosporanic acid prodn. an
CC intermediate for cephalosporin antibiotics. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 48 BP; 11 A; 18 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 55.3%; Score 16.6; DB 2; Length 48;
Best Local Similarity 82.6%; Pred. No. 5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 ACCCGCAGCAGCCGCGCTTGAAG 28
||| ||| ||| ||| ||| ||| ||| |||
DB 18 ACCGCGCGCGCGCGCTTGAAG 40
||| ||| ||| ||| ||| ||| ||| |||
RESULT 12
ACI28074
ID ACI28074 standard; DNA; 25 BP.
XX
AC ACI28074;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 28065.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
FN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
DR New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 28065; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
```

CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 3 A; 9 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 9; Length 25;
 Best Local Similarity 85.7%; Pred. No. 6.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACCCCGAGCGCCGCC 22
 ||||| ||||| ||||| |||||
 Db 4 CGGTACCTAGGAGCCCGTC 24

RESULT 13
 AC141032
 ID AC141032 standard; DNA; 25 BP.

XX AC AC141032;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 41023.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

KW genetic variation; biallelic marker; polymorphism; human;

KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 XX Southern, Northern or dot-blot hybridization to identify or detect the
 XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 41023; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,

CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 9; Length 25;
 Best Local Similarity 85.7%; Pred. No. 6.8e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACCCCGAGCGCCGCC 22
 ||||| ||||| ||||| |||||
 Db 3 CGGTACCTAGGAGCCCGTC 23

RESULT 14
 AAZ35754
 ID AAZ35754 standard; DNA; 28 BP.

XX AC AAZ35754;

XX 01-FEB-2000 (first entry)

XX Human IL17RLP PCR 3' primer SEQ ID NO:11.

XX Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
 KW detection; immune system related disorder; haemostasis;
 KW cellular activation; angiogenesis; tumour metastasis; ovulation;
 KW cellular migration; neurogenesis; infection; T-cell proliferation;
 KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
 KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;
 KW immunosuppression; immunity; inflammatory bowel disease;
 KW myelo suppression; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9914240-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019121.

XX 17-SEP-1997; 97US-0059133P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Shi Y, Ruben SM;

XX WPI; 2000-061918/05.

XX New human interleukin-17 receptor like protein, e.g. to treat disorders
 XX relating to cellular activation.

XX Example 3; Page 100; 133pp; English.

XX The present invention describes human interleukin 17 receptor like
 CC protein (IL17RLP), isolated from a cDNA library of human adult pulmonary
 CC tissue. The present sequence represents a PCR primer for human IL17RLP.
 CC IL17RLP and its agonists can be used to treat disorders relating to
 CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
 CC cellular migration and ovulation, and neurogenesis. They can also be used
 CC to enhance host defences against resistant chronic and acute infections,
 CC e.g. mycobacterial infections via the attraction and activation of
 CC microbial leukocytes. IL17RLP may also be used to increase T-cell

CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
 CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
 CC regulate haematopoiesis by regulating the activation and differentiation
 CC of various haematopoietic progenitor cells, e.g. to release mature
 CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
 CC mobilisation or to treat sepsis. The products can also be used for the
 CC diagnosis or treatment of immune system related disorders e.g. tumours,
 CC cancers, interstitial lung disease, and any dysregulation of immune cell
 CC function including autoimmunity, arthritis, leukaemias, lymphomas,
 CC immunosuppression, immunity, humoral immunity, inflammatory bowel
 CC disease, or myelo suppression
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GGTACCCCGAGCCCGGCTT 23
 Db 6 GGTACCCCGAGCTCCCGCTT 26
 RESULT 15
 AAZ35756
 ID AAZ35756 standard; DNA; 28 BP.
 AC AAZ35756;
 DT 01-FEB-2000 (first entry)
 XX Human IL17RLP PCR primer SEQ ID NO:13.
 KW Human; interleukin 17 receptor like protein; IL17RLP; IL-17; diagnosis;
 KW detection; immune system related disorder; haemostasis;
 KW cellular activation; angiogenesis; tumour metastasis; ovulation;
 KW cellular migration; neurogenesis; infection; T-cell proliferation;
 KW autoimmune disease; lymphocytic leukaemia; haematopoiesis; regulation;
 KW sepsis; tumour; cancer; interstitial lung disease; arthritis; lymphoma;
 KW immunosuppression; immunity; inflammatory bowel disease;
 KW myelo suppression; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9914240-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-US019121.
 XX
 PR 17-SEP-1997; 97US-0059133P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Shi Y, Ruben SM;
 XX WPI; 2000-061918/05.
 DR
 XX New human interleukin-17 receptor like protein, e.g. to treat disorders
 XX relating to cellular activation.
 PT
 XX Example 3; Page 102; 133pp; English.
 PS
 XX The present invention describes human interleukin 17 receptor like
 CC protein (IL17RLP), isolated from a cDNA library of human adult pulmonary
 CC tissue. The present sequence represents a PCR primer for human IL17RLP.
 CC IL17RLP and its agonists can be used to treat disorders relating to
 CC cellular activation, haemostasis, angiogenesis, tumour metastasis,
 CC cellular migration and ovulation, and neurogenesis. They can also be used
 CC to enhance host defences against resistant chronic and acute infections,
 CC e.g. mycobacterial infections via the attraction and activation of
 CC microbial leukocytes. IL17RLP may also be used to increase T-cell

CC proliferation by the stimulation of IL-2 biosynthesis for the treatment
 CC of T-cell mediated autoimmune diseases and lymphocytic leukaemias, to
 CC regulate haematopoiesis by regulating the activation and differentiation
 CC of various haematopoietic progenitor cells, e.g. to release mature
 CC leukocytes from the bone marrow following chemotherapy, i.e. in stem cell
 CC mobilisation or to treat sepsis. The products can also be used for the
 CC diagnosis or treatment of immune system related disorders e.g. tumours,
 CC cancers, interstitial lung disease, and any dysregulation of immune cell
 CC function including autoimmunity, arthritis, leukaemias, lymphomas,
 CC immunosuppression, immunity, humoral immunity, inflammatory bowel
 CC disease, or myelo suppression
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GGTACCCCGAGCCCGGCTT 23
 Db 6 GGTACCCCGAGCTCCCGCTT 26
 RESULT 16
 AAZ52043
 ID AAZ52043 standard; DNA; 28 BP.
 AC AAZ52043;
 DT 09-AUG-2000 (first entry)
 XX 3'primer for amplification of IL-17RLP cDNA.
 DE
 XX Interleukin-17-like receptor protein; IL-17RLP; cytokine receptor;
 KW resistant chronic infection; acute infection; mycobacterial infection;
 KW T-cell proliferation; IL-2 biosynthesis; lymphocytic leukaemia;
 KW T-cell mediated autoimmune disease; hematopoiesis; sepsis; hybridoma;
 KW IL-6 expression; myeloma; plasmacytoma; Lennert's Lymphoma;
 KW immunoprotective; cytostatic; hematopoietic; proliferative;
 KW antibacterial; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS WO200015759-A1.
 PN
 XX 23-MAR-2000.
 PD
 XX 15-SEP-1999; 99WO-US021048.
 XX
 PF 16-SEP-1998; 98US-00154219.
 PR
 PR 16-SEP-1998; 98WO-US019121.
 PR 16-MAR-1999; 99US-00268311.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Shi Y;
 XX WPI; 2000-271403/23.
 DR
 XX Novel polynucleotides encoding interleukin-17-like receptor protein,
 XX useful for diagnosis and treatment of immune system-related disorders,
 XX e.g. sepsis and cancers.
 PT
 XX Example 3; Page 102; 147pp; English.
 PS
 XX The patent relates to novel interleukin-17-like receptor protein (IL-
 CC 17RLP). IL-17RLP is a homologue of the IL-17 receptor and has a wide
 CC range of cytokine receptor-like activities. IL-17RLP or its agonists may
 CC be used to enhance host defenses against resistant chronic and acute
 CC infections, e.g. mycobacterial infections, via the attraction and
 CC activation of microbicidal leukocytes. It may also be used to increase T-
 CC cell proliferation by stimulating IL-2 biosynthesis, for the treatment of
 CC T-cell mediated autoimmune diseases and lymphocytic leukaemias. IL-17RLP

CC may also be used to regulate hematopoiesis and to treat sepsis.
 CC Extracellular IL-17RLP domains may be used as antagonists of IL-17RLP. IL
 CC -17RLP agonists and antagonists can also be used to modulate IL-6
 CC expression, useful in treatment of cancers such as myelomas,
 CC plasmacytomas and hybridomas and Lennert's lymphoma. The present sequence
 CC is the 3'PCR primer used for the amplification of IL-17RLP cDNA. This
 CC primer comprises Asp18 and 17 of nucleotides complementary to the
 CC 3'coding region immediately before the stop codon. This is used in the
 CC construction of vectors for expression in E. coli
 XX
 SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTT 23
 Db 6 GGTACCCAGCAGCTCCCGGCTT 26

RESULT 17
 AAA75769
 ID AAA75769 standard; DNA; 28 BP.
 XX
 AC AAA75769;
 DT 22-JAN-2001 (first entry)
 XX
 DE PCR primer for a human interleukin 17 receptor-like cDNA fragment.
 XX
 KW Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
 KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
 KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.
 XX

OS Homo sapiens.

PN WO200055204-A1.

PD 21-SEP-2000.

PF 06-MAR-2000; 2000WO-US005759.

PR 16-MAR-1999; 99US-00268311.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Shi Y, Ruben SM;

DR WPI; 2000-647065/62.

XX Novel gene encoding a polypeptide of the interleukin-17 receptor family,
 PT and an antagonist and agonist of the polypeptide, useful for treating,
 PT diagnosing, detecting and/or preventing immune system related disorders.
 XX
 PS Example 3a; Page 182; 247pp; English.

XX PCR primers AAA75768-69 were used to amplify a fragment of cDNA encoding
 CC a human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP
 CC polypeptide is useful for screening for agonists and antagonists. These
 CC antagonists and agonists are useful for treating, diagnosing, detecting
 CC and or preventing disorders related to cellular activation, haemostasis,
 CC angiogenesis, tumour metastasis, cellular migration, ovulation or
 CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
 CC e.g. systemic lupus erythromatosus
 XX

SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;
 Best Local Similarity 85.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTT 23
 Db 6 GGTACCCAGCAGCTCCCGGCTT 26

RESULT 18

AAA75771

ID AAA75771 standard; DNA; 28 BP.

XX AAA75771;

DT 22-JAN-2001 (first entry)

DE PCR primer for a human interleukin 17 receptor-like DNA fragment.

XX Human; interleukin 17-receptor-like protein; IL17RLP; osteoporosis;
 KW cellular activation; haemostasis; angiogenesis; tumour metastasis;
 KW cellular migration; ovulation; neurogenesis; arthritis;
 KW autoimmune disorder; systemic lupus erythromatosus; PCR primer; ss.

OS Homo sapiens.

PN WO200055204-A1.

PD 21-SEP-2000.

PF 06-MAR-2000; 2000WO-US005759.

PR 16-MAR-1999; 99US-00268311.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Shi Y, Ruben SM;

DR WPI; 2000-647065/62.

XX Novel gene encoding a polypeptide of the interleukin-17 receptor family,
 PT and an antagonist and agonist of the polypeptide, useful for treating,
 PT diagnosing, detecting and/or preventing immune system related disorders.
 XX

PS Example 3b; Page 185; 247pp; English.

XX PCR primers AAA75770-71 were used to amplify a fragment of DNA encoding a
 CC human interleukin 17-receptor-like protein (IL17RLP). The IL17RLP
 CC polypeptide is useful for screening for agonists and antagonists. These
 CC antagonists and agonists are useful for treating, diagnosing, detecting
 CC and or preventing disorders related to cellular activation, haemostasis,
 CC angiogenesis, tumour metastasis, cellular migration, ovulation or
 CC neurogenesis, such as osteoporosis, arthritis and autoimmune disorders
 CC e.g. systemic lupus erythromatosus
 XX

SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 3; Length 28;

Best Local Similarity 85.7%; Pred. No. 6.9e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCCGGCTT 23
 Db 6 GGTACCCAGCAGCTCCCGGCTT 26

RESULT 19

ADT93853

ID ADT93853 standard; DNA; 28 BP.

XX ADT93853;

DT 16-DEC-2004 (first entry)

XX Human interleukin 17 receptor-like protein extracellular domain primer 3.
 DE ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;
 KW

KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
KW hemostasis; angiogenesis; tumor metastasis; cellular migration;
KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
KW graft versus host disease; chromosomal identification; primer; PCR.
XX
OS Homo sapiens.
XX
XX AU2004200961-A1.
PN
XX 01-APR-2004.
PD
XX 09-MAR-2004; 2004AU-00200961.
PF
XX 09-MAR-2004; 2004AU-00200961.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Shi Y, Ruben SM;
PI
XX WPI; 2004-662639/65.
DR
XX Novel isolated interleukin 17-receptor-like protein useful for treating
PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
PT disease.
XX
PS Example 3; SEQ ID NO 13; 145pp; English.
XX
XX The invention relates to an isolated interleukin 17-receptor-like protein
CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
CC identical to a sequence e.g., sequence having amino acids from positions
CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
CC the specification, sequence having amino acids from positions 18-407 of
CC (S1) that comprises N-terminal methionine or sequence having amino acids
CC from positions 1-407 of (S1). (I) is useful for treating disorders
CC related to cellular activation, hemostasis, angiogenesis, tumor
CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
CC for treating immune-related disorders e.g., Crohn's disease, tumor,
CC inflammatory bowel disease, autoimmune diseases, lymphocytic
CC or graft versus host disease. (II) is useful for chromosomal
CC identification. (I) exhibits enhanced activity, solubility and stability,
CC and is produced in large quantities. This sequence corresponds to a PCR
CC primer to amplify the extracellular domain from the human IL17RLP cDNA
CC sequence (ADT93841) for expression in Chinese Hamster Ovary (CHO) cells.
XX
SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 13; Length 28;
Best Local Similarity 85.7%; Pred. No. 6.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGATCCCGCAGCGCCGCGCT 23
Db 6 GGATCCCGCAGCTCCCGGCTT 26

RESULT 20
ADT93851
ID ADT93851 standard; DNA; 28 BP.
XX
XX ADT93851;
AC
XX 16-DEC-2004 (first entry)
DT
XX Human interleukin 17 receptor-like protein extracellular domain primer.
DE
XX ss; antiinflammatory; cytostatic; gastrointestinal; immunosuppressive;
KW interleukin 17-receptor-like protein; IL17RLP; cellular activation;
KW hemostasis; angiogenesis; tumor metastasis; cellular migration;
KW ovulation; neurogenesis; immune-related disorder; Crohn's disease; tumor;
KW inflammatory bowel disease; autoimmune disease; lymphocytic leukemia;
KW graft versus host disease; chromosomal identification; primer; PCR.

XX
OS Homo sapiens.
XX
XX AU2004200961-A1.
PN
XX 01-APR-2004.
PD
XX 09-MAR-2004; 2004AU-00200961.
PF
XX 09-MAR-2004; 2004AU-00200961.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Shi Y, Ruben SM;
PI
XX WPI; 2004-662639/65.
DR
XX Novel isolated interleukin 17-receptor-like protein useful for treating
PT immune-related disorders e.g., Crohn's disease, tumor, inflammatory bowel
PT disease, autoimmune diseases, lymphocytic leukemias, or graft versus host
PT disease.
XX
PS Example 3; SEQ ID NO 11; 145pp; English.
XX
XX The invention relates to an isolated interleukin 17-receptor-like protein
CC (IL17RLP) (I) comprising an amino acid sequence that is 95% or more
CC identical to a sequence e.g., sequence having amino acids from positions
CC 19-407 of a fully defined sequence (S1) of 426 amino acids as given in
CC the specification, sequence having amino acids from positions 18-407 of
CC (S1) that comprises N-terminal methionine or sequence having amino acids
CC from positions 1-407 of (S1). (I) is useful for treating disorders
CC related to cellular activation, hemostasis, angiogenesis, tumor
CC metastasis, cellular migration, ovulation or neurogenesis. (I) is useful
CC for treating immune-related disorders e.g., Crohn's disease, tumor,
CC inflammatory bowel disease, autoimmune diseases, lymphocytic
CC or graft versus host disease. (II) is useful for chromosomal
CC identification. (I) exhibits enhanced activity, solubility and stability,
CC and is produced in large quantities. This sequence corresponds to a PCR
CC primer to amplify the extracellular domain from the human IL17RLP cDNA
CC sequence (ADT93841).
XX
SQ Sequence 28 BP; 2 A; 13 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 13; Length 28;
Best Local Similarity 85.7%; Pred. No. 6.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGATCCCGCAGCGCCGCGCT 23
Db 6 GGATCCCGCAGCTCCCGGCTT 26

RESULT 21
ADT72771
ID ADF72771 standard; DNA; 38 BP.
XX
XX ADF72771;
AC
XX 26-FEB-2004 (first entry)
DT
XX Fusarium solani cutinase gene primer, Exon1B.
DE
XX immobilizing; functional organic molecule; predetermined density;
KW mixed monolayer surface; MMS; reducing end; peracetylated sugar;
KW chemoselective; ss; primer; cutinase.
XX
XX Synthetic.
OS
XX Fusarium solani.
XX WO2003018854-A2.
PN
XX 06-MAR-2003.
PD
XX

```
PF 27-AUG-2002; 2002WO-US027195.
XX
XX 27-AUG-2001; 2001US-0315261P.
XX 28-AUG-2001; 2001US-0315544P.
PR 15-FEB-2002; 2002US-0358765P.
PR 15-FEB-2002; 2002US-0358412P.
PR 19-FEB-2002; 2002US-0357136P.
PR 20-FEB-2002; 2002US-0375023P.
PR 26-APR-2002; 2002US-0380259P.
XX
XX (SURF-) SURFACE LOGIX INC.
XX
XX Hodneland C, Campbell S, Duffy D, Agosto M, Wang E;
XX
XX WPI; 2003-393250/37.
XX
XX Immobilizing functional organic molecule in a predetermined density on a
PT mixed monolayer surface, by contacting the surface with the organic
PT molecule to form a covalent bond and to immobilize the organic molecule.
XX
XX Example 6; SEQ ID NO 2; 234pp; English.
XX
XX The invention relates to a novel method for immobilizing a functional
CC organic molecule in a predetermined density on a mixed monolayer surface
CC (MMS). The novel method comprises a first monolayer moiety (MM1) having a
CC covalent bond forming reactive group and a second monolayer moiety (MM2)
CC having an inert group. The method involves contacting MMS with the
CC functional organic molecule to form a covalent bond between the
CC functional organic molecule and MM1 to immobilize the functional organic
CC molecule. The novel method of the invention is useful for immobilizing a
CC functional organic molecule in a predetermined density on a mixed
CC monolayer surface, where the functional organic molecule is selected from
CC oligopeptides, peptides, polypeptides, proteins, nucleosides, nucleotides,
CC oligonucleosides, carbohydrates, ligands, receptors, antibodies, antigens,
CC enzymes, enzyme substrates, ligands, receptors, antibodies, antigens,
CC lipids, and small molecules, but preferably a carbohydrate. The
CC carbohydrate comprises a reducing end, the reducing end comprises a
CC peracetylated sugar having an n-pentenyl group. This polynucleotide
CC sequence represents a primer used in the exemplification of the
CC invention.
XX
XX Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
SQ
Query Match 54.0%; Score 16.2; DB 10; Length 38;
Best Local Similarity 72.4%; Pred. No. 7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 CGGTACCCAGCAGCCGCGCTTGAAGAA 30
| | | | | | | | | | | | | | | | | |
Db 2 CGGTACCCAGCAGTTGCCCGTCTCTGTGAA 30
| | | | | | | | | | | | | | | | | |
RESULT 22
ADH34521
ID ADH34521 standard; DNA; 38 BP.
XX
XX ADH34521;
XX
XX 11-MAR-2004 (first entry)
XX
XX PCR primer #2 for Fusarium solani cutinase gene.
XX
XX Alkanethiol; reactant ligand; substrate; protein chip;
KW polypeptide immobilisation; enzyme activity; antibody detection;
KW cutinase; PCR; primer; ss.
XX
XX Fusarium solani.
XX
XX US2003119054-A1.
XX
XX 26-JUN-2003.
XX
XX 07-AUG-2001; 2001US-00923760.
```

```
XX 07-AUG-2001; 2001US-00923760.
PR
XX (MRKS/) MRKSICH M.
PA (HODN/) HODNELAND C.
XX
XX Mrksich M, Hodneland C;
XX
XX WPI; 2004-080248/08.
XX
XX New alkanethiols substituted with a reactant ligand useful for
PT immobilizing polypeptides on gold surfaces, e.g. for determining enzyme
PT activity or detecting antibodies.
XX
XX Example 7; SEQ ID NO 2; 57pp; English.
XX
XX The present invention relates to alkanethiols substituted with a reactant
CC ligand. Also disclosed is a substrate comprising a surface and a
CC plurality of moieties on the surface. The moieties are of formula Surf-L-
CC Q-T where T comprises a reactant ligand, and Surf designates where the
CC moiety attaches to the surface. The substrate can be incorporated into a
CC protein chip comprising a substrate bearing the reaction product of a
CC reactant ligand and a fusion polypeptide comprising a capture polypeptide
CC corresponding to the reactant ligand. The alkanethiols of the invention
CC are useful for immobilising polypeptides on gold surfaces, e.g. for
CC determining enzyme (especially kinase or protease) activity or detecting
CC antibodies. The present invention represents a PCR primer used in the
CC examples of the present invention.
XX
XX Sequence 38 BP; 5 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
SQ
Query Match 54.0%; Score 16.2; DB 12; Length 38;
Best Local Similarity 72.4%; Pred. No. 7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 CGGTACCCAGCAGCCGCGCTTGAAGAA 30
| | | | | | | | | | | | | | | | | |
Db 2 CGGTACCCAGCAGTTGCCCGTCTCTGTGAA 30
| | | | | | | | | | | | | | | | | |
RESULT 23
ABK49653
ID ABK49653 standard; DNA; 29 BP.
XX
XX ABK49653;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human intron 1 3' acceptor site.
XX
XX RhCG; mouse; human; non-erythroid Rh type C glycoprotein; ss; intron.
XX
XX Homo sapiens.
XX
XX WO200220719-A2.
XX
XX 14-MAR-2002.
XX
XX 05-SEP-2001; 2001WO-US027503.
XX
XX 07-SEP-2000; 2000US-0230660P.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX Huang C, Liu Z;
XX
XX WPI; 2002-351774/38.
XX
XX Nucleic acid sequences encoding novel mammalian nonerythroid Rh type C
PT and glycoproteins which have a characteristic twelve transmembrane domain
PT structure.
XX
XX Example; Fig 6; 53pp; English.
PS
```

XX	CC	This invention relates to the nucleic acid and protein sequences of novel
CC	CC	human and mouse non-erythroid Rh type C glycoprotein (RhCG). The RhCG
CC	CC	protein and the mouse homologue (rhcg) have a characteristic 12
CC	CC	transmembrane domain structure and are expressed in kidneys and testis.
CC	CC	The invention also comprises a method for antibody that specifically
CC	CC	binds an epitope of the glycoprotein and a method for detecting the
CC	CC	protein using this antibody. The antibodies of the invention may be used
CC	CC	in Western blots, enzyme linked immunosorbent assays (ELISA) or
CC	CC	immunohistochemical assays to identify the non- erythroid tissues,
CC	CC	particularly kidney and testis, that express the RhCG or Rhcg
CC	CC	glycoproteins. The methods are used for detecting an Rhcg or and RhCG
CC	CC	glycoprotein in a sample. The present sequence represents the intronic
CC	CC	sequence at an intron/exon splice site of the rhcg gene of the invention
XX	XX	
SQ	SQ	Sequence 29 BP; 5 A; 11 C; 10 G; 3 T; 0 U; 0 Other;
		Query Match 53.3%; Score 16; DB 6; Length 29;
		Best Local Similarity 79.2%; Pred. No. 8.3e+03;
		Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	3	GGTACCCAGCAGCAGCCGCGCCTTGA 26
Db	6	GGCACCCCTGCAGCATGCGCCTGGA 29
RESULT 24		
AAI73703/c		
ID	AAI73703	standard; DNA; 50 BP.
XX		
AC	AAI73703;	
XX		
DT	09-NOV-2001	(first entry)
XX		
DE	Human silent SNP containing nucleic acid SEQ:644.	
XX		
KW	Human; single nucleotide polymorphism; SNP; genome; gene therapy;	
KW	protein therapy; vaccine; probe; diagnostic assay; detection;	
KW	quantitation; restorative therapy; polymorphic; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200140521-A2.	
XX		
PD	07-JUN-2001.	
XX		
PF	30-NOV-2000; 2000WO-US032758.	
XX		
PR	30-NOV-1999; 99US-0168138P.	
PR	29-NOV-2000; 2000US-00726173.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Shimkets RA, Leach M;	
XX		
DR	WPI; 2001-356160/37.	
XX		
PT	Polymorphic nucleic acid sequences, useful in genetic testing and	
PT	therapy.	
XX		
PS	Claim 1; Page 251; 2653pp; English.	
XX		
CC	AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide	
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).	
CC	AAW53114 to AAM53329 represent peptides related to human polymorphic	
CC	polynucleotide sequences. The sequences can be used in gene and protein	
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by	
CC	them may be used in the prevention, diagnosis and treatment of diseases	
CC	associated with inappropriate expression of polymorphic polypeptides. For	
CC	example, (I) may be used to treat disorders by rectifying mutations or	
CC	deletions in a patient's genome that affect the activity of polypeptides	
CC	by expressing inactive proteins or to supplement the patients own	
CC	production of polypeptide. Additionally, (I) and its complementary	

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTATCCCGAGCGCGGCC 22
 ||||| ||||| |||||
 Db 19 GTATCCCTGCAGCGCGGCC 1

RESULT 26

ACD82353/c
 ID ACD82353 standard; DNA; 19 BP.

XX
 AC ACD82353;

DT 19-SEP-2003 (first entry)

XX Nucleic acid cloning associated adaptor molecule #54.

KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
 KW internal deletion mutagenesis analysis; cloning vehicle; ss.

XX Synthetic.

XX US2003044791-A1.

XX PD 06-MAR-2003.

XX PF 13-JUN-2001; 2001US-00880313.

XX PR 13-JUN-2001; 2001US-00880313.

XX PA (FLEM/) FLEMINGTON E K.

XX PI Flemington EK;

XX DR WPI; 2003-521745/49.

XX New adaptor molecules, useful for cloning nucleic acid molecules that
 PT does not require the design and synthesis of oligonucleotides or PCR
 PT primers.

XX PS Claim 12; Fig 1; 100pp; English.

XX The invention describes adaptor molecules, where each end of the adaptor
 CC is compatible with a nucleic acid digested with a restriction enzyme or a
 CC nucleic acid comprising an end that is compatible with a nucleic acid
 CC digested with a restriction enzyme. The adaptor molecules, compositions,
 CC kits and arrays are useful for cloning nucleic acid molecules that does
 CC not require the design and synthesis of oligonucleotides or PCR primers.
 CC The adaptors, kits and arrays are also useful for ligating two ends of a
 CC single nucleic acid molecule, or ligating two or more nucleic acid
 CC molecules. The kits can also be used for performing internal deletion
 CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
 CC vehicle, making the cloning procedure more rapid and efficient, and less
 CC error-prone. This sequence represents a nucleic acid cloning associated
 CC adaptor molecule

SQ Sequence 19 BP; 2 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 52.7%; Score 15.8; DB 9; Length 19;

Best Local Similarity 89.5%; Pred. No. 9.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTATCCCGAGCGCGGCC 22

Db 19 GTATCCCTGCAGCGCGGCC 1

RESULT 27

ACF79913/c

ID ACF79913 standard; DNA; 39 BP.

XX AC ACF79913;

XX

DT 15-JAN-2004 (first entry)

XX Human Her-2 protein cytoplasmic kinase domain PCR primer.

KW Human; Her-2; chitin binding domain; affinity tag; protein purification;
 KW PCR; primer; ss.

XX Homo sapiens.

XX WO2003074660-A2.

XX PD 12-SEP-2003.

XX PF 26-FEB-2003; 2003WO-US005851.

XX PR 28-FEB-2002; 2002US-0360354P.

XX PA (NEWE) NEW ENGLAND BIOLABS INC.

XX PI Xu M, Ferrandon SM, Taron CH, Colussi PA;

XX DR WPI; 2003-712883/67.

XX A (mutant) chitin binding domain capable of reversibly binding a chitin
 PT substrate under a selected non-denaturing condition, useful for producing
 PT and purifying a target protein molecule.

XX Example 1; Page 29; 74pp; English.

XX The present sequence is that of a primer used, with the primer given in
 CC ACF79912, for the PCR amplification of cDNA encoding the human Her-2
 CC protein cytoplasmic kinase domain. The PCR product was used in the
 CC construction of a fusion protein comprising the Her-2 kinase domain and a
 CC modified (W687F mutant) chitin binding domain (CBD) of Bacillus circulans
 CC WL-12 chitinase A1. The modified CBD acted as an affinity tag for
 CC purification of the Her-2 kinase domain, allowing protein elution under
 CC non-denaturing conditions

SQ Sequence 39 BP; 4 A; 16 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 52.7%; Score 15.8; DB 10; Length 39;

Best Local Similarity 89.5%; Pred. No. 1e+04;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCGGCC 21

Db 28 GGTACCCCGAGCGCGGCC 10

RESULT 28

ABN86094

ID ABN86094 standard; DNA; 41 BP.

XX AC ABN86094;

XX DT 02-OCT-2002 (first entry)

XX Lymphocyte activator protein 33 related probe 1.

KW Lymphocyte activator protein 33; body fluid immunity disorder; tumour;
 KW probe; ss.

XX Unidentified.

XX CN1340527-A.

XX PD 20-MAR-2002.

XX PF 31-AUG-2000; 2000CN-00119839.

XX PR 31-AUG-2000; 2000CN-00119839.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

```
XX
PI Mao Y, Xie Y;
DR WPI; 2002-436421/47.
XX
XX Lymphocyte activator protein 33 and encoding polynucleotide, useful for
XX treating body fluid disorder and tumor.
XX
XX Example 6; Page 19 (disclosure); 33pp; Chinese.
XX
XX The invention relates to a lymphocyte activator protein 33, the encoding
XX polynucleotide, and a method for preparing the polypeptide by DNA
XX recombination technique. The polypeptide is used in treating diseases
XX such as body fluid immunity disorder and tumours. The current sequence
XX represents a lymphocyte activator protein 33 related probe sequence
XX
SQ Sequence 41 BP; 11 A; 13 C; 13 G; 4 T; 0 U; 0 Other;
Query Match 52.7%; Score 15.8; DB 6; Length 41;
Best Local Similarity 74.1%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4 GTACCCACGAGCCCGCCTTGAGAA 30
Db 2 GGACCCACGAGCCCGCCTTGAGAA 28
RESULT 29
AAL33786/c
ID AAL33786 standard; DNA; 50 BP.
XX
XX AAL33786;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #6994.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 95US-0173419P.
XX
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 3387; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
SQ Sequence 50 BP; 7 A; 20 C; 18 G; 5 T; 0 U; 0 Other;
Query Match 52.7%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 CCCACGAGCCCGCCCTTG 25
Db 21 CCCACGAGCCCGCCCTTG 3
RESULT 30
AAX16927/c
ID AAX16927 standard; DNA; 43 BP.
XX
XX AAX16927;
XX
XX 11-MAY-1999 (first entry)
XX
XX Primer #17 for constructing plasmid M13IX30.
XX
XX Heteromeric; receptor; immunoglobulin; superfamily; plasmid; primer; PCR;
XX bacteriophage; fusion protein; amplification; heavy chain; light chain;
XX immune system; diagnosis; ss.
XX
XX Synthetic.
XX
XX US5871974-A.
XX
XX 16-FEB-1999.
XX
XX 02-DEC-1994; 94US-00349131.
XX
XX 28-SEP-1990; 90US-00590219.
XX
XX 27-SEP-1991; 91US-00767136.
XX
XX 13-SEP-1993; 93US-00120648.
XX
XX (IXSY-) IXSYS INC.
XX
XX Huse WD;
XX
XX WPI; 1999-166647/14.
XX
XX New surface expression libraries expressing heteromeric receptors -
XX comprising cells containing vectors containing combinations of DNA
XX sequences encoding first and second polypeptides.
XX
XX Example 1; Col 12; 58pp; English.
XX
XX The invention relates to the expression of heteromeric receptor proteins,
XX e.g. from an immunoglobulin (Ig) superfamily, in cells containing the
XX heteromeric receptor genes on a single plasmid. Especially mentioned, the
XX cell may be a bacteriophage, where the receptor protein are expressed as
XX fusion proteins with the surface protein gVIII. Primers AAX16911-X16936
XX were used in the construction of plasmid M13IX30 (AAX16937) for
XX expression of receptor heavy chain proteins. Light chain genes are cloned
XX into the plasmid M13IX11 (AAX16953). The methods can be used to generate
XX diverse populations of heteromeric receptors which mimic the natural
XX immune system and can be used for diagnostic and therapeutic purposes
XX
```

```
SQ Sequence 43 BP; 12 A; 8 C; 15 G; 8 T; 0 U; 0 Other;
Query Match 52.0%; Score 15.6; DB 2; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCGTTACCCAGCAGCCGCGCTTGAAGAA 30
   ||| |||| ||| ||| |||| |||
DB 42 GCGTTACCCAGCTTAATCGCTTGCAGAA 13

RESULT 31
AAZ91566/c
ID AAZ91566 standard; DNA; 43 BP.
XX
AC AAZ91566;
XX
DT 25-MAY-2000 (first entry)
XX
DE Lac Z mutagenesis oligonucleotide SEQ ID NO:43.
XX
KW Bacteriophage M13 vector; prokaryotic cell; heteromeric receptor;
KW antibody; immune system; filamentous bacteriophage; cloning; screening;
KW coexpression; PCR primer; mutagenesis; ss.
XX
OS Enterobacteria phage M13.
OS Synthetic.
XX
PN US6027933-A.
XX
PD 22-FEB-2000.
XX
PF 05-JUN-1995; 95US-00470297.
XX
PR 28-SEP-1990; 90US-00590219.
PR 27-SEP-1991; 91US-00767136.
PR 13-SEP-1993; 93US-00120648.
PR 01-DEC-1994; 94US-00349131.
XX
PA (IXSY-) IXSYS INC.
XX
PI Huse WD;
XX
DR WPI; 2000-194835/17.
XX
PT Kit for the preparation of vectors for the coexpression of two or more
PT DNA sequences encoding proteins that form heteromeric receptors.
XX
PS Example 1; Col 13; 58pp; English.
XX
CC The present invention describes a kit (I) for the preparation of vectors
CC for the coexpression of two or more DNA sequences encoding polypeptides
CC comprising two vectors which operatively combine through two pairs of
CC restriction sites to form a single vector. The kit is useful for the
CC preparation of vectors for the coexpression of two or more DNA sequences
CC encoding polypeptides which form heteromeric receptors. The kit simply
CC and efficiently generates a large repertoire of diverse combinations of
CC heteromeric receptors. Only proper combinations of vector portions are
CC randomly brought together for the coexpression of different DNA sequences
CC without loss of population size or diversity. AAZ91524 to AAZ91528
CC represent bacteriophage M13 vector nucleotide sequences constructed in
CC the exemplification of the present invention. AAZ91529 to AAZ91599
CC represent oligonucleotides used in the construction of vectors in the
CC exemplification of the present invention
XX
SQ Sequence 43 BP; 12 A; 8 C; 15 G; 8 T; 0 U; 0 Other;
Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Pred. No. 1.2e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCGTTACCCAGCAGCCGCGCTTGAAGAA 30
   ||| |||| ||| ||| |||| |||
DB 42 GCGTTACCCAGCTTAATCGCTTGCAGAA 13

RESULT 32
ACD82542/c
ID ACD82542 standard; DNA; 20 BP.
XX
AC ACD82542;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #243.
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
PN US2003044791-A1.
XX
PD 06-MAR-2003.
XX
PF 13-JUN-2001; 2001US-00880313.
XX
PR 13-JUN-2001; 2001US-00880313.
XX
PA (FLEM/) FLEMINGTON E K.
XX
PI Flemington EK;
XX
PW WPI; 2003-521745/49.
XX
PT New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.
XX
PS Claim 12; Fig 5; 100pp; English.
XX
CC The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 51.3%; Score 15.4; DB 9; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GTACCCCGCAGCAGCCCGG 20
   ||||| ||||| |||||
DB 20 GTACCCCGCAGCAGCCCGG 4

RESULT 33
AAA93835
ID AAA93835 standard; DNA; 27 BP.
XX
AC AAA93835;
XX
DT 11-JAN-2001 (first entry)
XX
DE PCR primer for human MSH receptor DNA amplification.
XX
```

```

KW Viral vector; melanocyte-stimulating hormone receptor; MSH; cytostatic;
KW tumour; malignant melanoma; fibre protein; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200050618-A1.
XX
XX 31-AUG-2000.
XX
XX 24-FEB-2000; 2000WO-JP001069.
XX
XX 24-FEB-1999; 99JP-00093263.
XX
XX (NICA-) JAPANESE FOUND CANCER RES.
XX
XX Hamada H;
XX
XX WPI; 2000-549414/50.
XX
XX Virus vector useful in diagnosis and treatment of tumors particularly
XX malignant melanoma, constructed by fusing viral protein with ligand
XX binding specifically to melanocyte-stimulating hormone receptor.
XX
XX Example 4; Page 46; 145pp; Japanese.
XX
XX This invention relates to a viral vector constructed by the fusion of a
XX viral protein with a ligand which binding specifically to the melanocyte-
XX stimulating hormone (MSH) receptor. The vector contains one of four
XX linkers represented by sequences AAA93815-A93818 and AAB23583-B23586, and
XX DNA encoding a fibre protein selected from those represented by AAA93819-
XX A93826 and AAB23587-B23594. The vector has cytostatic activity, and can
XX be used for gene therapy and in the diagnosis and treatment of tumours,
XX particularly malignant melanomas. The present sequence represents a PCR
XX primer used in the construction of the vector
XX
XX Sequence 27 BP; 5 A; 10 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 3; Length 27;
Best Local Similarity 76.0%; Pred. No. 1.4e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTG 25
Db 3 GCGGTACCCAGCAGCATCGTGACCTG 27

RESULT 34
AAQ83899/c
ID AAQ83899 standard; DNA; 40 BP.
XX
XX AAQ83899;
XX
XX 25-MAR-2003 (revised)
XX 19-SEP-1995 (first entry)
XX
XX Hepatitis C virus reverse transcription PCR primer.
XX
XX Hepatitis C virus; HCV; non-A non-B; reverse transcription; diagnosis;
XX PCR primer; ss.
XX
XX Hepatitis C virus.
XX
XX WO9501442-A2.
XX
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007320.
XX
XX 29-JUN-1993; 93US-00086428.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Bukh J, Miller RH, Purcell RH;
XX
XX WPI; 1995-061006/08.
XX
XX Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
XX nucleotide(s), peptide(s) and proteins, used in diagnosis and in
XX vaccines.
XX
XX Claim 19; Page 119; 186pp; English.
XX
XX AAQ83896-Q83901 are primers for hepatitis C virus (HCV) reverse
XX transcription PCR. By contacting the amplification products of the PCR to
XX at least one of the genotype specific hybridisation probes described in
XX AAQ83902-Q83928, the genotype of the amplified HCV can be determined.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCAGCAGCCGCGCTTGAA 27
Db 27 GGCACATCAATAGCACGCGCTTGAA 3

RESULT 35
AAQ83897/c
ID AAQ83897 standard; DNA; 40 BP.
XX
XX AAQ83897;
XX
XX 25-MAR-2003 (revised)
XX 19-SEP-1995 (first entry)
XX
XX Hepatitis C virus reverse transcription PCR primer.
XX
XX Hepatitis C virus; HCV; non-A non-B; reverse transcription; diagnosis;
XX PCR primer; ss.
XX
XX Hepatitis C virus.
XX
XX WO9501442-A2.
XX
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007320.
XX
XX 29-JUN-1993; 93US-00086428.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Bukh J, Miller RH, Purcell RH;
XX
XX WPI; 1995-061006/08.
XX
XX Envelope 1 cDNAs of 51 hepatitis C virus isolates - and derived oligo-
XX nucleotide(s), peptide(s) and proteins, used in diagnosis and in
XX vaccines.
XX
XX Claim 19; Page 119; 186pp; English.
XX
XX AAQ83896-Q83901 are primers for hepatitis C virus (HCV) reverse
XX transcription PCR. By contacting the amplification products of the PCR to
XX at least one of the genotype specific hybridisation probes described in
XX AAQ83902-Q83928, the genotype of the amplified HCV can be determined.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

PA Bukh J, Miller RH, Purcell RH;
PI

```

```

QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      40  GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 36
AAT16692/c
ID  AAT16692 standard; cDNA; 40 BP.
XX
AC  AAT16692;
XX
DT  02-OCT-1996 (first entry)
XX
DE  Hepatitis C virus E1 gene RT-PCR primer.
XX
KW  HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW  hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.
XX
OS  Synthetic.
XX
PN  WO9605315-A2.
XX
PD  22-FEB-1996.
XX
PF  15-AUG-1995; 95WO-US010398.
XX
PR  15-AUG-1994; 94US-00290665.
XX
PA  (USSH ) US SEC DEPT HEALTH.
XX
PI  Bukh J, Miller RH, Purcell RH;
XX
WPI; 1996-139709/14.
XX
DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
determine HCV genotype and as vaccines against HCV infection.
XX
PS  Example 1; Page 224; 340pp; English.
XX
CC  AAT16689-T16694 are a set of RT-PCR primers used for the identification
of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
isolated sequences are useful for the prodn. of primers useful for
detecting the presence of HCV in a sample, the primers are also useful
for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
for immunising against HCV infection. The proteins may also be used to
detect antibodies against HCV in serum, saliva, lymphocytes or other
mononuclear cells. The antibodies may be used in the prevention of HCV
infection
XX
SQ  Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

PS  Example 1; Page 224; 340pp; English.
XX
CC  AAT16689-T16694 are a set of RT-PCR primers used for the identification
of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
isolated sequences are useful for the prodn. of primers useful for
detecting the presence of HCV in a sample, the primers are also useful
for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
for immunising against HCV infection. The proteins may also be used to
detect antibodies against HCV in serum, saliva, lymphocytes or other
mononuclear cells. The antibodies may be used in the prevention of HCV
infection
XX
SQ  Sequence 40 BP; 7 A; 9 C; 12 G; 12 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      27  GGCACATCAATAGCAGCGCCTTGAA 3

RESULT 37
AAT16690/c
ID  AAT16690 standard; cDNA; 40 BP.
XX
AC  AAT16690;
XX
DT  02-OCT-1996 (first entry)
XX
DE  Hepatitis C virus E1 gene RT-PCR primer.
XX
KW  HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
KW  hepatitis; reverse transcriptase polymerase chain reaction; RT-PCR; ss.

```

```

XX      Synthetic.
XX      WO9605315-A2.
XX      22-FEB-1996.
XX      15-AUG-1995; 95WO-US010398.
XX      15-AUG-1994; 94US-00290665.
XX      (USSH ) US SEC DEPT HEALTH.
XX      Bukh J, Miller RH, Purcell RH;
XX      WPI; 1996-139709/14.
XX      DNA and amino acid sequence of HCV envelope 1 and core proteins - used to
determine HCV genotype and as vaccines against HCV infection.
XX      Example 1; Page 224; 340pp; English.
XX      AAT16689-T16694 are a set of RT-PCR primers used for the identification
of the cDNA sequence of the E1 (envelope-1) gene of 51 HCV isolates. The
isolated sequences are useful for the prodn. of primers useful for
detecting the presence of HCV in a sample, the primers are also useful
for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines
for immunising against HCV infection. The proteins may also be used to
detect antibodies against HCV in serum, saliva, lymphocytes or other
mononuclear cells. The antibodies may be used in the prevention of HCV
infection
XX
SQ  Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match      51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 1.5e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GGTACCCAGCAGCCGGCCTTGAA 27
Db      40  GGCACATCAATAGCAGCGCCTTGAA 16

RESULT 38
ADF08491/c
ID  ADF08491 standard; DNA; 40 BP.
XX
AC  ADF08491;
XX
DT  12-FEB-2004 (first entry)
XX
DE  Hepatitis C virus (HCV) genomic DNA PCR primer #4.
XX
KW  Hepatitis C virus; HCV; inducible promoter; HCV infection; PCR; primer;
KW  ss.
XX
OS  Hepatitis C virus.
XX
PN  US2003148267-A1.
XX
PD  07-AUG-2003.
XX
PF  08-NOV-2002; 2002US-00292129.
XX
PR  09-NOV-2001; 2001US-0345405P.
XX
PA  (SCHM/) SCHMIDT E V.
PA  (CHUN/) CHUNG R T.
XX
PI  Schmidt EV, Chung RT;
XX
WPI; 2003-897533/82.

```

PT Identifying a compound that increases the mutation rate of hepatitis C
 PT virus (HCV) comprises detecting an increase in HCV quasi-species produced
 PT by the cell in the presence of the candidate compound.
 XX
 PS Example 10; SEQ ID NO 8; 35pp; English.
 XX
 CC The invention relates to a method for identifying a compound that
 CC increases the mutation rate of hepatitis C virus (HCV), comprising
 CC detecting an increase in HCV quasi-species produced by the cell in the
 CC presence of the candidate compound by e.g. sequencing HCV nucleic acid
 CC molecules isolated from the test cell. The method involves providing a
 CC test cell containing a nucleic acid molecule comprising a first
 CC nucleotide sequence consisting of an infectious hepatitis C viral genome
 CC or its DNA copy, a second nucleotide consisting of a ribozyme or its DNA
 CC copy and an inducible promoter operably linked to the first and second
 CC nucleotide sequences, where the ribozyme is configured to remove a 3'
 CC sequence unnecessary for replication of the hepatitis C viral genome from
 CC a transcript initiated by the promoter, inducing the inducible promoter,
 CC contacting the test cell with a candidate compound and detecting an
 CC increase in HCV quasi-species produced by the cell in the presence of the
 CC candidate compound compared to that in the absence of the compound, where
 CC an increase in the HCV quasi-species indicates that the compound increases
 CC the mutation rate of HCV. The method is useful in identifying compounds
 CC that may be used for treating HCV infection. This sequence represents a
 CC PCR primer used to amplify an HCV genomic DNA region, used in the method
 CC of the invention.
 XX

Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 10; Length 40;

Best Local Similarity 76.0%; Pred. No. 1.5e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCCGACGACCGCGCCTTGAA 27

Db 40 GGACATCAATAGACGCGCCTTGAA 16

RESULT 39

AAL31882

ID AAL31882 standard; DNA; 50 BP.

XX AAL31882;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #5090.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX

PS Claim 1; Page 2851; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
 CC protein coupled receptors and thioesterases. The present sequence is one
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms

Sequence 50 BP; 11 A; 17 C; 16 G; 6 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 4; Length 50;

Best Local Similarity 76.0%; Pred. No. 1.5e+04;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCGGTACCCCGACGACCGCGCCTTG 25

Db 22 GAGGCACAGCAGCAGCGCGCCTTG 46

RESULT 40

ADL96717

ID ADL96717 standard; DNA; 25 BP.

XX ADL96717;

XX 20-MAY-2004 (first entry)

XX M. paratuberculosis DNA PCR primer #57.

XX M. paratuberculosis; PCR; milk; faeces; blood;

KW M. paratuberculosis infection; John's disease; polypeptide purification;
 KW primer; ss; ds.

XX Mycobacterium avium subsp. paratuberculosis.

XX US2003175725-A1.

XX 18-SEP-2003.

XX 30-APR-2002; 2002US-00137113.

XX 06-MAR-2002; 2002US-0362396P.

XX (KAPU/) KAPUR V.

PA (BANN/) BANNANTINE J P.

XX Kapur V, Bannantine JP;

XX WPI; 2003-863842/80.

XX New isolated nucleic acids and encoded polypeptides useful for detecting
 PT Mycobacterium paratuberculosis, and as antibacterial vaccines.

XX Example 16; SEQ ID NO 108; 38pp; English.

XX The invention relates to Mycobacterium avium subsp. paratuberculosis (M.
 CC paratuberculosis) nucleic acid molecules. A nucleic acid of the invention

CC combined with a second nucleic acid will generate an amplification
CC product from M. paratuberculosis but not from human, Pseudomonas
CC aeruginosa, Streptomyces viridochromogenes, mouse, cat or Xanthomonas
CC campestris. The nucleic acids and other sequences specific for
CC Mycobacterium paratuberculosis are used to detect M. paratuberculosis in
CC e.g. milk, faeces or blood. The polypeptides encoded by these sequences,
CC and antibodies directed against them, are also used to detect M.
CC paratuberculosis by immunoassay. The nucleic acids and the polypeptides
CC are also used as vaccines to prevent infection (John's disease) by M.
CC paratuberculosis. The antibodies are also useful for polypeptide
CC purification. This sequence represents a PCR primer used to amplify an M.
CC paratuberculosis nucleic acid of the invention.

XX
SQ Sequence 25 BP; 6 A; 10 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 11; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ACCCCAGCAGCCCGCCTTG 25
|||
Db 6 ACTCCAGCAGCGCGCCTCG 25

Search completed: November 18, 2005, 11:52:28
Job time : 207.578 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1434.98 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCGCCGCTTGAGAA 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.8	52.7	50	1	AU104878
C 2	15.4	51.3	43	9	CU211120 W191D04 G
C 3	15	50.0	50	1	AU102519
C 4	14.8	49.3	50	1	AU105799
C 5	14.6	48.7	50	1	AU102973
C 6	14.6	48.7	50	1	AU102977
C 7	14.6	48.7	50	1	AU102978
C 8	14.6	48.7	50	1	AU104624
C 9	14.2	47.3	39	8	AZ810683
C 10	14	46.7	38	8	AZ487251
C 11	14	46.7	43	1	AA547556
C 12	14	46.7	43	8	BH892666
C 13	14	46.7	43	9	CC940831
C 14	14	46.7	45	8	AZ503949
C 15	13.8	46.0	36	8	BH909575
C 16	13.8	46.0	50	1	AU103064
C 17	13.8	46.0	50	1	AU103065
C 18	13.8	46.0	50	1	AU103067
C 19	13.8	46.0	50	1	AU104872
C 20	13.8	46.0	50	1	AU104893
C 21	13.8	46.0	50	1	AU104917
C 22	13.6	45.3	46	9	CU529006
C 23	13.6	45.3	50	1	AU105070
C 24	13.4	44.7	28	1	AI168501 ow90g01.s

C 25	13.4	44.7	36	4	BG717269
C 26	13.4	44.7	43	7	H99826
C 27	13.4	44.7	47	8	CC022113
C 28	13.4	44.7	47	9	AJ590023
C 29	13.2	44.0	29	8	AZ868876
C 30	13.2	44.0	37	7	W05202
C 31	13.2	44.0	40	9	CG774406
C 32	13.2	44.0	41	8	BZ586362
C 33	13.2	44.0	45	8	CC182796
C 34	13.2	44.0	46	1	AI019594
C 35	13.2	44.0	46	1	AL585781
C 36	13.2	44.0	46	1	AA238784
C 37	13.2	44.0	46	7	H38217
C 38	13.2	44.0	48	5	BX629147
C 39	13.2	44.0	48	8	BH902004
C 40	13.2	44.0	49	1	AA739463
C 41	13.2	44.0	49	8	BZ582545
C 42	13.2	44.0	50	1	AU105801
C 43	13.2	44.0	50	8	AZ920008
C 44	13	43.3	44	8	AZ783951
C 45	13	43.3	46	1	AA922868

ALIGNMENTS

RESULT 1
AU104878/c
LOCUS AU104878 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU104878 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP09640, mRNA sequence.
ACCESSION AU104878
VERSION AU104878.1 GI:13554399
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP09640"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 52.7%; Score 15.8; DB 1; Length 50;
Best Local Similarity 74.1%; Pred. No. 1e+05;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GCGTTACCCAGCGCCGCTTGAA 27
|||||
Db 40 GCGGTATCCAGCGGCTCGGCGCTGAA 14

RESULT 2
 CL211120
 LOCUS
 DEFINITION W191D04 GGTc Gene Trap Library GV04C04 Mus musculus cDNA clone
 W191D04, mRNA sequence.
 ACCESSION CL211120
 VERSION CL211120.2 GI:49489691
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 43)
 Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
 Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
 A large-scale, gene-driven mutagenesis approach for the functional
 analysis of the mouse genome
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 22810117
 PUBLISHED 12904583
 COMMENT On Jun 30, 2004 this sequence version replaced gi:40728021.
 Contact: GGTc
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de
 RoabetaGeo gene trap. Sequence tag generated by 5'RACE. Additional
 sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=W191D04' ES cell line harboring insertion mutation of
 target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
 1' Inhouse Sequence Identifier: 11106
 Class: Gene Trap.

FEATURES
 source
 Location/Qualifiers
 1..43
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="W191D04"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_lines="ES cells 129S2 (formerly 129/SvPas)"
 /clone_lib="GGTC Gene Trap Library GV04C04"
 /note="Vector: ROSAbetaGeo"

ORIGIN
 Query Match 51.3%; Score 15.4; DB 9; Length 43;
 Best Local Similarity 73.1%; Pred. No. 1.4e+05;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 GCGGTACCCAGCGCGCGCTTGA 26
 |||||
 Db 17 GCGGACCCAGCGCGCCACCTTGA 42

RESULT 3
 AU102519/c
 LOCUS
 DEFINITION AU102519 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 CAS01336, mRNA sequence.
 ACCESSION AU102519
 VERSION AU102519.1 GI:13552039
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 21270072
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yezuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS01336"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 50.0%; Score 15; DB 1; Length 50;
 Best Local Similarity 78.3%; Pred. No. 2.1e+05;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 6 ACCCCAGCAGCCCGCTTGAAG 28
 |||||
 Db 45 ACCCGAGCAGCCCGCCAGCAGCAG 23

RESULT 4

AU105799/c
 LOCUS
 DEFINITION AU105799 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 COLF5975, mRNA sequence.
 ACCESSION AU105799
 VERSION AU105799.1 GI:13555320
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yezuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="COLF5975"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match

Best Local Similarity 49.3%; Score 14.8; DB 1; Length 50;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      8  CCCAGAGCCCGCCTTG 25
MEDLINE PUBMED
COMMENT
Db      42  CCTAGACAGCCCGCCTTG 25

RESULT 5
AUI02973/c
LOCUS
DEFINITION
AUI02973 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP09976, mRNA sequence.
ACCESSION
AUI02973
VERSION
AUI02973.1 GI:13552494
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Location/Qualifiers
source
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP16119"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 48.7%; Score 14.6; DB 1; Length 50;
Best Local Similarity 69.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      2  CGGTACCCAGCAGCCCGCCTTGAAGAA 30
Db      30  CGAACACAGACAGCCCGTGGCGAGGAA 2

RESULT 7
AUI02978/c
LOCUS
DEFINITION
AUI02978 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP17663, mRNA sequence.
ACCESSION
AUI02978
VERSION
AUI02978.1 GI:13552499
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Location/Qualifiers
source
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP17663"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 48.7%; Score 14.6; DB 1; Length 50;
Best Local Similarity 69.0%; Pred. No. 3e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      2  CGGTACCCAGCAGCCCGCCTTGAAGAA 30
Db      43  CGAGACACAGACAGCCCGTGGAGGAGAA 15

RESULT 6
AUI02977/c
LOCUS
DEFINITION
AUI02977 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP16119, mRNA sequence.
ACCESSION
AUI02977
VERSION
AUI02977.1 GI:13552498
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
```



```

/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="3526 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match          46.7%; Score 14; DB 8; Length 43;
Best Local Similarity 77.3%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 8 CCCAGCAGCCGCGCTTGAGGA 29
    ||||| ||||| ||||| |||||
Db 20 CCCAGAGCGCGCAATTGAGGA 41

RESULT 13
LOCUS CC940831
DEFINITION CC940831 43 bp DNA linear GSS 18-AUG-2003
ACCESSION 01S0615-06B1-A12 UniformMu MutTAIL Library Zea mays genomic clone
VERSION 01S0615-06B1-A12, genomic survey sequence.
KEYWORDS CC940831.1 GI:33773697
SOURCE GSS.
ORGANISM Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 43)
AUTHORS Latschaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
        population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
        Plant Molecular and Cellular Biology Program
        University of Florida
        PO 110690 Gainesville, FL 32611-0690, USA
        Tel: 352-392-1928 x322
        Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
01S0615-06, Primer set: B
Class: transposon insertion site.

FEATURES
        Location/Qualifiers
            1..43
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="W22 (ACR, bz1-m9)"
                /cultivar="UniformMu"
                /db_xref="taxon:4577"
                /clone="01S0615-06B1-A12"
                /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                insertions in Mu inactive lines were extracted from the
                UniformMu maize population by the thermo asymmetric
                interlaced PCR (TAIL) protocol using primers specific for
                the Mu terminal inverted repeat and a set of 16 arbitrary
                primers. Amplicons were size enriched using Sepharose 400
                spin columns and cloned into the TOPO PCR4 vector."

/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="3526 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter
2000-2001. DNA was extracted from leaf punches, double
digested using BamHI and BglII, and ligated to form
circular plasmids. DH10B cells were transformed and then
screened on LB plates with ampicillin."

ORIGIN
Query Match          46.7%; Score 14; DB 8; Length 43;
Best Local Similarity 77.3%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 8 CCCAGCAGCCGCGCTTGAGGA 29
    ||||| ||||| ||||| |||||
Db 20 CCCAGAGCGCGCAATTGAGGA 41

RESULT 14
LOCUS AZ503949
DEFINITION AZ503949 45 bp DNA linear GSS 05-OCT-2000
ACCESSION 1M0343L24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION 1M0343L24R R, genomic survey sequence.
KEYWORDS AZ503949.1 GI:10685265
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 45)
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0343 row: L column: 24
          Seq primer: CACACAGGAAACACGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 45.
          Location/Qualifiers
            1..45
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0343L24"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

```

ORIGIN

Query Match 46.7%; Score 14; DB 8; Length 45;
 Best Local Similarity 77.3%; Pred. No. 5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCC 22
 |||||
 Db 9 GCGGTTCCCGCAGCGGCTGCC 30
 |||||

RESULT 15

BH909575/c
 LOCUS BH909575
 DEFINITION SALK_054521.15.30.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_054521.15.30.x, genomic
 survey sequence.

ACCESSION

VERSION BH909575.1 GI:22722508
 KEYWORDS GSS.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

Arabidopsis Genome

COMMENT

Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 Atg53460.

Class: TDNA tagged.

Location/Qualifiers

1..36
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_054521.15.30.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 46.0%; Score 13.8; DB 8; Length 36;
 Best Local Similarity 72.0%; Pred. No. 5.9e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GTACCCAGCAGCCGGCTTGAG 28
 |||||

Db 31 GTACCCATAAGCCAGCATTTGAG 7
 |||||

RESULT 16

AUI03064
 LOCUS AUI03064
 DEFINITION HRC00745, Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HRC00745, mRNA sequence.

ACCESSION

VERSION AUI03064.1 GI:13552585

KEYWORDS

EST.

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS

1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

JOURNAL

EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE

21270072

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

source

1..50
 /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC00745"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 46.0%; Score 13.8; DB 1; Length 50;
 Best Local Similarity 72.0%; Pred. No. 6.1e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCTTG 25
 |||||

Db 26 GAGGTCCCCCGCGCGCGGCGCTG 50
 |||||

RESULT 17

AUI03065

LOCUS AUI03065

DEFINITION AUI03065 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HRC01582, mRNA sequence.

ACCESSION

VERSION AUI03065.1 GI:13552586

KEYWORDS

EST.

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

JOURNAL

EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE

21270072

PUBMED

11375929

COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).


```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC08321"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCGCGGCTTG 25
    ||||| || || || || || || ||
Db 40 GCGGTATCCAGCGGCTCGGGCCTG 16

RESULT 21
AUI04917/c
LOCUS AUI04917 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION ADSE00422, mRNA sequence.
ACCESSION AUI04917
VERSION AUI04917.1 GI:13554438
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source location/Qualifiers
Qy 10 CAGCAGCCGCGCTTGAAGA 29
Db 25 CAGCAGGCTGGCAATGAAGA 44

ORIGIN
Query Match      45.3%; Score 13.6; DB 9; Length 46;
Best Local Similarity 80.0%; Pred. No. 7.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 CAGCAGCCGCGCTTGAAGA 29
    ||||| || || || || || || ||
Db 25 CAGCAGGCTGGCAATGAAGA 44

RESULT 23
AUI05070
LOCUS AUI05070 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION KAT06679, mRNA sequence.
ACCESSION AUI05070
VERSION AUI05070.1 GI:13554591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADSE00422"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCGCGGCTTG 25
    ||||| || || || || || || ||
Db 37 GCGGTATCCAGCGGCTCGGGCCTG 13

RESULT 22
CL529006
LOCUS CL529006 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HIV55A08 fwd HIV-vector integration sites in human IMR90 primary
lung fibroblasts
ACCESSION CL529006
VERSION CL529006.1 GI:47422217
KEYWORDS GSS.

```

[illegible]

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 43)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlffing, F., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyt not found
Insert Length: 732 Std Error: 0.00
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3872705"
/db_xref="taxon:9606"
/clone="IMAGE:263063"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCAGTTTTTTTTTTTTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 44.7%; Score 13.4; DB 7; Length 43;
Best Local Similarity 73.9%; Pred. No. 8.6e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CCCAGCAGCCCGCGCTTGAAGA 29
| ||||| ||| || |||||
Db 43 CTCAGCAGCCCGCAGCCTGCGA 21

RESULT 27
LOCUS CC022113/c
DEFINITION 3591.1.28.1_C03.2EL_Y_1_3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
ACCESSION CC022113
VERSION CC022113.1 GI:29436186
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 47)
AUTHORS Walbot, V.

TITLE
JOURNAL
COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591.1.28.1 row: 15
Class: transposon-tagged.
Location/Qualifiers
1..47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 44.7%; Score 13.4; DB 8; Length 47;
Best Local Similarity 73.9%; Pred. No. 8.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGCAGCCCGCGCTT 24
| ||||| ||| || |||||
Db 44 CCGTGCCCCCGCGCGCGAGCCTT 22

RESULT 28
LOCUS AJ590023
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
562D09, genomic survey sequence.
ACCESSION AJ590023
VERSION AJ590023.1 GI:37939647
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 47)
AUTHORS Balzerque, S.
Direct Submission
TITLE Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, France

COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES Location/Qualifiers
 source 1..47
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassillewskija"
 /db_xref="taxon:3702"
 /clone="562D09"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature 1..47
 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 44.7%; Score 13.4; DB 9; Length 47;
 Best Local Similarity 70.8%; Pred. No. 8.7e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 GTACCCAGCAGCGCGCTTGAA 27
 |||||
 Db 23 GTACTCCGCGCGGCATTA 46

RESULT 29
 AZ868876/c
 LOCUS 29 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0180F17R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0180F17 R, genomic survey sequence.

ACCESSION AZ868876
 VERSION AZ868876.1 GI:13072628
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0180 row: F column: 17

Seq primer: CACACAGAAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol_type="genomic DNA"

/strains="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0180F17"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 29;
 Best Local Similarity 83.3%; Pred. No. 1e+06;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 AGCAGCCCGCGCTTGAA 28
 |||||
 Db 25 AGCAGCGCGCGCTTGAA 8

RESULT 30
 W05202

LOCUS

DEFINITION 37 bp mRNA linear EST 23-APR-1996
 234201.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:295249 5' similar to SW:GSGS_BOVIN P30670 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-5 SUBUNIT. [1] ; mRNA sequence.

ACCESSION W05202.1 GI:1277934

VERSION W05202

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 37)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: mob.REGA+ET

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1240170"

/db_xref="taxon:9606"

/clone="IMAGE:295249"

/sex="male"

```

/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: p7T73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' - ACTCGAGAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p7T73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Donaldo."

```

ORIGIN

```

Query Match      44.0%; Score 13.2; DB 7; Length 37;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 5 TACCCAGAGCCGCGCCTTGAGAA 30
   ||||| ||||| |||||
Db 2 TCCTCCAGCGTCGCGCTATGAGAA 27

```

RESULT 31

```

CG774406
LOCUS      40 bp      DNA      linear      GSS 29-OCT-2003
DEFINITION 1123018G05.2EL_Y1 1123 - RescueMu Grid L Zea mays genomic, genomic
survey sequence.
ACCESSION  CG774406
VERSION     CG774406.1 GI:38030394
KEYWORDS   GSS.
SOURCE     Zea mays
           Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1 (bases 1 to 40)
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123018 row: 12
Class: transposon-tagged.
Location/Qualifiers
1..40
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid L was grown in Molokai in 2001. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

REFERENCE

```

AUTHORS
TITLE
JOURNAL
COMMENT

```

FEATURES

source

```

1..40
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid L was grown in Molokai in 2001. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

ORIGIN

```

Query Match      44.0%; Score 13.2; DB 9; Length 40;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 GCGGTACCCAGCAGCCGCGCTTGA 26
   ||||| ||||| |||||
Db 4 GTGGTCTCCAGCAGCAGGATCTGGA 29

```

RESULT 32

```

BZ586362
LOCUS      41 bp      DNA      linear      GSS 17-DEC-2002
DEFINITION 3590.1.16.1.D07.2EL_Y_1 3590 - RescueMu Grid M Zea mays genomic,
genomic survey sequence.
ACCESSION  BZ586362
VERSION     BZ586362.1 GI:27221423
KEYWORDS   GSS.
SOURCE     Zea mays
           Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1 (bases 1 to 41)
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590.1.16.1 column: 4
Class: transposon-tagged.
Location/Qualifiers
1..41
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3590 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHI and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
on LB plates with ampicillin."

```

ORIGIN

```

Query Match      44.0%; Score 13.2; DB 8; Length 41;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 GCGGTACCCAGCAGCCGCGCTTGA 26
   ||||| ||||| |||||
Db 5 GTGGTCTCCAGCAGCAGGATCTGGA 30

```

RESULT 33

```

CC182796/c
LOCUS CC182796 45 bp mRNA linear GSS 08-MAY-2003
DEFINITION XG533 BayGenomics Gene Trap Library pGTLxf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC182796
VERSION CC182796.1 GI:30426696
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS BayGenomics.
TITLE http://baygenomics.ucsf.edu/
JOURNAL Unpublished (2001)
COMMENT Contact: BayGenomics
Email: info@baygenomics.ucsf.edu
Bay Area Functional Genomics Consortium (BayGenomics)
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL LINE&KEY=XG533
Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1..45
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 ola"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /clone_lib="BayGenomics Gene Trap Library pGTLxf"
                     /note="Vector: pGTLxf"

ORIGIN
Query Match      44.0%; Score 13.2; DB 8; Length 45;
Best Local Similarity 83.3%; Pred. No. 1e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CCCGACGACCGCGCCTT 24
    ||| ||||| ||||| |||||
Db 45 CCACGACGACCGACCTT 28

RESULT 34
LOCUS AI019594/c
DEFINITION u91a06.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:1364818 5' similar to SW:BBP_HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ; mRNA sequence.
ACCESSION AI019594
VERSION AI019594.1 GI:3233930
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

```

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:898038
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
     source          1..46
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1364818"
                     /sex="male"
                     /tissue_type="mammary gland"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares mammary_gland NbMMG"
                     /notes="Organ: mammary gland; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site 1: Not I;
                     Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5',
                     TGTACCACATCTGAAGTGGGAGCGCGCGCAATGCTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."

ORIGIN
Query Match      44.0%; Score 13.2; DB 1; Length 46;
Best Local Similarity 83.3%; Pred. No. 1e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCGACGACCGCG 20
    ||| ||||| ||||| |||||
Db 19 GGCACCCCGCGAGCGCG 2

RESULT 35
LOCUS AL585781/c
DEFINITION AL585781 BP Chicken Embryo Library Gallus gallus cDNA clone
ROS029H11, mRNA sequence.
ACCESSION AL585781
VERSION AL585781.1 GI:13164514
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Murray,F.
TITLE BP Chicken Embryo Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
Seq primer: T3.
Location/Qualifiers
     source          1..46
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS029H11"

```

/tissue type="Embryo"
 /dev stage="5 days old"
 /lab host="DH10B"
 /clone lib="BP Chicken Embryo Library"
 /note="Vector: pBJUESCRIPT SK; Site 1: NotI; Site 2: SalI;
 Cloned unidirectionally. Primer: Oligo dt. 5' adaptor
 sequence: 5' TCAGCTCGAG 3'; 3' adaptor sequence: 5'
 GCGGCGCTTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 46;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 GTACCCAGCAGCCGCGCTTGAAGA 29

DB 46 GAACCCACCTGCTGGTTCATGAAGA 21

RESULT 36

AA238784/c

LOCUS AA238784 46 bp mRNA linear EST 03-MAR-1997
 DEFINITION wx2h02.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692883 5' similar to SW:NEB4_HUMAN P46934 NEDD-4 RELATED PROTEIN ; mRNA sequence.

ACCESSION AA238784

VERSION AA238784.1 GI:1862822

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 46)

REFERENCE

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL

COMMENT Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:426443

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..46

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:692883"

/tissue type="Liver"

/lab_host="DH10B"

/clone lib="Soares mouse NML"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGTGGAGCGCGCGATCTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 7; Length 46;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Query Match 44.0%; Score 13.2; DB 1; Length 46;
 Best Local Similarity 69.2%; Pred. No. 1e+06;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TACCCAGCAGCCGCGCTTGAAGAA 30

DB 36 TCCATCAGGAGCAGCGCTTCATAA 11

RESULT 37

H38217/c

LOCUS

DEFINITION H38217 46 bp mRNA linear EST 16-AUG-1995
 VP58c07.sl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:191628 3' similar to SP:KGUA_PIG P31006 GUANYLATE KINASE ; mRNA sequence.

ACCESSION H38217

VERSION H38217.1 GI:907716

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46)

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1641

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 1641 Std Error: 0.00

Seq primer: Promega -21ml3

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..46

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3761417"

/db_xref="taxon:9606"

/clone="IMAGE:191628"

/sex="male"

/dev stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone lib="Soares fetal liver spleen 1NFLS"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5', AACTGGAGAAATTAATTAAGATCTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

Qy 4 GTACCCAGCAGCCGGCCT 23
Db 46 GGAGCCAGNANCCGGCCT 27

RESULT 38
BX629147/C

LOCUS BX629147 NAPI Anopheles gambiae cDNA clone ANGNP2364C01T7, mRNA
DEFINITION sequence.
ACCESSION BX629147
VERSION BX629147.1 GI:33558282
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae

REFERENCE 1 (bases 1 to 48)
AUTHORS Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
TITLE Anopheles gambiae EST, Center for Tropical Disease Research and Training
JOURNAL Unpublished (2003)
COMMENT Contact: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-3996
Email: frank.h.collins.75@nd.edu.

FEATURES
source
1..48
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="ANGNP2364C01T7"
/lab_host="E. coli DH10B"
/clone_lib="NAPI"
/note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI;
Site 2: EcoRI; ESTs sequenced from the T7 priming site
that reads from the 5' end of cDNA. The NAPI is a
directionally cloned and normalized, oligo-T primed cDNA
library constructed from a mixture of Anopheles gambiae
developmental stages according to: Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
6, 791-806."

ORIGIN
Query Match 44.0%; Score 13.2; DB 5; Length 48;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGGCCTTGA 27
Db 40 GCGGTTCACCGCGCTGTCCTTGA 14

RESULT 39
BH902004

LOCUS BH902004 48 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_091114.48.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_091114.48.90.x, genomic
survey sequence.
ACCESSION BH902004
VERSION BH902004.1 GI:22712885
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 48)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_091114.48.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 44.0%; Score 13.2; DB 8; Length 48;
Best Local Similarity 69.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TACCCAGCAGCCGGCCTTGAAGAA 30
Db 10 TAATCAAGCATTCAGCCTTTAAGAA 35

RESULT 40
RA739463

LOCUS RA739463 49 bp mRNA linear EST 14-JAN-1998
DEFINITION vv54a11.r1 Soares_thymus_2NBMT Mus musculus cDNA clone
IMAGE:1226204 5' similar to SW:GBG5_BOVIN_P30670 GUANINE
NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-5 SUBUNIT. ;, mRNA
sequence.
ACCESSION AA739463
VERSION AA739463.1 GI:2775649
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 49)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

1 (bases 1 to 49)
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:651796

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..49

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1226204"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: pT7D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TGTTACCAATCTGAAGTGGAGCGCGCGTTTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 49;
Best Local Similarity 59.2%; Pred. No. 1e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 3 GGTACCCAGCAGCGCGCGCTTGAG 28
||| ||||| ||| |||
Db 22 GGTGTCCAGCAGCTCCGCGCTGAG 47

Search completed: November 18, 2005, 21:12:48
Job time : 1436.98 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-6
Perfect score: 30
Sequence: 1 GCGGTACCCAGCAGCCGCGCTTGAGAA 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-6
2	18.2	60.7	26	4	US-09-268-311-9
3	18.2	60.7	26	4	US-09-154-219-9
4	16.6	55.3	48	1	US-08-592-411-11
5	16.6	55.3	48	1	US-08-591-501-11
6	16.4	54.7	30	1	US-08-244-010-1
7	16.2	54.0	28	4	US-09-268-311-11
8	16.2	54.0	28	4	US-09-268-311-13
9	16.2	54.0	28	4	US-09-154-219-11
10	16.2	54.0	28	4	US-09-154-219-13
11	16.2	54.0	33	1	US-07-640-476-20
12	16	53.3	25	4	US-09-396-196G-25759
13	15.8	52.7	25	4	US-09-396-196G-109792
14	15.6	52.0	32	2	US-09-396-196G-125627
15	15.6	52.0	32	2	US-08-403-852D-43
16	15.6	52.0	32	3	US-08-510-646B-45
17	15.6	52.0	32	3	US-09-231-818-43
18	15.6	52.0	32	4	US-09-635-359B-43
19	15.6	52.0	43	1	US-08-464-136-43
20	15.6	52.0	43	1	US-08-440-787A-42
21	15.6	52.0	43	2	US-08-349-131-43
22	15.6	52.0	43	3	US-08-470-287A-43
23	15.6	52.0	43	3	US-08-367-685-42
24	15.6	52.0	43	5	PCT-US91-07149-42
25	15.6	52.0	43	5	PCT-US91-07149-43
26	15.4	51.3	25	4	US-09-396-196G-25761
27	15.4	51.3	40	1	US-08-086-428B-104

C 28	15.4	51.3	40	1	US-08-086-428B-106	Sequence 106, App
C 29	15.4	51.3	40	2	US-08-468-570-104	Sequence 104, App
C 30	15.4	51.3	40	2	US-08-468-570-106	Sequence 106, App
C 31	15.4	51.3	40	2	US-08-290-665A-208	Sequence 208, App
C 32	15.4	51.3	40	2	US-08-290-665A-210	Sequence 210, App
C 33	15.4	51.3	40	4	US-08-466-601A-104	Sequence 104, App
C 34	15.4	51.3	40	4	US-08-466-601A-106	Sequence 106, App
C 35	15.4	51.3	40	5	PCT-US95-10398-208	Sequence 208, App
C 36	15.4	51.3	40	5	PCT-US95-10398-210	Sequence 210, App
C 37	15.2	50.7	25	4	US-09-396-196G-91572	Sequence 91572, A
C 38	15.2	50.7	25	4	US-09-396-196G-91573	Sequence 91573, A
C 39	14.8	49.3	32	4	US-09-673-198-23	Sequence 23, Appl
C 40	14.6	48.7	27	3	US-08-998-099-161	Sequence 161, App
C 41	14.6	48.7	44	1	US-08-471-791-37	Sequence 37, Appl
C 42	14.6	48.7	44	5	PCT-US91-01746-37	Sequence 37, Appl
C 43	14.6	48.7	48	1	US-08-471-791-35	Sequence 35, Appl
C 44	14.6	48.7	48	5	PCT-US91-01746-35	Sequence 35, Appl
C 45	14.4	48.0	29	4	US-09-304-232-405	Sequence 405, App

ALIGNMENTS

RESULT 1
US-07-989-160-6
; Sequence 6, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-989-160-6

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCGGTACCCAGCAGCCGCGCTTGAGAA 30
|||||

```
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
;
; TITLE OF INVENTION: 3-(Carboxymethylthio)propionyl-7-ADCA
; NUMBER OF SEQUENCES: 17
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA: US/08/592,411
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: oligonucleotide 11
; US-08-592-411-11
;
Query Match 55.3%; Score 16.6; DB 1; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ACCCCAGCAGCCGCGCTTGAAG 28
||| ||| ||| ||| ||| ||| ||| |||
Db 18 ACCGCGCGCGCGCGCTTGAAG 40

RESULT 5
US-08-591-501-11
; Sequence 11, Application US/08591501
; Patent No. 5795733
; GENERAL INFORMATION:
; APPLICANT: BOVENBERG, ROELOF ARY LANS
; APPLICANT: KOEKMAN, BERTUS PIETER
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: VAN DER LAAN, JAN METSKE
; APPLICANT: VERWEIJ, JAN
; APPLICANT: DE VROOM, ERIK
; TITLE OF INVENTION: PROCESS FOR THE EFFICIENT PRODUCTION OF
; TITLE OF INVENTION: 7-ADCA VIA 3-(CARBOXYETHYLTHIO) PROPIONYL-7-ADCA
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,501
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 24615-20065.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
;

Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
;
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF3981
; CURRENT APPLICATION NUMBER: US/09/268,311
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; EARLIER APPLICATION NUMBER: 09/154,219
; EARLIER FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-268-311-9
;
Query Match 60.7%; Score 18.2; DB 4; Length 26;
Best Local Similarity 87.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCT 23
||||| ||| ||| ||| ||| ||| |||
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24

RESULT 3
US-09-154-219-9
; Sequence 9, Application US/09154219
; Patent No. 6635443
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/09/154,219
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-9
;
Query Match 60.7%; Score 18.2; DB 4; Length 26;
Best Local Similarity 87.0%; Pred. No. 2.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCT 23
||||| ||| ||| ||| ||| ||| |||
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24

RESULT 4
US-08-592-411-11
; Sequence 11, Application US/08592411
; Patent No. 5726032
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for the Efficient Production of
; TITLE OF INVENTION: 7-ADCA via 2-(Carboxyethylthio)acetyl-7-ADCA and
```

RESULT 7
US-09-268-311-11
; Sequence 11, Application US/09268311
; Patent No. 6482923
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangqu

```

; SOFTWARE: PatentIn Ver. 2.0

```

```
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-11

Query Match          54.0%; Score 16.2; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
Db 6 GGTACCCCGAGCGCTCCGCGCT 26

RESULT 10
US-09-154-219-13
; Sequence 13, Application US/09154219
; Patent No. 6635443
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguo
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/09/154,219
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/059,133
; EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-219-13

Query Match          54.0%; Score 16.2; DB 4; Length 28;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCT 23
Db 6 GGTACCCCGAGCGCTCCGCGCT 26

RESULT 11
US-07-640-476-20/c
; Sequence 20, Application US/07640476
; Patent No. 5376536
; GENERAL INFORMATION:
; APPLICANT: QUAX, WILHELMUS
; APPLICANT: LUITEN, RUDOLF G.M.
; APPLICANT: SCHUURHUIZEN, PAUL W.
; APPLICANT: MRABET, NADIR
; TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/640,476
; FILING DATE: 19910110
```

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kate H. Murashige
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20009.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-7250
; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
US-07-640-476-20

Query Match          54.0%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCGCCGCGCTTGAAGAA 30
Db 32 CGGACTCCATCATCTCGACCTTCAGAA 4

RESULT 12
US-09-396-196G-25759/c
; Sequence 25759, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25759

Query Match          53.3%; Score 16; DB 4; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTACCCCGAGCGCCGCGCTTGA 27
Db 25 GTAGCCCGAGCATGCCGAGCTTGA 2

RESULT 13
US-09-396-196G-109792/c
; Sequence 109792, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
```

;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 109792
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-109792

Query Match 52.7%; Score 15.8; DB 4; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGCAGCCCGCCTTGAAG 28
||||| | | | | | | | | | | | | | | | | | | | |
DB 20 CAGCAGCTGCGCCTTGAAG 2

RESULT 14
US-09-396-196G-125627
;; Sequence 125627, Application US/09396196G
;; Patent No. 6821724
;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 125627
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-125627

Query Match 52.0%; Score 15.6; DB 4; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CCCAGCAGCCCGCCTTGAAGA 29
||||| | | | | | | | | | | | | | | | | | | | |
DB 3 CCCAGCAGCTCAGCCTGGCAGA 24

RESULT 15
US-08-403-852D-43/c
;; Sequence 43, Application US/08403852D
;; Patent No. 5891695
;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington

;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,852D
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-403-852D-43

Query Match 52.0%; Score 15.6; DB 2; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGTACCCAGCAGCCCGCCTTG 25
||||| | | | | | | | | | | | | | | | | | | | |
DB 32 CGGTACCCAGSAGSGGCGCTTS 9

RESULT 16
US-08-510-646B-45/c
;; Sequence 45, Application US/08510646B
;; Patent No. 6077699
;; GENERAL INFORMATION:
;; APPLICANT: Blanc, Veronique
;; APPLICANT: Blanche, Francis
;; APPLICANT: Crouzet, Joel
;; APPLICANT: Jacques, Nathalie
;; APPLICANT: Lacroix, Patricia
;; APPLICANT: Thibaut, Denis
;; APPLICANT: Zagorec, Monique
;; APPLICANT: Debussche, Laurent
;; APPLICANT: De Crecy-Lagard, Valerie
;; TITLE OF INVENTION: Polypeptides Involved In The
;; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
;; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/510,646B

;; FILING DATE: 03-AUG-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/403,852
;; FILING DATE: 10-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR 93/00923
;; FILING DATE: 25-SEP-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-01000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4400
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-510-646B-45

Query Match 52.0%; Score 15.6; DB 3; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCGGCCTTG 25
Db 32 CGGTACCASAGSGGGCTTS 9

RESULT 17
US-09-231-818-43/c
; Sequence 43, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,818
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 92/11441
;; FILING DATE: 25-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 03806.0054-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-231-818-43

Query Match 52.0%; Score 15.6; DB 3; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGGTACCCAGCAGCCGGCCTTG 25
Db 32 CGGTACCASAGSGGGCTTS 9

RESULT 18
US-09-635-359B-43/c
; Sequence 43, Application US/09635359B
; Patent No. 6670157
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; Biosynthesis Of Streptogramins, Nucleotide Sequences
; Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/635,359B
; FILING DATE: 09-AUG-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/231,818
; FILING DATE: 15-JAN-1999
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-03000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-635-359B-43

Query Match 52.0%; Score 15.6; DB 4; Length 32;
Best Local Similarity 62.5%; Pred. No. 2.9e+03;
Matches 15; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGGTACCCAGCAGCCGCGCTTG 25
Db 32 CGGTACCCAGSAGSGGCTTS 9

RESULT 19
US-08-464-136-43/c
; Sequence 43, Application US/08464136
; Patent No. 5698426
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-136-43

Query Match 52.0%; Score 15.6; DB 1; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGTACCCAGCAGCCGCGCTTGAGAA 30
Db 42 CGGTACCCAGCTTAATCGCCTTGAGAA 13

RESULT 20
US-08-440-787A-42/c
; Sequence 42, Application US/08440787A

; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-440-787A-42

Query Match 52.0%; Score 15.6; DB 1; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGGTACCCAGCAGCCGCGCTTGAGAA 30
Db 42 CGGTACCCAGCTTAATCGCCTTGAGAA 13

RESULT 21
US-08-349-131-43/c
; Sequence 43, Application US/08349131
; Patent No. 5871974
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,131

```
;
; FILING DATE: 435
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,648
; FILING DATE:
; APPLICATION NUMBER: US/07/767,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-349-131-43

Query Match 52.0%; Score 15.6; DB 2; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 22
US-08-470-297A-43/c
; Sequence 43, Application US/08470297A
; Patent No. 6027933
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-470-297A-43

Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
```

```
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 23
US-08-367-685-42/c
; Sequence 42, Application US/08367685
; Patent No. 6258530
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,494
; FILING DATE:
; APPLICATION NUMBER: US/07/767,436
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-367-685-42

Query Match 52.0%; Score 15.6; DB 3; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCCTTGCAAA 13

RESULT 24
PCT-US91-07141-42/c
; Sequence 42, Application PC/TUS9107141
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
```

```
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07141
; FILING DATE: 19910927
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US91-07141-42

Query Match          52.0%; Score 15.6; DB 5; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGGCGCTTGAAGAA 30
    |||||
Db 42 GCGTTACCAAGCTTAATCGCGCTTGCAGAA 13

RESULT 25
PCT-US91-07149-43/c
; Sequence 43, Application PC/TUS9107149
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 SO. FLOWER STREET, SUITE 200
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07149
; FILING DATE: 19910927
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
PCT-US91-07149-43

Query Match          52.0%; Score 15.6; DB 5; Length 43;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGGCGCTTGAAGAA 30
    |||||
Db 42 GCGTTACCAAGCTTAATCGCGCTTGCAGAA 13

RESULT 26
US-09-396-196G-25761/c
; Sequence 25761, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-25761

Query Match          51.3%; Score 15.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 GCGGTACCCAGCAGCCGGCGCTTG 25
    |||||
Db 25 GCGGTACCCAGCATGCCGAGCTTG 1

RESULT 27
US-08-086-428B-104/c
; Sequence 104, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086.428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-086-428B-104

Query Match 51.3%; Score 15.4; DB 1; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCGGCTTGAA 27
Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 28

US-08-086-428B-106/c
; Sequence 106, Application US/08086428B
; Patent No. 5514539
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,428B
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-086-428B-106

Query Match 51.3%; Score 15.4; DB 1; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCGGCTTGAA 27
Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 29

US-08-468-570-104/c
; Sequence 104, Application US/08468570
; Patent No. 5871962
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 159
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,570
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-468-570-104

Query Match 51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCGCGGCTTGAA 27
Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 30

US-08-468-570-106/c
; Sequence 106, Application US/08468570
; Patent No. 5871962
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE


```

Query Match          51.3%; Score 15.4; DB 2; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCAGCCGCGCTTGAA 27
    |||||
Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 33
US-08-466-601A-104/c
; Sequence 104, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; ATORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-466-601A-104

Query Match          51.3%; Score 15.4; DB 3; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCAGCCGCGCTTGAA 27
    |||||
Db 40 GGCACATCAATAGCAGCGCTTGAA 16

RESULT 34
US-08-466-601A-106/c
; Sequence 106, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:

```

```

; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; ATORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-466-601A-106

Query Match          51.3%; Score 15.4; DB 4; Length 40;
Best Local Similarity 76.0%; Pred. No. 3.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTACCCGAGCAGCCGCGCTTGAA 27
    |||||
Db 27 GGCACATCAATAGCAGCGCTTGAA 3

RESULT 35
PCT-US95-10398-208/c
; Sequence 208, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:

```

RESULT 38
US-09-396-196G-31573/c
; Sequence 91573, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic A
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,19
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-91573

Query Match      50.7%; Score 15.2; DB 4; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CAGCAGCCCGCGCTTGAAGA 29
      ||||| ||| ||||| |||
Db 21 CAGCATCCACACTTGAAGA 2

RESULT 39
US-09-673-198-23
; Sequence 23, Application US/09673198
; Patent No. 6806076
; GENERAL INFORMATION:
; APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;
; APPLICANT: OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
; TITLE OF INVENTION: A process for producing isoprenoid compounds by
; TITLE OF INVENTION: microorganisms and a method for screening compounds with
; TITLE OF INVENTION: antibiotic or weeding activity
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/673,198
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: JP98/103101
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: JP98/221910
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: JP99/035739
; PRIOR FILING DATE: 1999-02-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-673-198-23

Query Match      49.3%; Score 14.8; DB 4; Length 32;
Best Local Similarity 73.1%; Pred. No. 6.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGCTTGA 26
      ||||| ||| ||||| |||||
Db 1 GGGGATCCTCGCAGCCAGCGCTTGA 26

RESULT 40
US-08-998-099-161/c
; Sequence 161, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18

; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Hammerhead Ribozyme
; OTHER INFORMATION: The letter "n" represents stem II region of a HH ribozyme.
US-08-998-099-161

Query Match      48.7%; Score 14.6; DB 3; Length 27;
Best Local Similarity 77.3%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCCGCGGCC 22
      ||||| ||| ||||| |||||
Db 23 GCGTTTCATCATCAGCCCGGCC 2

Search completed: November 18, 2005, 11:22:00
Job time : 58.289 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 403.232 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-6

Perfect score: 30

Sequence: 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

```

1: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-469-172-6	Sequence 6, Appli
2	30	100.0	30	US-10-788-779-6	Sequence 6, Appli
3	18.2	60.7	26	US-09-796-844-9	Sequence 9, Appli
4	18.2	60.7	26	US-10-645-702-9	Sequence 9, Appli
5	18.2	60.7	26	US-10-686-639-9	Sequence 9, Appli

6	18.2	60.7	26	24	US-10-645-702-9	Sequence 9, Appli
7	16.8	56.0	25	22	US-10-719-900-167892	Sequence 167892,
8	16.8	56.0	25	22	US-10-719-900-189296	Sequence 189296, A
9	16.2	54.0	25	16	US-10-098-263B-28065	Sequence 28065, A
10	16.2	54.0	25	16	US-10-098-263B-41023	Sequence 41023, A
11	16.2	54.0	28	11	US-09-796-844-11	Sequence 11, Appl
12	16.2	54.0	28	11	US-09-796-844-13	Sequence 11, Appl
13	16.2	54.0	28	20	US-10-645-702-11	Sequence 11, Appl
14	16.2	54.0	28	20	US-10-645-702-13	Sequence 13, Appl
15	16.2	54.0	28	20	US-10-686-639-11	Sequence 11, Appl
16	16.2	54.0	28	20	US-10-686-639-13	Sequence 13, Appl
17	16.2	54.0	28	24	US-10-645-702-11	Sequence 11, Appl
18	16.2	54.0	28	24	US-10-645-702-13	Sequence 13, Appl
19	16.2	54.0	38	10	US-09-923-760-2	Sequence 2, Appli
20	16	53.3	25	22	US-10-809-189-25759	Sequence 25759, A
21	16	53.3	29	9	US-09-949-145-26	Sequence 26, Appl
22	15.8	52.7	19	10	US-09-880-313A-54	Sequence 54, Appl
23	15.8	52.7	19	10	US-09-880-313A-140	Sequence 140, App
24	15.8	52.7	25	22	US-10-809-189-109792	Sequence 109792,
25	15.8	52.7	39	18	US-10-375-913-39	Sequence 39, Appl
26	15.8	52.7	39	26	US-11-110-001-39	Sequence 39, Appl
27	15.8	52.7	39	26	US-11-110-002-39	Sequence 39, Appl
28	15.6	52.0	25	22	US-10-719-900-48748	Sequence 48748, A
29	15.6	52.0	25	22	US-10-719-900-48748	Sequence 125627,
30	15.6	52.0	25	22	US-10-809-189-125627	Sequence 186720,
31	15.6	52.0	25	24	US-10-719-956-186720	Sequence 220107,
32	15.6	52.0	25	24	US-10-719-956-220107	Sequence 254406,
33	15.6	52.0	25	24	US-10-719-956-254406	Sequence 273121,
34	15.6	52.0	25	24	US-10-719-956-273121	Sequence 627239,
35	15.6	52.0	25	24	US-10-719-956-627239	Sequence 627240,
36	15.6	52.0	25	24	US-10-719-956-627240	Sequence 43, Appl
37	15.6	52.0	32	21	US-10-716-803-43	Sequence 42, Appl
38	15.6	52.0	43	9	US-09-727-311-42	Sequence 43, Appl
39	15.6	52.0	43	22	US-10-767-869-43	Sequence 243, App
40	15.4	51.3	20	10	US-09-880-313A-243	Sequence 468543,
41	15.4	51.3	25	22	US-10-719-900-468543	Sequence 675526,
42	15.4	51.3	25	22	US-10-719-900-675526	Sequence 763075,
43	15.4	51.3	25	22	US-10-719-900-763075	Sequence 25761, A
44	15.4	51.3	25	22	US-10-809-189-25761	Sequence 292888,
45	15.4	51.3	25	22	US-10-956-157-292888	

ALIGNMENTS

RESULT 1
US-08-469-172-6
; Sequence 6, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-6

Query Match 100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 2
US-10-788-779-6
; Sequence 6, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-788-779-6

Query Match 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30

RESULT 3
US-09-796-844-9
; Sequence 9, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-9

Query Match 60.7%; Score 18.2; DB 11; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCGGTACCCAGCAGCCGCGCTT 23
Db 2 GCGGTACCCAGCAGCCGCGCTT 24

RESULT 4
US-10-645-702-9
; Sequence 9, Application US/10645702
; Publication No. US20040115698A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-9
```

```
Query Match      60.7%; Score 18.2; DB 20; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||||| |||||
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24
```

RESULT 5

```
; Sequence 9, Application US/10686639
; Publication No. US20040175790A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398
; CURRENT APPLICATION NUMBER: US/10/686,639
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US/09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-9
```

```
Query Match      60.7%; Score 18.2; DB 20; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||||| |||||
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24
```

RESULT 6

```
; Sequence 9, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
```

```
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-9
```

```
Query Match      60.7%; Score 18.2; DB 24; Length 26;
Best Local Similarity 87.0%; Pred. No. 7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 GCGGTACCCAGCAGCCCGGCTT 23
    ||||||||| |||||
Db 2 GCGGTACCCAGCAGCTCCCGGCTT 24
```

RESULT 7

```
; Sequence 167892, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 167892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-167892
```

```
Query Match      56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 11 AGCAGCCCGGCTTGAAGAA 30
    ||||||||| |||||
Db 1 AGCAGCCCGGCATAGAGAA 20
```

RESULT 8

```
; Sequence 189296, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 189296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-189296

Query Match          56.0%; Score 16.8; DB 22; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 AGCAGCCCGGCTTGAAGAA 30
    ||||| ||||| |||||
Db 1 AGGAGCCTGGCTTGAAGAA 20

RESULT 9
US-10-098-263B-28065
; Sequence 28065, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28065
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-28065

Query Match          54.0%; Score 16.2; DB 16; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCCCGGCC 22
    ||||| ||||| |||||
Db 4 CGGTACCTAGGAGCCCGGTC 24

RESULT 10
US-10-098-263B-41023
; Sequence 41023, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41023
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-41023

Query Match          54.0%; Score 16.2; DB 16; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCCCGGCC 22
    ||||| ||||| |||||
Db 3 CGGTACCTAGGAGCCCGGTC 23

RESULT 11
US-09-796-844-11
; Sequence 11, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-11

Query Match          54.0%; Score 16.2; DB 11; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCCCGGCTT 23
    ||||| ||||| |||||
Db 6 GGTACCCCGAGCCCGGCTT 26

RESULT 12
US-09-796-844-13
; Sequence 13, Application US/09796844
; Publication No. US20040096935A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanguu
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF398P2
; CURRENT APPLICATION NUMBER: US/09/796,844
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 09/268,311
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-844-13
```

; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/21048

27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
86

; PRIOR APPLICATION NUMBER: 60/059,133
 ;
 ; PRIOR FILING DATE: 1997-09-17

```
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-13

Query Match      54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGCCT 23
Db 6 GGTACCCCGAGCCTCCCGCCT 26

RESULT 17
US-10-645-702-11
; Sequence 11, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF39822
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/187,015
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US00/05759
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: PCT/US99/21048
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US98/19121
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 09/154,219
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/059,133
; PRIOR FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-645-702-11

Query Match      54.0%; Score 16.2; DB 24; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGCCT 23
Db 6 GGTACCCCGAGCCTCCCGCCT 26

RESULT 18
US-10-645-702-13
; Sequence 13, Application US/10645702
; Publication No. US20050181372A9
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve M.
; TITLE OF INVENTION: Interleukin 17 Receptor-Like Protein
; FILE REFERENCE: PF39822
; CURRENT APPLICATION NUMBER: US/10/645,702
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US/09/796,844

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-686-639-13

Query Match      54.0%; Score 16.2; DB 20; Length 28;
Best Local Similarity 85.7%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCAGCCCGCCT 23
Db 6 GGTACCCCGAGCCTCCCGCCT 26

RESULT 19
US-09-923-760-2
; Sequence 2, Application US/09923760
; Publication No. US20030119054A1
; GENERAL INFORMATION:
; APPLICANT: Mrksich, Milan
; APPLICANT: Hoehnland, Christian
; TITLE OF INVENTION: POLYPEPTIDE IMMOBILIZATION
; FILE REFERENCE: 7814/45
; CURRENT APPLICATION NUMBER: US/09/923,760
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer sequence, Exon1B, for F. solani cutinase gene
US-09-923-760-2

Query Match      54.0%; Score 16.2; DB 10; Length 38;
Best Local Similarity 72.4%; Pred. No. 4.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 CGGTACCCCGAGCAGCCCGCCTTGAAGAA 30
Db 2 CGGTACCCCGAGCAGCCTCCCGCCTTGAAGAA 30

RESULT 20
US-10-809-189-25759/c
; Sequence 25759, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
```

; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-189-25759

Query Match 53.3%; Score 16; DB 22; Length 25;
Best Local Similarity 79.2%; Pred. No. 6e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTACCCAGAGCCCGCGCTTGAA 27
Db 25 GTAGCCAGCATGCGAGCTTGA 2

RESULT 21

US-09-949-145-26
; Sequence 26, Application US/0949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:

; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glyco
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-145-26

Query Match 53.3%; Score 16; DB 9; Length 29;
Best Local Similarity 79.2%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTACCCAGAGCCCGCGCTTGA 26
Db 6 GGCACCCCTGCAGCATGCGCTTGA 29

RESULT 22

US-09-880-313A-54/c
; Sequence 54, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:

; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide

Query Match 52.7%; Score 15.8; DB 10; Length 19;

Best Local Similarity 89.5%; Pred. No. 7.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GTACCCAGAGCCCGCGGCC 22
Db 19 GTACCCCTGCAGCGCGGCC 1

RESULT 23

US-09-880-313A-140/c
; Sequence 140, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:

; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide

US-09-880-313A-140

Query Match 52.7%; Score 15.8; DB 10; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTACCCAGAGCCCGCGGCC 22
Db 19 GTACCCCTGCAGCGCGGCC 1

RESULT 24

US-10-809-189-109792/c
; Sequence 109792, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus

US-10-809-189-109792

Query Match 52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CAGCAGCCCGCGCTTGAAG 28
Db 20 CAGCAGTCTGCGCCTTGAAG 2

RESULT 25

US-10-375-913-39/c

```
; Sequence 39, Application US/10375913
; Publication No. US20030216550A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/10/375,913
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,354
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-10-375-913-39

Query Match          52.7%; Score 15.8; DB 18; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
   |||||
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 26
US-11-110-001-39/c
; Sequence 39, Application US/11110001
; Publication No. US20050196804A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/11/110,001
; CURRENT FILING DATE: 2005-04-20
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/10/375,913
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-11-110-001-39

Query Match          52.7%; Score 15.8; DB 26; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
   |||||
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 27
US-11-110-002-39/c
; Sequence 39, Application US/11110002
; Publication No. US20050196841A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Ming-Qun
; APPLICANT: Ferrandon, Sebastien
; APPLICANT: Taron, Christopher
; APPLICANT: Colussi, Paul
; TITLE OF INVENTION: Modified Chitin Binding Domain And Uses Thereof
; FILE REFERENCE: NEB-200-US
; CURRENT APPLICATION NUMBER: US/11/110,002
; CURRENT FILING DATE: 2005-04-20
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,354
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 39
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: primer
; US-11-110-002-39

Query Match          52.7%; Score 15.8; DB 26; Length 39;
Best Local Similarity 89.5%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGC 21
   |||||
Db 28 GGTACCCCGAGCGCGCGC 10

RESULT 28
US-10-719-900-48747
; Sequence 48747, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-48747

Query Match          52.0%; Score 15.6; DB 22; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTACCCCGAGCGCCGCGCTT 24
   |||||
Db 3 GATAACCCGAGAGCGCGCAT 24

RESULT 29
US-10-719-900-48748
; Sequence 48748, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
```


Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels

```

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

```

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0

```
RESULT 38
US-09-727-311-42/c
; Sequence 42, Application US/09727311
; Patent No. US20010024782A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/767,436
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-727-311-42
Query Match 52.0%; Score 15.6; DB 9; Length 43;
Best Local Similarity 70.0%; Pred. No. 8.3e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 GCGGTACCCAGCAGCCGCGCTTGAAGAA 30
Db 42 GCGTTACCAAGCTTAATCGCTTGACAGAA 13
RESULT 40
US-09-880-313A-243/c
; Sequence 243, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; US-09-880-313A-243
Query Match 51.3%; Score 15.4; DB 10; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GTACCCCGCAGCAGCCCGG 20
Db 20 GTACCCCTGCAGCCCGG 4
Search completed: November 18, 2005, 15:41:06
Job time : 403.232 secs

RESULT 39
US-10-767-869-43/c
; Sequence 43, Application US/10767869
; Publication No. US20050003384A1
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott Will & Emery
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 832.357 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATTCGGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	6	I12900 Sequence 7
2	18.8	62.7	50	6	CQ848568 Sequence
3	15.2	54.0	23	6	AR030683 Sequence
4	16.2	54.0	23	6	AR076191 Sequence
5	16.2	54.0	23	6	AR124104 Sequence
6	16.2	54.0	23	6	E23386 DNA encodin
7	16.2	54.0	31	6	BD226997 Plasmid i
8	16.2	54.0	38	6	A37856 Sequence 26
9	16.2	54.0	38	6	AR069894 Sequence
10	16.2	54.0	38	6	AR099291 Sequence
11	16.2	54.0	38	6	AR124175 Sequence
12	16.2	54.0	38	6	AR442782 Sequence
13	15.4	51.3	41	6	AX515690 Sequence
14	15.4	51.3	41	6	AX518285 Sequence
15	15.2	50.7	24	6	CQ818454 Sequence
16	15.2	50.7	33	6	E30624 Antibody an
17	15.2	50.7	33	6	E31233 Device for
18	15.2	50.7	33	6	AR566423 Sequence
19	15	50.0	31	6	AS1539 Sequence 24

20	15	50.0	31	6	A51567	Sequence 27	
21	15	50.0	31	6	AR084293	Sequence	
22	15	50.0	31	6	CQ795411	Sequence	
23	15	50.0	31	6	I95571	Sequence 26	
24	14.8	49.3	26	6	AR307679	Sequence	
25	14.8	49.3	27	6	AR003508	Sequence	
26	14.8	49.3	27	6	AR070729	Sequence	
27	14.8	49.3	27	6	AR118062	Sequence	
28	14.8	49.3	27	6	I17115	Sequence 8	
29	14.8	49.3	27	6	I62404	Sequence 8	
30	14.8	49.3	27	6	I86716	Sequence 4	
31	14.8	49.3	27	6	I86724	Sequence 12	
32	14.8	49.3	30	6	AR049388	Sequence	
33	14.8	49.3	30	6	AR095549	Sequence	
34	14.6	48.7	32	6	CQ818101	Sequence	
35	14.6	48.7	50	6	AR444529	Sequence	
c	36	14.4	48.0	26	6	CQ857433	Sequence
37	14.4	48.0	31	6	BD002760	Gene comp	
c	38	14.4	48.0	44	6	AR274129	Sequence
c	39	14.4	48.0	44	6	AR444946	Sequence
c	40	14.2	47.3	31	6	BD271888	Methods f
41	14.2	47.3	31	6	AX080183	Sequence	
42	14.2	47.3	31	6	AX592510	Sequence	
43	14.2	47.3	34	6	CQ756616	Sequence	
44	14.2	47.3	39	6	AR009935	Sequence	
45	14.2	47.3	39	6	I76260	Sequence 88	

ALIGNMENTS

RESULT 1	I12900	Sequence 7 from patent US 5429923.	30 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12900	Sequence 7 from patent US 5429923.	30 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	I12900	Sequence 7 from patent US 5429923.	30 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	I12900	Sequence 7 from patent US 5429923.	30 bp	DNA	linear	PAT 26-JUL-1995
VERSION	I12900.1	GI:910877	30 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 30)					
AUTHORS	Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.					
TITLE	Method for detecting hypertrophic cardiomyopathy associated mutations					
JOURNAL	Patent: US 5429923-A 7 04-JUL-1995;					
FEATURES	Location/Qualifiers					
source	1..30					
ORIGIN	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	100.0%;	Score 30;	DB 6;	Length 30;		
Best Local Similarity	100.0%;	Pred. No. 0.034;				
Matches	30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	GGGAATTCGGAGCCAGCGCACTGAAG 30				
Db	1	GGGAATTCGGAGCCAGCGCACTGAAG 30				
RESULT 2	CQ848568	Sequence 28 from Patent WO2004065628.	50 bp	DNA	linear	PAT 19-AUG-2004
LOCUS	CQ848568	Sequence 28 from Patent WO2004065628.	50 bp	DNA	linear	PAT 19-AUG-2004
DEFINITION	CQ848568	Sequence 28 from Patent WO2004065628.	50 bp	DNA	linear	PAT 19-AUG-2004
ACCESSION	CQ848568	Sequence 28 from Patent WO2004065628.	50 bp	DNA	linear	PAT 19-AUG-2004
VERSION	CQ848568.1	GI:51469996	50 bp	DNA	linear	PAT 19-AUG-2004
KEYWORDS	Human sapiens (human)					
SOURCE	Human sapiens (human)					
ORGANISM	Human sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					

```
AUTHORS Fu,G.
TITLE Quantitative multiplex detection of nucleic acids
JOURNAL Patent: WO 2004065628-A 28 05-AUG-2004;
Fu, Guoliang (GB)
FEATURES
    source
        Location/Qualifiers
            1..50
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match 62.7%; Score 18.8; DB 6; Length 50;
Best Local Similarity 76.7%; Pred. No. 2.5e+03;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCCAGCCACTGAAG 30
Db 14 GAGAATTCGAGCATCCAGGTGTCACCTGAAG 43
RESULT 3
AR030683 LOCUS 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861294.
ACCESSION AR030683
VERSION AR030683.1 GI:5943897
KEYWORDS Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Cowart,M.Daniel., Halbert,D.N., Kerwin,J.F. Jr. and McNally,T.
TITLE Adenosine kinase polypeptides
JOURNAL Patent: US 5861294-A 20 19-JAN-1999;
FEATURES
    source
        Location/Qualifiers
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 GAATTCGGAGCCAGCCAGCCG 23
Db 1 GAATTCGTGGAGCCCAACCG 21
RESULT 4
AR076191 LOCUS 23 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 5 from patent US 5958748.
ACCESSION AR076191
VERSION AR076191.1 GI:10002937
KEYWORDS Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 5958748-A 5 28-SEP-1999;
FEATURES
    source
        Location/Qualifiers
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCCAGCCAGCG 21
Db 1 GGGAAATTCGGAGCCAGGAGG 21
RESULT 5
AR124104 LOCUS 23 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6171841.
ACCESSION AR124104
VERSION AR124104.1 GI:14109465
KEYWORDS Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 6171841-A 5 09-JAN-2001;
FEATURES
    source
        Location/Qualifiers
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GGGAAATTCGGAGCCAGCCAGCG 21
Db 1 GGGAAATTCGGAGCCAGGAGG 21
RESULT 6
E23386 LOCUS 23 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA encoding serine/threonine kinase.
ACCESSION E23386
VERSION E23386.1 GI:13024388
KEYWORDS JP 199098984-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Shizuo,S. and Taro,K.
TITLE DNA encoding serine/threonine kinase
JOURNAL Patent: JP 199098984-A 3 13-APR-1999;
COMMENT SCIENCE & TECH AGENCY
OS Unidentified
PN JP 199098984-A/3
PD 13-APR-1999
PF 26-SEP-1997 JP 1997261589
PR SHIZUO SHINRA,TARO KAWAI
PC C12N15/09,C12N1/21,C12N9/12/(C12N15/09,C12R1:91), (C12N1/21,
PC C12R1:19),
PC (C12N9/12,C12R1:19),C12N15/00, (C12N15/00,C12R1:91) CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT 1..23 /organism="Unidentified".
FEATURES
    source
        Location/Qualifiers
            1..23
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY 1 GGGAAATTCGGGAGCCAGCAGC 21
    |||||
Db 1 GGGAAATTCGGGAGCCAGCAGC 21
    |||||

RESULT 7
BD226997 31 bp DNA linear PAT 17-JUL-2003
LOCUS Plasmin inhibitor from Australia brown snake Pseudonaja textilis
DEFINITION textilis.
ACCESSION BD226997
VERSION BD226997.1 GI:33036767
KEYWORDS JP 2002514404-A/17.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 31)
AUTHORS Masci, P., Lavin, M.F. and Gaffney, P.J.
TITLE Plasmin inhibitor from Australia brown snake Pseudonaja textilis
JOURNAL Patent: JP 2002514404-A 17 21-MAY-2002;
        THE UNIVERSITY OF QUEENSLAND, NATIONAL INSTITUTE OF BIOLOGICAL
        STANDARDS AND CONTROL UNITED KINGDOM
COMMENT OS Artificial Sequence
        PN JP 2002514404-A/17
        PD 21-MAY-2002
        PF 07-MAY-1999 JP 2000548371
        PR 11-MAY-1998 AU PP 3450
        PI PANTALEONE PAUL MASCI, MARTIN FRANCIS LAVIN, PATRICK JOSEPH PI
        GAFFNEY
        PC C12N15/09, A61K38/00, A61K39/44, A61P7/04, A61P35/00, PC
        A61P43/00,
        PC C07K14/81, C12N15/00, A61K37/02, A61K37/465
        CC Description of Artificial Sequence: gene-specific reverse CC
        primer for Txnl
        FH Key Location/Qualifiers
        FT -source 1..31
        FT /organism='Artificial Sequence'.
        FT Location/Qualifiers
        source 1..31
        /organism='synthetic construct'
        /mol_type='genomic DNA'
        /db_xref='taxon:32630'

ORIGIN
Query Match 54.0%; Score 16.2; DB 6; Length 31;
Best Local Similarity 85.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGC 21
    |||||
Db 4 GGGAAATTCAGAGCCACAGC 24
    |||||

RESULT 8
A37856 38 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 26 from Patent WO9408014.
DEFINITION A37856
ACCESSION A37856
VERSION A37856.1 GI:2294536
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
        Thibaut, D., Zagorec, M.
TITLE POLYPEPTIDES INVOLVED IN STREPTOGRAMIN BIOSYNTHESIS, NUCLEOTIDE
        SEQUENCES CODING FOR SAID POLYPEPTIDES AND USE THEREOF
JOURNAL Patent: WO 9408014-A 26 14-APR-1994;
        RHONE POULENC RORER SA (FR)
COMMENT Other publication AU 4823993 940426

```

```

Other publication CA 2145523 940414
Other publication ZA 9307102 940422
Other publication FI 951403 950324
Other publication FR 2696189 940401
Other publication JP 85016961 960227.
        Location/Qualifiers
        source 1..38
        /organism='unidentified'
        /mol_type='unassigned DNA'
        /db_xref='taxon:32644'

```

FEATURES

```
source
```

ORIGIN

```

Query Match 54.0%; Score 16.2; DB 6; Length 38;
Best Local Similarity 66.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGCAGC 27
    |||||
Db 11 GSGAGTTTCGCGCGCTGGGACGCGCACG 37
    |||||

```

RESULT 9

```
AR069894 38 bp DNA linear PAT 18-FEB-2000
```

```
LOCUS Sequence 42 from patent US 5891695.
DEFINITION AR069894
ACCESSION AR069894
VERSION AR069894.1 GI:7220782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
        Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
        nucleotide sequences coding for these polypeptides and their use
        Patent: US 5891695-A 42 06-APR-1999;
        Location/Qualifiers
        source 1..38
        /organism='unknown'
        /mol_type='unassigned DNA'

```

ORIGIN

```

Query Match 54.0%; Score 16.2; DB 6; Length 38;
Best Local Similarity 66.7%; Pred. No. 3.3e+04;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGCAGCAGC 27
    |||||
Db 11 GSGAGTTTCGCGCGCTGGGACGCGCACG 37
    |||||

```

RESULT 10

```
AR099291 38 bp DNA linear PAT 14-FEB-2001
```

```
LOCUS Sequence 44 from patent US 6077699.
DEFINITION AR099291
ACCESSION AR099291
VERSION AR099291.1 GI:12809057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Blanc, V., Blanchet, F., Crouzet, J., Jacques, N., Lacroix, P.,
        Thibaut, D., Zagorec, M., Debussche, L. and De Crecy-Lagard, V.
TITLE Polypeptides involved in the biosynthesis of streptogramins,
        nucleotide sequences coding for these polypeptides and their use
        Patent: US 6077699-A 44 20-JUN-2000;
        Location/Qualifiers
        source 1..38
        /organism='unknown'
        /mol_type='unassigned DNA'

```

ORIGIN

ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Roth,C.W., Brey,F.T., Holm,I., Graillies,M. and Rzhetsky,A.
 TITLE Multidrug resistance proteins in drosophila and anopheles
 JOURNAL Patent: WO 2004029088-A 15 08-APR-2004;
 INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
 (CNRS) (FR)
 FEATURES Location/Qualifiers
 source 1..24
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Description of Artificial Sequence: primer"
 ORIGIN
 Query Match 50.7%; Score 15.2; DB 6; Length 24;
 Best Local Similarity 85.0%; Pred. No. 9.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 Db 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 RESULT 16
 E30624 33 bp DNA linear PAT 18-JUN-2001
 LOCUS Antibody and nucleic acid encoding the same.
 DEFINITION E30624
 ACCESSION E30624
 VERSION E30624.1 GI:13017190
 KEYWORDS JP 1999332563-A/11.
 SOURCE unidentified
 ORGANISM unidentified
 1 (bases 1 to 33)
 REFERENCE
 AUTHORS Mitsuhashi,O., Takayuki,K. and Ikuo,M.
 TITLE Antibody and nucleic acid encoding the same
 JOURNAL Patent: JP 1999332563-A 11 07-DEC-1999;
 ASahi CHEM IND CO LTD
 COMMENT OS Unidentified
 PN JP 1999332563-A/11
 PD 07-DEC-1999
 PF 26-MAY-1998 JP 1998163034
 PR MITSUHASHI ONO,TAKAYUKI KUSAKA,IKUO MORIMOTO
 PC C12N15/02,A61K39/395,A61K39/395,C07K16/28,C12N15/09,C12P21/08,
 PC C12N15/00,
 PC C12N15/00
 CC Key Location/Qualifiers
 FH source 1..33
 FT source /organism='Unidentified'.
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 ORIGIN
 Query Match 50.7%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 9.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 Db 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 RESULT 17
 E31233 33 bp DNA linear PAT 18-JUN-2001
 LOCUS E31233
 DEFINITION E31233
 TITLE Device for separating CD4-positive cells and separation method.
 ACCESSION E31233
 VERSION E31233.1 GI:13017326

KEYWORDS JP 1999332594-A/11.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Mitsuhashi,O., Takayuki,K. and Ikuo,M.
 TITLE Device for separating CD4-positive cells and separation method
 JOURNAL Patent: JP 1999332594-A 11 07-DEC-1999;
 ASahi CHEM IND CO LTD
 COMMENT OS Unidentified
 PN JP 1999332594-A/11
 PD 07-DEC-1999
 PF 26-MAY-1998 JP 1998163023
 PR MITSUHASHI ONO,TAKAYUKI KUSAKA,IKUO MORIMOTO
 PC C12Q1/04,C07K16/28,C07K16/46,C12M1/34,G01N33/53 CC
 FH Key Location/Qualifiers
 FT source 1..33
 /organism='Unidentified'.
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 ORIGIN
 Query Match 50.7%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 9.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 Db 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 RESULT 18
 AR566423 33 bp DNA linear PAT 08-OCT-2004
 LOCUS AR566423
 DEFINITION Sequence 3 from patent US 6768004.
 ACCESSION AR566423
 VERSION AR566423.1 GI:53983440
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified
 1 (bases 1 to 33)
 AUTHORS Muller,S. and Kohler,H.
 TITLE Nucleotide sequences encoding variable regions of heavy and light
 chains of monoclonal antibody 1F7, an anti-idiotypic antibody
 reactive with anti-HIV antibodies
 JOURNAL Patent: US 6768004-A 3 27-JUL-2004;
 FEATURES Location/Qualifiers
 source 1..33
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 50.7%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 9.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 Db 1 GGGAAATTCGGGAGCCAGAC 20
 |||||
 RESULT 19
 A51539 31 bp DNA linear PAT 10-MAR-1997
 LOCUS A51539
 DEFINITION Sequence 24 from Patent EP0728842.
 ACCESSION A51539
 VERSION A51539.1 GI:2304360
 KEYWORDS

SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 31)
AUTHORS Audonnet,J.-C.Francis,, Bublot,M.Joseph.Marie., Darteil,R.Jean.,
and Riviere,M.A.
TITLE Live recombinant avian vaccine based on an avianherpes virus,
against Gumboro disease
JOURNAL Patent: EP 0728842-A 24 28-AUG-1996;
RHONE MERIEUX (FR)
COMMENT Other publication FR 2728794 960705
Other publication CA 2166371 960701
Other publication AU 4063095 960711.
FEATURES Location/Qualifiers
source 1..31
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GAATTCGGGAGCCAGCGGCAC 25
Db 6 GAATTCGCGAAGAGAGGAAC 28
RESULT 20
A51567
LOCUS A51567 31 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 27 from Patent EP0719864.
ACCESSION A51567
VERSION A51567.1 GI:2304395
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 31)
AUTHORS Audonnet,J.F., Bublot,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L.
and Riviere,M.A.
TITLE Recombinant live avian vaccin, using an avian herpes virus as
vector
JOURNAL Patent: EP 0719864-A 27 03-JUL-1996;
RHONE MERIEUX (FR)
COMMENT Other publication FR 2728795 960705
Other publication CA 2166367 960701
Other publication AU 4071595 960711.
FEATURES Location/Qualifiers
source 1..31
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GAATTCGGGAGCCAGCGGCAC 25
Db 6 GAATTCGCGAAGAGAGGAAC 28
RESULT 21
AR084293
LOCUS AR084293 31 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 27 from patent US 5980906.
ACCESSION AR084293
VERSION AR084293.1 GI:10011064
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Audonnet,J.-C.Francis,, Bublot,M.Joseph.Marie., Darteil,R.Jean.,
Duinat,C.Veronique,, Laplace,E.Louise.Francedillaoise. and
Riviere,M.Albert.Emile.
TITLE Live recombinant avian vaccine using an avian herpesvirus as vector
JOURNAL Patent: US 5980906-A 27 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..31
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GAATTCGGGAGCCAGCGGCAC 25
Db 6 GAATTCGCGAAGAGAGGAAC 28
RESULT 22
CQ795411
LOCUS CQ795411 31 bp DNA linear PAT 19-APR-2004
DEFINITION Sequence 27 from Patent EP1403375.
ACCESSION CQ795411
VERSION CQ795411.1 GI:46407501
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Audonnet,J.C., Bublot,M., Darteil,R., Duinat,C., Laplace,E. and
Riviere,M.
TITLE Recombinant live avian vaccin, using avian herpes virus as vector
JOURNAL Patent: EP 1403375-A 27 31-MAR-2004;
FEATURES Location/Qualifiers
source 1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucl otide servant d'amorce de PCR"
ORIGIN
Query Match 50.0%; Score 15; DB 6; Length 31;
Best Local Similarity 78.3%; Pred. No. 1.1e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GAATTCGGGAGCCAGCGGCAC 25
Db 6 GAATTCGCGAAGAGAGGAAC 28
RESULT 23
I95571
LOCUS I95571 31 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 26 from patent US 5733554.
ACCESSION I95571
VERSION I95571.1 GI:3940041
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Audonnet,J.-C.Francedillais., Bublot,M.Joseph.Marie.,
Darteil,R.Jean., Duinat,C.Veronique.,
Laplace,E.Louise.Francedillaoise. and Riviere,M.Albert.Emile.
TITLE Avian herpesvirus-based live recombinant avian vaccine, in
particular against Gumboro disease
JOURNAL Patent: US 5733554-A 26 31-MAR-1998;

```
FEATURES
  source
    Location/Qualifiers
    1..31
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match 50.0%; Score 15; DB 6; Length 31;
  Best Local Similarity 78.3%; Pred. No. 1.1e+05;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGAATTCGGAGCCAGACGGCAC 25
    |||||
Db 6 GGAATTCGCAAGAGAGGAAC 28
    |||||

RESULT 24
AR307679 AR307679 26 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 26 from patent US 6551821.
ACCESSION AR307679
VERSION AR307679.1 GI:31698384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and Grant,S.
TITLE Brain cyclic nucleotide gated ion channel and uses thereof
JOURNAL Patent: US 6551821-A 26 22-APR-2003;
FEATURES
  source
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
  Query Match 49.3%; Score 14.8; DB 6; Length 26;
  Best Local Similarity 73.1%; Pred. No. 1.4e+05;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ATTTCGGAGCCAGCGGCTGGAAG 30
    |||||
Db 1 ATGTTCCGAGCAGAAGCGGTGGAG 26
    |||||

RESULT 25
AR003508 AR003508 27 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 4 from patent US 5744310.
ACCESSION AR003508
VERSION AR003508.1 GI:3964767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C.
TITLE Bax promoter sequence and screening assays for indentifying agents that regulate bax gene expression
JOURNAL Patent: US 5744310-A 4 28-APR-1998;
FEATURES
  source
    Location/Qualifiers
    1..27
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match 49.3%; Score 14.8; DB 6; Length 27;
  Best Local Similarity 73.1%; Pred. No. 1.4e+05;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGACGGCACTG 27
    |||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26
    |||||

RESULT 26
AR070729 AR070729 27 bp DNA linear PAT 18-FEB-2000
LOCUS
DEFINITION Sequence 8 from patent US 5908750.
ACCESSION AR070729
VERSION AR070729.1 GI:7221617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
TITLE Screening assays for identifying agents that regulate the expression of genes involved in cell death
JOURNAL Patent: US 5908750-A 8 01-JUN-1999;
FEATURES
  source
    Location/Qualifiers
    1..27
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match 49.3%; Score 14.8; DB 6; Length 27;
  Best Local Similarity 73.1%; Pred. No. 1.4e+05;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGACGGCACTG 27
    |||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26
    |||||

RESULT 27
AR118062 AR118062 27 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 1 from patent US 6140484.
ACCESSION AR118062
VERSION AR118062.1 GI:14098968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Bitler,C.Mastroni., Bowersox,S.Scott., Crea,R., Demo,S.Dunham., Horne,W.A. and Zhou,M.
TITLE Bax .omega. protein and methods
JOURNAL Patent: US 6140484-A 1 31-OCT-2000;
FEATURES
  source
    Location/Qualifiers
    1..27
    /organism="unknown"
    /mol_type="unassigned DNA"

ORIGIN
  Query Match 49.3%; Score 14.8; DB 6; Length 27;
  Best Local Similarity 73.1%; Pred. No. 1.4e+05;
  Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGACGGCACTG 27
    |||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26
    |||||

RESULT 28
I17115 I17115 27 bp DNA linear PAT 03-APR-1996
LOCUS
DEFINITION Sequence 8 from patent US 5484710.
ACCESSION I17115
VERSION I17115.1 GI:1252023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
```

AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
TITLE Method of down-regulating a gene linked to a P-53 responsive element
JOURNAL Patent: US 5484710-A 8 16-JAN-1996;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCCGCGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 29
162404
LOCUS I62404 27 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5659024.
ACCESSION I62404
VERSION I62404.1 GI:2480352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
TITLE Promoters that regulate the expression of genes involved in cell death
JOURNAL Patent: US 5659024-A 8 19-AUG-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 30
186716
LOCUS I86716 27 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5702897.
ACCESSION I86716
VERSION I86716.1 GI:3206434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 4 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 31
186724
LOCUS I86724 27 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 12 from patent US 5702897.
ACCESSION I86724
VERSION I86724.1 GI:3206442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 12 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 32
AR049388
LOCUS AR049388 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 25 from patent US 5824513.
ACCESSION AR049388
VERSION AR049388.1 GI:6005427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Katz,L., Donadio,S. and McAlpine,J.B.
TITLE Recombinant DNA method for producing erythromycin analogs
JOURNAL Patent: US 5824513-A 25 20-OCT-1998;
FEATURES Location/Qualifiers
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGGCACTG 27
Db 2 GGAATTCGCGGTGATGGACGGGTCCG 27

RESULT 33
AR095549
LOCUS AR095549 30 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 25 from patent US 6004787.
ACCESSION AR095549
VERSION AR095549.1 GI:10023513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Reed,J.C. and Sato,T.
TITLE Interaction of proteins involved in a cell death pathway
JOURNAL Patent: US 5702897-A 4 30-DEC-1997;
FEATURES Location/Qualifiers
source 1. .27
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.3%; Score 14.8; DB 6; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
REFERENCE 1 (bases 1 to 30)
AUTHORS Katz,L., Donadio,S. and McAlpine,J.B.
TITLE Method of directing biosynthesis of specific polyketides
JOURNAL Patent: US 6004787-A 25 21-DEC-1999;
FEATURES
    source
        1..30
        /organism="unknown"
        /mol_type="unassigned DNA"
ORIGIN
Query Match 49.3%; Score 14.8; DB 6; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGACGCGACTG 27
Db 2 GGAATTCGGTGGAGCATGTCGGGACTG 27
RESULT 34
CQ818101
LOCUS CQ818101 32 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 128 from Patent WO2004044004.
ACCESSION CQ818101
VERSION CQ818101.1 GI:48426915
KEYWORDS
    synthetic construct
    synthetic construct
    other sequences; artificial sequences.
ORIGIN
REFERENCE 1
AUTHORS Jakobsen,B.K., Andersen,T.B., Molloy,P.E., Li,Y. and Boulter,J.M.
TITLE T cell receptor display
JOURNAL Patent: WO 2004044004-A 128 27-MAY-2004;
Avidex Limited (GB)
FEATURES
    source
        1..32
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"
ORIGIN
Query Match 48.7%; Score 14.6; DB 6; Length 32;
Best Local Similarity 69.0%; Pred. No. 1.7e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGACGCGACTGAAG 30
Db 1 GGAATTCATCGATGCAGAGGAAGTGGAG 29
RESULT 35
AR444529
LOCUS AR444529 50 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 940 from patent US 6670464.
ACCESSION AR444529
VERSION AR444529.1 GI:42672308
KEYWORDS
    Unknown.
    Unknown.
ORIGIN
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: US 6670464-A 940 30-DEC-2003;
FEATURES
    source
        1..50
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
Query Match 48.7%; Score 14.6; DB 6; Length 50;
Best Local Similarity 69.0%; Pred. No. 1.7e+05;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGACGCGACTGAAG 30
Db 1 GGAATTCATCGATGCAGAGGAAGTGGAG 29
RESULT 36
CQ857433
LOCUS CQ857433 26 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 161 from Patent WO2004069211.
ACCESSION CQ857433
VERSION CQ857433.1 GI:51851714
KEYWORDS
    synthetic construct
    synthetic construct
    other sequences; artificial sequences.
ORIGIN
REFERENCE 1
AUTHORS Houtzager,E., Vijn,I.M., Sijmons,P.C., Valinotti,T., Mudge,G. and
Fadel,A.
TITLE Affinity proteins for controlled application of cosmetic substances
JOURNAL Patent: WO 2004069211-A 161 19-AUG-2004;
L-Mabs B.V. (NL)
FEATURES
    Location/Qualifiers
        source
            1..26
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: primer Pr817"
ORIGIN
Query Match 48.0%; Score 14.4; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 2e+05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCAG 18
Db 25 GGGAAATTCGGGAGCCAG 8
RESULT 37
BD002760
LOCUS BD002760 31 bp DNA linear PAT 31-JAN-2002
DEFINITION Gene composition and method.
ACCESSION BD002760
VERSION BD002760.1 GI:18630721
KEYWORDS
    JP 2000245487-A/426.
    unidentified
    unidentified
    unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 426 12-SEP-2000;
AFIMETRICS INC
COMMENT
    OS Unknown
    PN JP 2000245487-A/426
    PD 12-SEP-2000
    PF 27-JAN-2000 JP 2000019392
    PR 27-JAN-1999 US 09/238 402
    PI NIRA SHA, JANET WALINTON, NIRA PATEL
    CC C12N15/09, C12Q1/68, C12N15/00
    FT Key
    FT source
    FT Location/Qualifiers
    FT 1..31
    FT /organism="Unknown".
    FT Location/Qualifiers
    FT 1..31
    FT /organism="unidentified"
    FT /mol_type="genomic DNA"
    FT /db_xref="taxon:32644"
ORIGIN
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 206.578 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATTCGGCGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	2	AAQ91127
2	30	100.0	30	9	ACK28325
3	30	100.0	30	13	ADRS05303
4	18.8	62.7	50	13	ADQ31570
5	17.2	57.3	31	3	AZ58040
6	16.8	56.0	35	3	AZ54807
7	16.2	54.0	23	2	AAT48848
8	16.2	54.0	23	2	AA01108
9	16.2	54.0	23	2	AA34658
10	16.2	54.0	31	3	AZ229034
11	16.2	54.0	33	8	ABZ39945
12	16.2	54.0	36	6	AA598482
13	16.2	54.0	39	6	AA155433
14	16.2	54.0	39	6	ABQ76067
15	16.2	54.0	39	8	ABV75124
16	16.2	54.0	39	12	ADI80425
17	15.8	52.7	29	3	AA11359
18	15.8	52.7	41	6	ABZ47699
19	15.8	52.7	41	6	ABZ45104
20	15.6	52.0	25	9	ACI97483

c	21	15.6	52.0	25	9	ACK28325
c	22	15.6	52.0	41	3	AZ54975
	23	15.4	51.3	34	3	AAA30422
	24	15.2	50.7	24	12	ADN97120
	25	15.2	50.7	33	2	AAQ90440
	26	15.2	50.7	33	3	AAZ44213
	27	15.2	50.7	33	3	AZ58671
	28	15.2	50.7	33	3	AAA39128
	29	15.2	50.7	33	5	AAH41120
	30	15.2	50.7	33	6	AA148649
	31	15.2	50.7	40	3	AZ96102
	32	15	50.0	28	13	ADS18341
	33	15	50.0	29	6	ABA03393
	34	15	50.0	31	2	AAT35896
	35	15	50.0	31	2	AAT39333
	36	15	50.0	31	2	AAT35930
	37	15	50.0	31	12	ADM41163
	38	15	50.0	45	13	ADR13841
	39	14.8	49.3	27	2	AAT62767
	40	14.8	49.3	27	2	AAT03167
	41	14.8	49.3	27	2	AAT48489
	42	14.8	49.3	27	2	AAV25511
	43	14.8	49.3	27	2	AZ19765
	44	14.8	49.3	30	2	AAQ46803
	45	14.8	49.3	36	10	ADD35981

ALIGNMENTS

RESULT 1

AAQ91127
ID AAQ91127 standard; cdna; 30 BP.

AC AAQ91127;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer C'.

KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.

OS Synthetic.

PN US5429923-A.

PD 04-JUL-1995.

PF 11-DEC-1992; 92US-00989160.

PR 11-DEC-1992; 92US-00989160.

PA (HARD) HARVARD COLLEGE.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
(GCHO-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

WPI; 1995-245715/32.

PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

XX Example 1; Col 10; 22pp; English.

XX AAQ91121-Q91130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
CC a broad applicability and may be used to detect mutations responsible for
CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAAATTCGGAGCCAGACGGCACTGAAG 30

Db 1 GGGAAATTCGGAGCCAGACGGCACTGAAG 30

RESULT 2

ACA63117

ID ACA63117 standard; DNA; 30 BP.

XX

AC ACA63117;

DT 28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer C'.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
KW familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

XX 20-MAR-2003.

PF 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

DR WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with

PT hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

PT hemophilia, by detecting a mutation in an amplified product of a beta

XX cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
CC and FHC) comprises detecting a mutation associated with hypertrophic
CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy
CC chain DNA. The mutations associated with SHC/FHC are detected in the
CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-
CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
CC sample). FHC associated point mutation can be classified and used to
CC determine life expectancy in affected individuals e.g. using a Kaplan-
CC Meier curve for the classified type of FHC causing point mutation. Also
CC included are an RNA probe comprising ribonucleotides arranged in a
CC sequence which is complementary to at least a portion of beta-cardiac
CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
CC DNA. The method is useful for detecting the presence or absence of a
CC mutation associated with hypertrophic cardiomyopathy. This method is
CC especially useful for diagnosing SHC and FHC, as well as for determining
CC the estimated life expectancy of a person with familial hypertrophic
CC cardiomyopathy. In particular, the method is useful for determining an
CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
CC is a nested PCR primer used to amplify a region of the beta cardiac
CC myosin heavy chain cDNA containing an FHC-associated mutation

XX Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAAATTCGGAGCCAGACGGCACTGAAG 30

Db 1 GGGAAATTCGGAGCCAGACGGCACTGAAG 30

RESULT 3

ADR05303

ID ADR05303 standard; DNA; 30 BP.

XX

AC ADR05303;

DT 21-OCT-2004 (first entry)

DE Human beta cardiac myosin heavy chain mutation detection primer C'.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;
KW familial hypertrophic cardiomyopathy;
KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

OS US2004152121-A1.

XX 05-AUG-2004.

PF 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

PR 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

DR WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to
PT diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac
PT myosin heavy-chain DNA and detecting the mutation in the amplified
PT product.

XX Claim 18; SEQ ID NO 7; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
CC amplified product, and detecting the presence or absence of a mutation
CC associated with hypertrophic cardiomyopathy in the amplified product,
CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
CC included are a set of DNA oligonucleotide primers for amplifying beta-
CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
 CC oligonucleotide primers being useful for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
 CC cardiomyopathy-associated mutation) and a kit for facilitating the
 CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
 CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
 CC heavy chain DNA, where the RNA probe is capable of detecting a
 CC hypertrophic cardiomyopathy-associated mutation, a second container
 CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
 CC instructions for using the components of the kit to detect the presence
 CC or absence of a hypertrophic cardiomyopathy-associated mutation in
 CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
 CC detecting the presence or absence of a mutation associated with
 CC hypertrophic cardiomyopathy for facilitating the diagnosis of
 CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
 CC having hypertrophic cardiomyopathy relies on the presence of typical
 CC clinical symptoms and the demonstration of unexplained ventricular
 CC hypertrophy. The present invention is non-invasive and based, at least in
 CC part, on the discovery that hypertrophic cardiomyopathy is caused by
 CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
 CC reveals that there are no extensive studies involving a large number of
 CC families which established that this particular disease or disorder was
 CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
 CC The present sequence is a PCR primer used to amplify a region of the beta
 CC cardiac myosin heavy chain having a disease-related point mutation.
 CC
 SQ Sequence 30 BP; 8 A; 7 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGAGGACGACGCGCATCTGAAG 30
 |||||
 DB 1 GGGAAATTCGGAGGACGACGCGCATCTGAAG 30

RESULT 4
 ID ADQ31570 standard; DNA; 50 BP.
 XX ADQ31570;
 AC ADQ31570;
 XX
 XX 21-OCT-2004 (first entry)
 XX
 DE Multiplex detection of human SNPs, primer F7C.
 XX
 XX Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;
 KW single nucleotide polymorphism.
 XX
 XX Homo sapiens.
 XX
 XX US2004146866-A1.
 XX
 XX 29-JUL-2004.
 XX
 XX 24-JAN-2003; 2003US-00349780.
 XX
 XX 24-JAN-2003; 2003US-00349780.
 XX
 XX (FUGG/) FU G.
 XX
 XX Fu G;
 XX
 XX WPI; 2004-552653/53.

XX Analyzing multiple targets in polynucleotide, by providing multiple
 PT primers with target nucleic acids, digesting nucleic acid products with
 PT cognate restriction enzymes, amplifying digested products, and detecting
 PT amplified products.
 XX
 XX Example 1; SEQ ID NO 28; 65pp; English.

CC The invention relates analysing multiple targets in polynucleotide,
 CC involves providing a set or sets of multiple primers with target nucleic
 CC acids in separate reactions of primer extension or amplification, where
 CC the reactions produce nucleic acid products in that each nucleic acid
 CC fragments comprise at least one restriction site, digesting nucleic acid
 CC products of the separate reactions on the restriction sites with cognate
 CC restriction enzymes, joining digested products derived from the separate
 CC reactions together, where randomly joining nucleic acid fragments from
 CC the separated reactions are created, amplifying the joined products, and
 CC detecting the amplified products. Also included are an oligonucleotide
 CC primer for detecting target nucleic acid sequence (comprising a 3'
 CC complementary portion and 5' non-complementary portion, where the 5' non-
 CC complementary portion comprises a restriction enzyme site, where the
 CC restriction site acts as detection marker in the process of detecting
 CC target nucleic acid sequence, where the detection signal generated from
 CC enzymatic manipulation on restriction site of reaction product is
 CC indicative of the presence of target nucleic acid sequence) and a kit for
 CC use in analysis and detection of multiple targets in a polynucleotide
 CC (comprising a set or sets of multiple primers, universal primers,
 CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
 CC in a polynucleotide and for genotyping mutations, preferably single
 CC nucleotide polymorphisms (SNPs), and for analysing differential gene
 CC expression profiles, genomic methylation patterns and any specific
 CC nucleic acids from any source. The method enables analysis of multiple
 CC targets quantitatively. An experiment was performed, using the method of
 CC the invention, where 8 SNPs were detected in human genomic DNA,
 CC simultaneously. The present sequence is a primer used in the above
 CC experiment.
 CC
 XX
 SQ Sequence 50 BP; 16 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 62.7%; Score 18.8; DB 13; Length 50;
 Best Local Similarity 76.7%; Pred. No. 2.2e+02;
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGAGGACGACGCGCATCTGAAG 30
 |||||
 DB 14 GAGAAATTCGACGATCCAGGTGTCTACTGAAG 43

RESULT 5
 ID AAZ58040 standard; DNA; 31 BP.
 XX AAZ58040;
 AC AAZ58040;
 XX
 XX 06-AUG-2003 (revised)
 DT 25-APR-2000 (first entry)
 XX
 XX Porcine reproductive and respiratory syndrome virus ORF3 3' primer.
 XX
 XX PRRS; racoonpox virus; vaccine; homology vector 934-64.2; PCR primer;
 KW ss.
 XX
 XX Porcine reproductive and respiratory syndrome virus.
 OS
 XX WO200003030-A2.
 XX
 XX 20-JAN-2000.
 XX
 XX 09-JUL-1999; 99WO-US015565.
 XX
 XX 10-JUL-1998; 98US-00113750.
 XX
 XX (SCHE) SCHERING-PLOUGH LTD.
 XX
 XX Cochran MD, Junker DE;
 XX
 XX WPI; 2000-171150/15.
 XX
 XX New recombinant racoonpox virus containing foreign DNA inserted into a
 PT non-essential region within the HindIII U genomic region, useful as a

PT vaccine against pathogens in mammalian and avian species.
XX Disclosure; Page 55; 164pp; English.
XX

CC The present sequence is that of downstream primer 9/97.10 used in the PCR
CC amplification of open reading frame 3 (ORF3) of swine reproductive and
CC respiratory syndrome virus (PPRS). It is based on the 3' end of the PPRS
CC ORF3, and introduces an EcoRI site at the 3' end of the gene. The PCR
CC product was used in the construction of homology vector 934-64.2, which
CC incorporates a beta-glucuronidase marker gene and the PPRS ORF3 gene
CC flanked by raccopox virus (RPV) DNA, and was constructed for the
CC purpose of inserting foreign DNA into recombinant RPV. Recombinant RPVs
CC of the invention have foreign DNA inserted into non-essential regions of
CC the RPV genome. They can be included in vaccines against animal
CC pathogens, useful for immunising animals (especially avian species or
CC mammals, including humans) against animal pathogens (claimed), e.g.
CC feline pathogens (claimed) or human pathogens such as hepatitis B virus,
CC human immunodeficiency virus, human influenza etc. (Updated on 06-AUG-
CC 2003 to correct OS field.)
XX

SQ Sequence 31 BP; 6 A; 9 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 57.3%; Score 17.2; DB 3; Length 31;
Best Local Similarity 73.3%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGCGCACTGAAG 30
| | | | | | | | | | | | | | | | | | | | |
Db 2 GGGAAATTCCTATCGCCGTACGCGCACTGAGG 31

RESULT 6
AAZ54807
ID AAZ54807 standard; DNA; 35 BP.
XX
AC AAZ54807;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria species ORF cloning PCR primer #192.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy; PCR primer; ss.
XX
OS Synthetic.
OS Neisseria sp.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizzo M, Rappuoli R, Ratti G, Scarlato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI; 2000-062150/05.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics.
XX Example 16; Page 145; 1453pp; English.
XX

CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX

SQ Sequence 35 BP; 16 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 56.0%; Score 16.8; DB 3; Length 35;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCAGCAGCGCACTGAAG 30
| | | | | | | | | | | | | | | | | | | | |
Db 7 GAATTCGCACAGCAAAACGGTTTGAAG 34

RESULT 7
AAT48848
ID AAT48848 standard; DNA; 23 BP.
XX
AC AAT48848;
XX
DT 30-MAR-1997 (first entry)
XX
DE Rat brain adenosine kinase outer forward primer.
XX
KW Adenosine kinase; agonist; antagonist; monoclonal antibody;
KW polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9640937-A2.
XX
PD 19-DEC-1996.
XX
PF 31-MAY-1996; 96WO-US008097.
XX
PR 07-JUN-1995; 95US-00480019.
XX
PA (ABBO) ABBOTT LAB.
XX
XX Cowart MD, Halbert DN, Kerwin JP, McNally T;
XX WPI; 1997-052334/05.
XX
XX Rat brain, and human placenta short and long forms of adenosine kinase -
XX used, e.g. for assaying for AK (ant)agonists or for prodn. of monoclonal
XX antibodies against AK.
XX
XX Disclosure; Page 52; 75pp; English.
XX
XX Nested PCR primers (AAT48848-51) were designed to obtain a full-length
XX coding sequence for rat brain adenosine kinase (AK). These primers bind
XX to the 5' and 3' untranslated regions of the gene. Rat brain cDNA was
XX initially amplified with outer primers (AAT48848, AAT48850) and then with
XX the inner primers (AAT48849, AAT48851). The PCR fragment was cloned into
XX pGEM-T and inserts from multiple clones were sequenced. A full-length
XX consensus sequence (AAT48843) coding for rat brain AK (AAW08369) was obtd
XX
XX Sequence 23 BP; 6 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

```

Query Match          54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAATTCGGCGGAGCCAGCGC 23
    ||||| ||||| |||||
DB 1 GAATTCGTGGAGCCAAACGCG 21

RESULT 8
ID AAX01108
AC AAX01108 standard; DNA; 23 BP.
XX
XX AAX01108;
XX
DT 23-MAR-1999 (first entry)
XX
XX PCR primer for rat adenosine kinase coding sequence.
XX
XX Adenosine kinase; cytotoxic nucleoside resistance; anticancer; antiviral;
KW liver tumour; gout; acquired immune deficiency syndrome; tissue injury;
KW adenosine concentration; cytoprotection; rat; PCR primer; ss.
XX
XX Synthetic.
OS
OS Rattus sp.
XX
XX US5861294-A.
PN
XX
XX 19-JAN-1999.
PD
XX
XX 07-JUN-1995; 95US-00479614.
PF
XX
XX 07-JUN-1995; 95US-00479614.
PR
XX
XX (ABBO ) ABBOTT LAB.
PA
XX
XX Halbert DN, Kerwin JF, McNally T, Cowart MD;
PI
XX
XX WPI; 1999-130392/11.
DR
XX
XX New nucleic acid encoding adenosine kinases and related oligo-nucleotides
PT - expression vectors and transformed cells, used to modulate adenosine
PT levels and to screen for specific modulators.
XX
XX Disclosure; Col 43; 39pp; English.
PS
XX
XX This sequence is a PCR primer for DNA encoding the rat brain adenosine
CC kinase (AK) of the invention. Cells transformed with the DNA are used to
CC produce recombinant AK. The AK is used: (i) to screen for specific
CC agonists and antagonists; (ii) to raise antibodies; and (iii)
CC therapeutically (reduced levels of AK are associated with resistance to
CC nucleoside analogues with cytotoxic, anticancer and antiviral properties,
CC with liver tumours, gout and acquired immune deficiency syndrome).
CC Fragments of the DNA sequence are used as primers and probes to screen
CC DNA libraries and for identifying AK-encoding nucleic acid, also as
CC antisense therapeutics (particularly to increase local adenosine
CC concentrations at the site of tissue injury, increasing the level of
CC cytoprotection)
XX
XX Sequence 23 BP; 6 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match          54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAATTCGGCGGAGCCAGCGC 23
    ||||| ||||| |||||
DB 1 GAATTCGTGGAGCCAAACGCG 21

RESULT 9
ID AAX34658
AC AAX34658 standard; DNA; 23 BP.
XX
XX AAX34658;
XX
DT 01-JUL-1999 (first entry)
XX
XX Sense primer for leucine zipper domain of mouse ATF4.
XX
XX Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
KW human; murine; PCR primer; ss.
XX
XX Synthetic.
OS
OS Mus sp.
XX
XX EP911408-A2.
PN
XX
XX 28-APR-1999.
PD
XX
XX 24-SEP-1998; 98EP-00307747.
PF
XX
XX 26-SEP-1997; 97JP-00261589.
PR
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA
XX
XX Akira S, Kawai T;
PI
XX
XX WPI; 1999-246420/21.
DR
XX
XX New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase) protein
PT and DNA, useful as anticancer agents.
XX
XX Example 1; Page 6; 33pp; English.
PS
XX
XX The invention provides human and murine recombinant Zipper Interacting
CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
CC kinases which bind the leucine zipper domain of transcription factor
CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
CC acids are used for the recombinant expression of the proteins. ZIP-kinase
CC protein and DNA are useful as gene therapeutic agents against cancer, and
CC as anti-cancer agents
XX
XX Sequence 23 BP; 5 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match          54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGCGGAGCCAGCG 21
    ||||| ||||| |||||
DB 1 GGGAAATTCGGCGGAGCCAGCG 21

RESULT 10
ID AAZ29034
AC AAZ29034 standard; DNA; 31 BP.
XX
XX AAZ29034;
AC
XX
XX 07-FEB-2000 (first entry)
DT
XX
XX Txln 1 gene-specific reverse primer, R1.
DE
XX
XX Textilin gene; Txln; plasmin inhibitor; reverse primer R1; ss;
KW increase GC content; untranslated region; UTR; Australian brown snake.
XX
XX Synthetic.
OS
XX
XX WO9958569-A1.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-AU000343.
PF

```

```
XX PR 11-MAY-1998; 98AU-00003450.
XX PA (UYOU ) UNIV QUEENSLAND.
XX PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.
XX PA (MASC/) MASC P P.
XX PA (LAVI/) LAVIN M P.
XX PA (GAFF/) GAFFNEY P J.
XX PI Masci PP, Lavin MF, Gaffney PJ, Sorokina NI, Filippovich IV;
XX WPI; 2000-039073/03.
XX DR
XX PT Pseudonaja textilis textilis plasmin inhibitors useful as anti-tumor
XX agents.
XX PS
XX PS Example 2; Page 61; 112pp; English.
XX CC The present DNA sequence is the Txln 1 gene specific reverse primer, R1.
XX CC This is specifically designed, increasing the GC content, to determine
XX CC the 5' and 3' untranslated regions (UTR) of the Txln cDNA, from the
XX CC Australian brown snake, Pseudonaja textilis textilis. It includes an
XX CC EcoRI restriction site and a stop codon
XX CC
XX SQ Sequence 31 BP; 8 A; 9 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 3; Length 31;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCACG 21
DB 4 GGGAAATTCAGAGCCACG 24
RESULT 11
ABZ99545
ID ABZ99545 standard; DNA; 33 BP.
XX AC
XX AC ABZ99545;
XX DT
XX DT 27-JUN-2003 (first entry)
XX DE Human guanosine monophosphate reductase GMPR2 PCR primer 2.
XX KW Human; guanosine monophosphate reductase; GMPR2; tumour; PCR; primer; ss.
XX OS Homo sapiens.
XX PN CN1380407-A.
XX XX
XX PD 20-NOV-2002.
XX PF
XX PF 12-APR-2001; 2001CN-00105966.
XX XX
XX PF 12-APR-2001; 2001CN-00105966.
XX XX
XX PF (IMMU-) INST IMMUNOLOGY NO 2 MILITARY MEDICAL CO.
XX PA
XX PI Zhang J, Zhang W, Wan T;
XX XX
XX DR WPI; 2003-230990/23.
XX XX
XX PT New human-phosphoguanosine reductase, its coding sequence and
XX PT application.
XX PS
XX PS Example 2; Page 19; 30pp; Chinese.
XX CC The invention relates to a novel human guanosine monophosphate reductase
XX CC GMPR2, and the polynucleotide encoding it. The zymological activity and
XX CC the relationship of GMPR2 and tumour cell multiplication and cell
XX CC differentiation are verified. The invention also discloses the strategy
XX CC of resisting GMPR2 for diagnosing and curing diseases, specially for
```

```
CC diagnosing and curing the diseases of tumour. The present sequence
CC represents a PCR primer used to amplify the human GMPR2 of the invention
XX SQ Sequence 33 BP; 8 A; 9 C; 9 G; 7 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 8; Length 33;
Best Local Similarity 72.4%; Pred. No. 2.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 GGAATTCGGGAGCCAGCGCACTGAAG 30
DB 1 GGAATTCGTCAGCGACGCTCACTGAAG 29
RESULT 12
AAS98482/c
ID AAS98482 standard; cDNA; 36 BP.
XX XX
XX AC AAS98482;
XX XX
XX DT 12-MAR-2002 (first entry)
XX XX
XX DE Human protective DNA sequence CNI-00738 open reading frame DNA #41.
XX XX
XX KW Human; protective sequence; cell death; central nervous system; stroke;
XX KW ischaemia; open reading frame; ORF; cerebral herniation; septic embolism;
XX KW cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733; ss;
XX KW metazoal infection; vascular disease; eye; macular degeneration; trauma;
XX KW diabetic retinopathy; epidural haematoma; tumour; degenerative disease;
XX KW nutritional condition; environmental condition; metabolic condition;
XX KW CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.
XX OS Homo sapiens.
XX XX
XX PN WO200181361-A1.
XX XX
XX PD 01-NOV-2001.
XX XX
XX PF 09-APR-2001; 2001WO-US011501.
XX XX
XX PF 11-APR-2000; 2000US-00547938.
XX XX
XX PF (COGE-) COGENT NEUROSCIENCE INC.
XX PA
XX PI Portbury SD, Puranam K, Katz LC, Lo DC, Barney S, Thomas MB;
XX XX
XX DR WPI; 2002-066433/09.
XX DR P-PSDB; AAU73320.
XX XX
XX PT Polypeptides and polynucleotides comprising protective sequences useful
XX PT for preventing, delaying or rescuing a cell from death in disease,
XX PT condition or disorders such as Alzheimer's disease, stroke, tumors,
XX PT trauma.
XX PS
XX PS Claim 2; Fig 6AR; 228pp; English.
XX CC
XX CC The invention relates to an isolated polypeptide encoded by a protective
XX CC sequence, which is a polynucleotide comprising sequences which, when
XX CC introduced into a cell either predisposed to undergo cell death or in the
XX CC process of undergoing cell death, prevent delay or rescue the cell from
XX CC death, relative to a corresponding cell into which exogenous nucleic
XX CC acids have been introduced. The sequences of the invention are useful for
XX CC diagnosing a protective sequence-mediated condition, disorder or disease
XX CC in an individual. The treatable disorders are preferably of the central
XX CC nervous system of humans including ischaemia-related conditions such as
XX CC stroke, cerebral herniation, septic embolism, cerebral oedema, infections
XX CC such as meningitis, protozoal infections such as malaria, metazoal
XX CC infections such as echinococcosis, vascular diseases such as ischaemic
XX CC encephalopathy, conditions involving the eye such as macular
XX CC degeneration, diabetic retinopathy, trauma such as epidural haematoma,
XX CC tumours such as primary intracranial tumours, degenerative diseases such
XX CC as Alzheimer's disease and nutritional, environmental and metabolic
XX CC conditions. Sequences AAS98409-AAS98544 represent human protective
```

CC sequence DNA and open reading frames of the polynucleotides
XX SQ Sequence 36 BP; 4 A; 13 C; 7 G; 12 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 36;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCCAGACGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 33 GGAATCTCGGAGGAGGAGCGGCACAAAGAAG 5

RESULT 13
AAL55433
ID AAL55433 standard; DNA; 39 BP.

XX AC AAL55433;

XX DT 22-MAY-2003 (first entry)

XX DE Specific tumour cell proliferation related PCR primer, SEQ ID No 3.

XX KW Recombination virus; proliferating; tumour cell; anti-oncogene;
XX KW proliferation; telomerase promoter; therapy; tumour; PCR; primer; ss.

XX OS Unidentified.

XX PN WO2003006640-A1.

XX PD 23-JAN-2003.

XX PF 12-JUL-2002; 2002WO-CN000493.

XX PR 12-JUL-2001; 2001CN-00126113.

XX PA (QIAN/) QIAN Q.

XX PI Qian Q, Wu M, Shan S;

XX DR WPI; 2002-464081/22.

XX PT Telomerase promoter-controlled recombinant viruses proliferating
XX PT specifically in tumor cells to highly express antioncogene to kill tumor
XX PT cells by synergism, applicable in treating tumor.

XX PS Example 1; Page 22; 56pp; Chinese.

XX CC The invention relates to a recombination virus proliferating in a tumour
XX CC cell, which can express an anti-oncogene with high efficiency. The
XX CC invention also relates to the method of its proliferation. A telomerase
XX CC promoter controlling the transcription of at least one necessary gene for
XX CC a recombination virus proliferating, can make the virus optionally
XX CC proliferate in a tumour cell, which has the activity of telomerase and
XX CC basically does not proliferate in a normal cell without the activity of a
XX CC telomerase. The recombination virus can be used in therapy of many kinds
XX CC of tumours. This polynucleotide sequence represents a PCR primer relating
XX CC to the specific proliferation in a tumour cell of the invention

XX SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 39;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCCAGACGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 1 GGAATCTCGGAGGAGGAGCGGCACAAAGAAG 29

RESULT 14
ABQ76067
ID ABQ76067 standard; DNA; 39 BP.

XX ABQ76067;
XX DT 30-SEP-2002 (first entry)
XX DE Anticancer gene-associated PCR primer #3.
XX KW Proliferation; anticancer gene; tumour cell; telomerase; promoter;
XX KW early virus gene; PCR; primer; ss.
XX OS Unidentified.

XX PN CN139584-A.

XX PD 13-MAR-2002.

XX PF 12-JUL-2001; 2001CN-00126113.

XX PR 12-JUL-2001; 2001CN-00126113.

XX PA (QIAN/) QIAN Q.

XX PI Qian Q, Wu M, Cen X;

XX DR WPI; 2002-464081/50.

XX PT Telomerase promoter-controlled recombinant viruses proliferating
XX PT specifically in tumor cells to highly express antioncogene to kill tumor
XX PT cells by synergism, applicable in treating tumor.

XX PS Example 1; Page 10; 25pp; Chinese.

XX CC This invention describes a novel recombinant virus for specific
XX CC proliferation and efficient expression of an anticancer gene in tumour
XX CC cells. By inserting a telomerase promoter in the upstream area of an
XX CC early virus gene, the recombinant virus is made to proliferate
XX CC selectively in tumour cells with telomerase activity rather than in
XX CC normal cells without telomerase activity. This recombinant virus may be
XX CC used to treat several kinds of tumours. This sequence represents a PCR
XX CC primer used to illustrate the method described in the disclosure of the
XX CC invention

XX SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 6; Length 39;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCCAGACGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 1 GGAATTCGGAGCCAGATCTCAGACG 29

RESULT 15
ABV75124/C
ID ABV75124 standard; DNA; 39 BP.

XX AC ABV75124;

XX DT 19-FEB-2003 (first entry)

XX DE Mutant HGFL constructing mutagenic oligonucleotide.

XX KW HGFL; RON; MSP; transmembrane; glycoprotein; receptor tyrosine kinase;
XX KW hepatocytic; liver; hepatocyte growth factor-like protein; human;
XX KW macrophage stimulating protein; mutagenic; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO200283074-A2.

XX PD 24-OCT-2002.

XX	15-APR-2002; 2002WO-US011724.
PF	
XX	
XX	13-APR-2001; 2001US-0283788P.
XX	
XX	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
PA	
XX	Waltz SE, Leonis MA, Degan SJ;
PI	WPI; 2003-067549/06.
XX	
DR	
XX	Pharmaceutical composition useful in prevention and treatment of hepatic
PT	disorders comprises heterodimeric transmembrane glycoprotein receptor
PT	tyrosine kinase inhibitor.
XX	
XX	Example 1; Page 36; 66pp; English.
XX	
CC	The invention relates to a pharmaceutical composition that comprises
CC	heterodimeric transmembrane glycoprotein (RON) receptor tyrosine kinase
CC	inhibitor with at least one additional component selected from carriers,
CC	adjuvants, emulsifiers, solubilizers and stabilizers. The compositions
CC	decrease the action of RON receptor tyrosine kinase in the liver
CC	physiology. The composition can be used in the treatment of hepatobiliary
CC	damage e.g. acute and chronic liver failure; for preventing hepatobiliary
CC	damage due to exposure to hepatotoxic agent (preferably anesthetic,
CC	neuropsychotropics, anticonvulsants, analgesics, antimicrobials,
CC	hormones, cardiovascular drugs, immunosuppressives, radiation and
CC	antineoplastic agents). It is also useful in the treatment and prevention
CC	of injury and diseases of liver, biliary tract, bile ducts, gall bladder
CC	and other related hepatobiliary system; to treat patient at risk of
CC	developing liver damage due to drug overdose, accidental exposure to
CC	infected blood samples, aggressive chemotherapy or liver transplantation.
CC	Sequences ABV75114-125 represent mutagenic oligonucleotides used for
CC	creating mutant forms of the human hepatocyte growth factor-like protein
CC	(HGFL), also known as macrophage stimulating protein (MSP)
XX	
XX	Sequence 39 BP; 2 A; 10 C; 18 G; 9 T; 0 U; 0 Other;
SQ	

Query Match	54.0%	Score 16.2	DB 8	Length 39
Best Local Similarity	85.7%	Pred. No. 2.9e+03		
Matches 18	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	8	CGCGGAGCCAGACGGCACTGA	28	
Db	26	CGCGGAACACAGACCGCGCTGA	6	

RESULT 16	
AD180425	
ID	AD180425 standard; DNA; 39 BP.
XX	
XX	
AC	AD180425;
XX	
DT	22-APR-2004 (first entry)
XX	
XX	
DE	Anti-tumour recombinant virus related primer, SEQ ID No 3.
XX	
XX	
KW	recombinant virus; tumour cell; antibody; cytostatic; primer; ss.

WPI; 2004-122938/12.

Recombinant viruses for expressing anti-tumor antibody or its fragment with high efficiency in tumor cells to kill or inhibit proliferation and transfer of tumors, useful in drug compositions to treat tumors.

Disclosure; SEQ ID NO 3; 79pp; Chinese.

The invention relates to a novel recombinant virus that is capable of specific replication in tumor cells, comprising a nucleotide sequence encoding an antibody or its fragment for treating a tumour. The invention further relates to: application of the virus for killing or inhibiting tumour cells after external infection of such cells with an effective dose of the virus; treating human tumours by external or internal infection of the tumour cells to limit their replication and upgrowth with selectivity after expressing a dose of the antibody or its fragment, with increase of the number of copies of the encoded nucleotide sequence if necessary, for direct killing of such tumour cells, and inhibiting formation of tumour, its growth and transfer; use of the virus to inhibit proliferation of tumour cells; use of virus producing remedies for treating a tumour; and drug compositions containing the recombinant virus and pharmaceutically-acceptable carriers. The recombinant virus has cytostatic activity. The viruses are applicable for killing or inhibiting tumour cells when used in drug compositions to treat tumours. This polynucleotide sequence represents a primer used in the exemplification of the invention.

Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

```

Query Match      54.0%; Score 16.2; DB 12; Length 39;
Best Local Similarity 72.4%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      2  GGAATTCGGCGGACCCAGACGGCACTGAAG  30
      |||||
Db      1  GGAATTCGGCGGCGCAGATCTCAGACG  29
      |||||

```

```

RESULT 17
AAAA11359
ID   AAAA11359 standard; DNA; 29 BP.
XX
XX
AC   AAAA11359;
XX
XX
DT   16-NOV-2000 (first entry)
XX
XX
DE   Human Myx cDNA primer #6.
XX
XX
KW   Human; Myx; Mad; C-myc; tumour; cancer; PCR primer; ss.
XX
XX
OS   Homo sapiens.
XX
XX
PN   CN1248626-A.
XX
XX
PD   29-MAR-2000.
XX
XX
PF   09-AUG-1999; 99CN-00113968.
XX
XX
PR   09-AUG-1999; 99CN-00113968.
XX
XX
PA   (UYFU-) UNIV FUDAN.
XX
XX
PI   Yu L, Fu Q, Zhao Y;
XX
XX
WPI  2000-483210/43.
XX
XX
Novel human gene coding sequence, its coded polypeptide and preparation
process thereof.
XX
XX
Example 4; Page 7; 13pp; Chinese.
XX
XX
Primers AAAA11358-All1359 were used to PCR amplify the cDNA (AAAA11353)
encoding the human Myx protein (AAV93137) for subcloning into the
CC
CC

```



```
XX PI Plaksin D;
XX WPI; 2000-387610/33.
XX Small functional units of antibody heavy chain variable regions useful
XX for diagnosis and treatment of disease.
XX Example 3; Page 21; 48pp; English.
XX The present sequence is an oligonucleotide designated pET-21aVH3'XhoI
XX which was used for large scale production of VH single-domain molecules.
XX A phage library was generated from a gene isolated from a mouse
XX hybridoma. Phage clones contained a random sequence coding for 9 amino
XX acids in the third hypervariable loop (CDR3). CDR3 typically makes most
XX antigen contacts in antibody combining sites. Phage clones capable of
XX binding a specific antigen, e.g. Tumour necrosis factor alpha (TNFalpha),
XX were selected by library panning. The present sequence was used to
XX reamplify plasmid DNA from positive-binding clones in order to insert
XX cloning sites for subcloning into the T7 promoter-based pET-21a
XX expression vector. Protein was expressed at high levels in BL21 cells
XX upon IPTG induction and accumulated in intracellular inclusion bodies
XX which could then be isolated and purified. Single-domain VH proteins can
XX be used to treat or diagnose disorders associated with the antigens that
XX they bind to. For example, disorders in which TNF plays a role include
XX inflammatory bowel disease, rheumatoid arthritis, septic shock, multiple
XX sclerosis, chronic inflammation and allograft rejection
XX SQ Sequence 34 BP; 6 A; 10 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 51.3%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 GGGAAATTCGGGAGCCAGCGGCAC 25
Db 1 GGGAAATTCCTCGAGCTATCGGGCAC 25
RESULT 24
ADN97120
ID ADN97120 standard; DNA; 24 BP.
XX AC ADN97120;
XX DT 01-JUL-2004 (first entry)
XX DE Primer of the invention #9.
XX KW multiple drug resistance protein; MRP; Drosophila melanogaster;
XX ANopheles gambiae; insecticide; ss; primer.
XX OS Synthetic.
XX PN WO2004029088-A2.
XX FD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-EP012400.
XX PR 26-SEP-2002; 2002US-0413469P.
XX FA (INSP ) INST PASTEUR.
XX PA (CNRS ) CENT NAT RECH SCI.
XX PI Roth CW, Brey PT, Holm I, Grailles M, Rzhetsky A;
XX WPI; 2004-305150/28.
XX New polynucleotide sequence encoding multiple drug resistance proteins
XX from Drosophila melanogaster or Anopheles gambiae, useful in developing
XX effective insecticides.
PS Disclosure; SEQ ID NO 15; 58pp; English.
XX The present invention relates to a purified polynucleotide or its
XX fragment and comprises a sequence encoding multiple drug resistance
XX proteins (MRPs) from Drosophila melanogaster or Anopheles gambiae. The
XX polynucleotide is useful in developing effective insecticides. The
XX present sequence represents a primer of the invention.
XX SQ Sequence 24 BP; 7 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 12; Length 24;
Best Local Similarity 85.0%; Pred. No. 7.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 GGGAAATTCGGGAGCCAGAC 20
Db 1 GGGAAATTCGGGTGGACAGAC 20
RESULT 25
AAQ90440
ID AAQ90440 standard; DNA; 33 BP.
XX AC AAQ90440;
XX DT 02-FEB-1996 (first entry)
XX DE RT-PCR primer for the production of anti-idiotypic antibodies.
XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX complementarity determining region, ss.
XX OS Mus sp.
XX PN JP07101999-A.
XX PD 18-APR-1995.
XX PF 06-OCT-1993; 93JP-00272950.
XX PR 06-OCT-1993; 93JP-00272950.
XX PA (HAGI/) HAGIWARA Y.
XX DR WPI; 1995-182987/24.
XX PT Novel anti-idiotypic antibody against an human anticancer monoclonal
XX antibody - and DNA sequences encoding the antibody, useful in
XX pharmacology, medicine and biochemical fields.
XX Example 5; Page 11; 28pp; Japanese.
XX AAQ90435-Q90441 are RT-PCR primers used for the production of anti-
XX idiotypic antibody clones of Idio1, Idio17, Idio20, Idio27 and Idio33
XX against a human anticancer monoclonal antibody. These antibodies and DNA
XX encoding them are useful in pharmacological, medical and biochemical
XX fields of research
XX SQ Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 2; Length 33;
Best Local Similarity 85.0%; Pred. No. 7.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 GGGAAATTCGGGAGCCAGAC 20
Db 1 GGGAAATTCATGGAGACAGAC 20
RESULT 26
AAZ44213
ID AAZ44213 standard; DNA; 33 BP.
XX
```

```

AC AA244213;
XX
XX 31-MAR-2000 (first entry)
XX
DE Murine CD4/CD34 recognising antibody PCR primer 7.
XX
XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
KW HIV infection; autoimmune disease; murine; PCR primer; ss.
XX
XX Mus sp.
XX
XX WO9961629-A1.
XX
XX 02-DEC-1999.
XX
XX 24-MAY-1999; 99WO-JP002711.
XX
XX 25-MAY-1999; 98JP-00159957.
XX
XX 26-MAY-1999; 98JP-00163023.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX (ASAH ) ASAH MEDICAL CO LTD.
XX
XX Ono M, Soka T, Morimoto I, Miyamura K;
XX WPI; 2000-086720/07.
XX
XX Devices containing antibodies recognising CD4 or CD34 and their use for
XX the separation of CD4 or CD34 positive cells.
XX
XX Example 2; Page 87; 11pp; Japanese.
XX
XX This invention describes a novel device (I) for separating cluster
XX differentiation (CD)-positive cells using a recombinant (chimeric or
XX single-chain) antibody recognising CD4 or CD34. The devices are useful
XX for the separation of CD4 or CD34 positive cells, which is useful for the
XX collection of hematopoietic undifferentiated cells, elimination of
XX lymphocytes from cells to be used in bone marrow transplantation, the
XX detection of leukemic cells and the production of medicinal compositions
XX for the treatment of HIV infection and autoimmune diseases. AA244207-
XX 244230 represent PCR primers used to illustrate the method of the
XX invention
XX
XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 3; Length 33;
Best Local Similarity 85.0%; Pred. No. 7.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
    ||||| ||||| |||||
Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 27
AAZ58671
ID AAZ58671 standard; DNA; 33 BP.
XX
XX AAZ58671;
XX
XX 17-APR-2000 (first entry)
XX
XX Anti-CD4 antibody 4H5 constructing primer.
XX
XX CD4 antigen; anti-human; antibody; 4H5; drug; PCR primer; ss.
XX
XX Mus sp.
XX
XX JP11332563-A.
XX
XX 07-DEC-1999.
XX

PF 26-MAY-1998; 98JP-00163034.
XX
XX 26-MAY-1998; 98JP-00163034.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX WPI; 2000-091351/08.
XX
XX An antibody and the nucleic acid coding the antibody.
XX
XX Example 5; Page 9; 25pp; Japanese.
XX
XX The invention provides an antibody having affinity to CD4 antigen. The
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and
XX application for drugs. It is highly safe in human dose. Sequences
XX AA258665-688 represent PCR primers used in the course of the invention
XX for constructing the anti-CD4 antibody 4H5
XX
XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 3; Length 33;
Best Local Similarity 85.0%; Pred. No. 7.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGAC 20
    ||||| ||||| |||||
Db 1 GGGAAATTCATGGAGACAGAC 20

RESULT 28
AAA39128
ID AAA39128 standard; DNA; 33 BP.
XX
XX AAA39128;
XX
XX 05-SEP-2000 (first entry)
XX
XX Murine monoclonal antibody 1F7 light chain PCR primer SEQ ID NO:3.
XX
XX 1F7 antibody; murine; monoclonal antibody; diagnosis; HIV; infection;
XX AIDS; anti-HIV; human immunodeficiency virus; detection;
XX acquired immunodeficiency syndrome; PCR primer; ss.
XX
XX Mus sp.
XX
XX US6057421-A.
XX
XX 02-MAY-2000.
XX
XX 03-DEC-1997; 97US-00984277.
XX
XX 30-NOV-1994; 94US-00351193.
XX
XX (IMMP-) IMMPPERON INC.
XX
XX Muller S, Kohler H;
XX
XX WPI; 2000-338622/29.
XX
XX Variable heavy and light chain regions of murine monoclonal antibody 1F7,
XX useful for treating HIV infection and AIDS.
XX
XX Disclosure; Col 5; 45pp; English.
XX
XX The present invention describes the variable heavy and light chain
XX regions (I) of murine monoclonal antibody (mAb) 1F7. AA91014 to AA91016
XX represent specifically claimed amino acid sequences of the variable light
XX chain, and AA91017 to AA91019 represent specifically claimed amino acid
XX sequence of the variable heavy chain. The antibodies are used for
XX treatment of HIV (human immunodeficiency virus) infection and AIDS
XX (acquired immunodeficiency syndrome). They are also used for detecting
XX HIV in serum and for stimulating HIV antigen related and committed B
XX cells to produce broadly reactive and neutralising antibodies by

```

CC clonotypic stimulation. The present sequence represents a PCR primer used
 CC in the amplification of the murine monoclonal antibody 1F7

SQ Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 50.7%; Score 15.2; DB 3; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20
 ||||| |||||
 Db 1 GGGAAATTCGGAGCCAGAC 20

RESULT 29

AAH41120
 ID AAH41120 standard; DNA; 33 BP.

AC AAH41120;

XX 17-AUG-2001 (first entry)

DE Murine immunoglobulin, IgkappaVL-B, PCR primer.

XX Murine; immunoglobulin E; monoclonal antibody; IGE; PCR primer; ss.

OS Mus musculus.

XX JP2001074737-A.

XX 23-MAR-2001.

XX 03-SEP-1999; 99JP-00249805.

XX 03-SEP-1999; 99JP-00249805.

XX (ASAK) ASAHI BREWERIES LTD.

XX WPI; 2001-311336/33.

XX Anti-human IGE monoclonal antibody.

XX Example 6; Page 6; 13pp; Japanese.

XX The present invention relates to anti-human immunoglobulin E (IGE)
 CC monoclonal antibody selected the monoclonal antibodies 4D3, 1A7, 3E8,
 CC 4D10, and 11D10, which combine specifically to human IGE. The monoclonal
 CC antibody can be used for the detection of human IGE. The present sequence
 CC was used in an example from the present invention

SQ Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 5; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20
 ||||| |||||
 Db 1 GGGAAATTCGGAGCCAGAC 20

RESULT 30

AAL48649
 ID AAL48649 standard; DNA; 33 BP.

XX AAL48649;

XX 11-OCT-2002 (first entry)

XX Murine Mab 1F7 light chain PCR primer #1.

DE Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;
 KW complementarity determining region; framework-determining region; FR;
 KW

KW heavy chain; light chain; HIV infection; PCR; primer; ss.

XX Mus sp.

XX WO200255668-A2.

XX 18-JUL-2002.

XX 11-JAN-2002; 2002WO-US000927.

XX 11-JAN-2001; 2001US-00759112.

XX (IMMP-) IMPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2002-590668/63.

XX New polynucleotide encoding a complementarity- or framework-determining
 PT region of an anti-idiotypic antibody that binds to human or primate anti-
 PT human immunodeficiency virus (HIV) antibodies, for use in vaccines
 PT against HIV.

XX Example; Page 16; 27pp; English.

XX The present invention relates to coding sequences of the murine 1F7 anti-
 CC idiotypic antibody complementarity-determining region (CDR) or framework-
 CC determining region (FR). The antibody binds to human or primate anti-
 CC human immunodeficiency virus (HIV) antibodies and can be used in the
 CC treatment of HIV infection. The present sequence is a PCR primer used to
 CC isolate a 1F7 coding sequence

XX Sequence 33 BP; 10 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 7.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGAC 20
 ||||| |||||
 Db 1 GGGAAATTCGGAGCCAGAC 20

RESULT 31

AAZ96102
 ID AAZ96102 standard; DNA; 40 BP.

XX AAZ96102;

XX 10-APR-2000 (first entry)

XX Polynucleotide sequence including binding site for BamHI.

DE Ligand binding; restriction enzyme; nucleic acid determination;
 KW pharmaceutical; BamHI; ss.

XX Synthetic.

XX WO9963077-A2.

XX 09-DEC-1999.

XX 04-JUN-1999; 99WO-US012516.

XX 04-JUN-1998; 98US-0087905P.

XX 03-JUN-1999; 99US-00324672.

XX (TWTE-) TM TECHNOLOGIES INC.

XX Lane MJ, Benight AS, Faldasz BD;

XX WPI; 2000-116369/10.

CC activator (tPA). The recombinant AV vectors are useful for directing the
 CC expression of one or more heterologous gene products in the absence of
 CC vector induced cytopathology. The present sequence is a PCR primer used
 CC in the construction of a vector containing the Sindbis virus nsp2 gene
 XX
 SQ Sequence 29 BP; 7 A; 10 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 6; Length 29;
 Best Local Similarity 78.3%; Pred. No. 9.2e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 GAATTCGGCGAGCCAGCGGCAC 25
 |||||
 Db 6 GAATTCGGCGGTATATCCGCAC 28
 |||||

RESULT 34

AAT35896
 ID AAT35896 standard; DNA; 31 BP.
 AC AAT35896;
 XX
 DT 18-MAR-1997 (first entry)
 XX
 DE Marek disease virus PCR primer MB048.
 XX
 KW HVT; turkey herpes virus; THV; UL41; Marek disease virus; MDV RNA1.8;
 KW promoter; live avian vaccine; Gumboro disease; PCR primer;
 KW polymerase chain reaction; infectious bursal disease virus; IBDV; ss.
 XX
 OS Synthetic.
 XX
 XN WO9621034-A1.
 XX
 PD 11-JUL-1996.
 XX
 PF 29-DEC-1995; 95WO-FR001763.
 XX
 PR 30-DEC-1994; 94FR-00016016.
 XX
 PA (INNR) RHONE MERIEUX SA.
 XX
 PI Audonnet J, Bublot MJM, Darteil R, Duinat CV, Laplace ELF;
 PI Riviere MA;
 XX

WPI; 1996-334009/33.

XX Live avian vaccine based on Marek disease virus - has sequence encoding
 PT antigenic polypeptide inserted into the UL13 gene.
 XX
 PS Example 11; Page 22; 75pp; French.
 XX
 CC Primers MB047 and MB048 (see AAT35895 and AAT35896) were used in a PCR to
 CC amplify a 163 bp fragment from DNA extracted from lymphocytes harvested
 CC from chickens infected by Marek disease virus (MDV) strain RB1B. The PCR
 CC product was subsequently used in the construction of a plasmid in which a
 CC VP2/MCMV-IE/RNA 1.8 kb/MDV GB double cassette was inserted into the UL41
 CC site of herpesvirus of turkeys. The final construct was useful as a viral
 CC vaccine to protect poultry against MDV
 XX

SQ Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 2; Length 31;
 Best Local Similarity 78.3%; Pred. No. 9.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGCGAGCCAGCGGCAC 25
 |||||

Db 6 GAATTCGGCGAGAGAGGAAC 28
 |||||

RESULT 35

AAT39333

ID AAT39333 standard; DNA; 31 BP.

XX AAT39333;

XX 25-MAR-2003 (revised)

DT 21-APR-1997 (first entry)

XX

DE Marek's disease virus 1.8 kb RNA gene upstream sequence primer MB048.

XX

XX Herpes virus of turkey; open reading frame; ORF; homology; vector;
 KW avian herpes virus; recombinant viral vaccine; intergenic region; IBDV;
 KW cytomegalovirus immediate early promoter; UL55 gene; repeat region; ILTV;
 KW antigen; infectious bursal disease virus; Marek's disease virus; MDV;
 KW infectious laryngotracheitis virus; avian anaemia virus; vaccination;
 KW infectious bronchitis virus; IBV; poultry; Gumboro disease;
 KW Newcastle disease; ss.

OS Synthetic.

XX EP719864-A2.

XX 03-JUL-1996.

PD 28-DEC-1995; 95EP-00402970.

PF 30-DEC-1994; 94FR-00016017.

XX

PR (INNR) RHONE MERIEUX SA.

XX

PI Audonnet J, Bublot MJM, Darteil RJ, Duinat CV, Laplace ELF;

PI Riviere MAE;

XX WPI; 1996-364150/37.

XX Live recombinant avian vaccine - comprises herpes virus as vector and
 PT having sequence encoding antigenic polypeptide inserted between UL55 gene
 PT and repeat region.

XX Example 13; Col 15; 50pp; French.

XX The invention relates to the generation of live recombinant avian
 CC vaccines using an avian herpes virus as the vector, esp. using the BamHI
 CC I fragment of herpes virus of turkeys (AAT393309). The fragment contains 6
 CC open reading frames (ORF) and 3 intergenic regions. The ORFs encode
 CC proteins having homology to other avian herpes viruses. The recombinant
 CC vectors are generated by inserting genes encoding proteins of interest
 CC into the intergenic regions of BamHI fragment. Pref. the inserted
 CC sequence is ligated between the ATG of the UL55 gene (ORF-6 of AAT39309)
 CC and the junction of UL with the adjacent repeat region. The primers
 CC AAT39332-3 were used to amplify a 163 bp fragment of the upstream region
 CC from the Marek's disease virus (MDV) 1.8 kb RNA gene which contains a
 CC promoter sequence. The template for the amplification was DNA extracted
 CC from chickens infected with MDV strain RB1B. The amplified fragment was
 CC placed in inverse orientation to the cytomegalovirus immediate early (CMV
 CC -IE) promoter in the plasmid pCD002 to generate plasmid pBS002. The
 CC double promoter sequence was then used to generate the plasmid pEL095
 CC which contains the VP2 gene from the infectious bursal disease virus
 CC (IBDV) under control of the CMV-IE promoter and the MDV GB gene under
 CC control of the MDV promoter, all inserted into the herpes virus of
 CC turkeys intergenic region 1 in plasmid pEL079 (see AAT39310-4) to produce
 CC plasmid pEL095. The recombinant vectors can be used to express proteins
 CC for vaccinating poultry against Gumboro disease (caused by IBDV),
 CC Newcastle disease, Marek's disease, infectious bronchitis, infectious
 CC laryngotracheitis and avian anaemia. (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX

SQ Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 2; Length 31;
 Best Local Similarity 78.3%; Pred. No. 9.3e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGCGAGCCAGCGGCAC 25

```

Db      ||||||| || || || || || || ||
        6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 36
AAT35930
ID      AAT35930 standard; DNA; 31 BP.
XX
XX
AC      AAT35930;
XX
XX
DT      25-MAR-2003 (revised)
DT      03-MAR-1997 (first entry)
XX
XX      Marek disease virus PCR primer MB048.
XX
XX      HVT; turkey herpes virus; THV; UL43; Marek disease virus; MDV RNA1.8;
KW      promoter; live avian vaccine; Gumboro disease; PCR primer;
KW      polymerase chain reaction; infectious bursal disease virus; IBDV; ss.
XX
XX      Synthetic.
XX
XX      FR2728794-A1.
XX
XX      05-JUL-1996.
XX
XX      30-DEC-1994; 94FR-00016015.
XX
XX      30-DEC-1994; 94FR-00016015.
XX
XX      (INNR ) RHONE MERIEUX SA.
XX
XX      Audonnet JC, Bublot MJM, Dartell R, Duinat CV, Laplace ELF;
PI      Riviere MEA;
XX
XX      WPI; 1996-335824/34.
XX
XX      Live recombinant avian vaccine based on herpes virus - with sequence
PT      encoding antigenic polypeptide inserted into the UL43 gene, esp. for
PT      protection against Gumboro disease.
XX
XX      Example 11; Page 22; 67pp; French.
XX
XX      Primers MB047 and MB048 (see AAT35929 and AAT35930) were used in a PCR to
CC      amplify a 163 bp fragment from DNA extracted from lymphocytes harvested
CC      from chickens infected by Marek disease virus (MDV) strain R81B. The PCR
CC      product was subsequently used in the construction of a plasmid in which a
CC      VP2/MCMV-IE/RNA 1.8 Kb/MDV GB double cassette was inserted into the UL43
CC      site of herpesvirus of turkeys. The final construct was useful as a viral
CC      vaccine to protect poultry against MDV. (Updated on 25-MAR-2003 to
CC      correct PI field.)
XX
XX      Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      50.0%; Score 15; DB 2; Length 31;
Best Local Similarity 78.3%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 GAATTCGCGGAGCCAGAGCGCAC 25
        ||||||| || || || || || || ||
Db      6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 37
ADM41163
ID      ADM41163 standard; DNA; 31 BP.
XX
XX
AC      ADM41163;
XX
XX
DT      17-JUN-2004 (first entry)
XX
XX      PCR primer MB048 used to produce plasmid pBS002.
DE
XX      avian vaccine; avian pathogen; BamHI fragment; vaccine; Gumboro;
KW

```

```

KW      infectious bursal; Marek disease; Newcastle disease;
KW      infectious bronchitis; infectious laryngotracheitis; avian anaemia; ss;
KW      THV; PCR; primer.
XX
XX      Synthetic.
XX
XX      EP1403375-A2.
XX
XX      31-MAR-2004.
XX
XX      28-DEC-1995; 2003EP-00025194.
XX
XX      30-DEC-1994; 94FR-00016017.
XX
XX      28-DEC-1995; 95EP-00402970.
XX
XX      (MERI-) MERIAL.
XX
XX      Audonnet J, Bublot M, Dartell R, Duinat C, Laplace E, Riviere M;
PI      WPI; 2004-271923/26.
XX
XX      Use of a recombinant turkey herpes virus (HVT) with an antigen-coding
PT      sequence inserted into an intergene region, to prepare vaccines for
PT      preventing e.g. Marek or Gumboro disease in poultry.
XX
XX      Example 13; Page 11; 63pp; French.
XX
XX      The specification describes the use of a recombinant turkey herpes virus
CC      (THV) for production of live, recombinant avian vaccines, intended for
CC      vaccination in ovo, of day-old chicks, or of adults to protect against an
CC      avian pathogen. The recombinant THV includes at least one nucleic acid
CC      that encodes and expresses an antigen of the avian pathogen, inserted
CC      into intergene region 1, 2 or 3 of the BamHI fragment of the THV genome.
CC      The nucleic acid especially encodes the VP2, VP3 or a combination of VP2,
CC      3 and 4, from infectious bursal disease (Gumboro disease) virus; GB, GC,
CC      GD or GH plus GL of Marek disease or infectious laryngotracheitis viruses
CC      ; F or NH of Newcastle disease virus; S or M of infectious bronchitis
CC      virus; or VPI (52 kD) or VP2 (24 kD) of avian anaemia virus. The nucleic
CC      acid is inserted under control of the cytomegalovirus immediate-early
CC      (CMV-IE) promoter (human or murine), or the Marek RNA1.8 promoter
CC      (especially used in combination with CMV-IE for increased levels of
CC      expression). The recombinant viruses of the invention are used to
CC      vaccinate chickens against one or more of the viruses that cause Gumboro
CC      (infectious bursal), Marek or Newcastle diseases, infectious bronchitis,
CC      infectious laryngotracheitis or avian anaemia. PCR primers ADM41162-
CC      ADM41163 were used to produce plasmid pBS002, comprising the Marek RNA1.8
CC      promoter.
XX
XX      Sequence 31 BP; 11 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      50.0%; Score 15; DB 12; Length 31;
Best Local Similarity 78.3%; Pred. No. 9.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 GAATTCGCGGAGCCAGAGCGCAC 25
        ||||||| || || || || || || ||
Db      6 GAATTCGCGAAGAGAGAGGAAC 28

RESULT 38
ADR13841
ID      ADR13841 standard; DNA; 45 BP.
XX
XX
AC      ADR13841;
XX
XX      21-OCT-2004 (first entry)
XX
XX      Human hereditary Haemochromatosis (HFE) gene Flanking probe HC63-2.
XX
XX      HFE; hereditary haemochromatosis; human; ss; probe; genetic polymorphism;
KW      single nucleotide polymorphism; SNP.
XX
XX      Homo sapiens.
OS

```

OS Synthetic.

XX Key Location/Qualifiers

FT misc_binding 1. .3

FT /*tag= a

FT /bound_moiety= "Nucleotides 24-22 of SEQ ID 15"

FT /note

FT modified_base 2

FT /*tag= b

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

FT modified_base 14

FT /*tag= c

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

FT misc_binding 43. .45

FT /*tag= d

FT /bound_moiety= "Nucleotides 3-1 of SEQ ID 15"

FT /note

FT modified_base 44

FT /*tag= e

FT /mod_base= OTHER

FT /note= "Non-nucleosidic cross-linking moiety"

XX US2004152118-A1.

XX 05-AUG-2004.

XX 27-JAN-2004; 2004US-00766266.

XX 29-JAN-2003; 2003US-0443820P.

XX (VATT)/ VAN ATTA R B.

XX (WOOD)/ WOOD M L.

XX Van Atta RB, Wood ML;

XX WPI; 2004-592583/57.

DR Probe set useful for detecting genetic polymorphism in target nucleic

XX acid suspected of containing polymorphism, comprises first flanking

FT probe, capture probe and second flanking probe.

XX Claim 16; SEQ ID NO 17; 31pp; English.

XX The invention relates to a probe set for detecting genetic polymorphisms

CC in target nucleic acids suspected of containing the polymorphisms,

CC comprising a first flanking probe comprising a sequence complementary to

CC a first portion of the nucleic acid sequence, a capture probe comprising

CC a sequence complementary to a second portion of the nucleic acid sequence

CC (the second portion comprising the location of the polymorphism, and

CC being adjacent to the first portion) and a second flanking probe

CC comprising sequence complementary to a third portion of target nucleic

CC acid sequence. The probes further comprise stem regions at the 3' and

CC 5' ends which can form non-covalent bonds with the stem regions of

CC adjacent probes and contain a photoactivatable cross-linking agent. Also

CC included is detecting a genetic polymorphism in a nucleic acid sequence

CC of a target nucleic acid suspected of containing the polymorphism,

CC comprising combining, in a hybridising medium, a nucleic acid sample

CC having the target and several probes, where several probes comprises the

CC probe set above, and comparing the degree of hybridisation of the capture

CC probe to the sequence portion containing the polymorphism to the

CC hybridisation of a capture probe to the target sequence lacking the

CC polymorphism, where the polymorphism is determined. The probe set

CC comprises an additional capture probe which is complementary to the

CC normal nucleic acid sequence of the second portion lacking the

CC polymorphism and a reporter moiety comprising a detectable label. The

CC probe is useful for detecting a genetic polymorphism in a nucleic acid

CC sequence of a target nucleic acid suspected of containing the

CC polymorphism, such as a single nucleotide polymorphism, a point mutation

CC (G1691A) in the Factor V gene, and a point mutation (C187G) or (G845A) in

CC the HFE gene (hereditary haemochromatosis). The probe set diminishes the

CC constraints imposed upon capture probe design, alleviates the need for

CC

CC the cross-linking site near the single nucleotide polymorphism (SNP) site

CC in the target sequence, provides more sites for introducing detectable

CC labels, and permits cross-linking in the stem to include reactions

CC between pairs of unnatural nucleotide analogues, thus expanding the

CC available option from which to select an appropriate choice of reactants.

CC The probe set enables detection of a genetic polymorphism with increased

CC sensitivity and improved data reliability and allows for high-stringency

CC washes of the hybridised probe-target complexes, which significantly

CC lower background contamination levels and result in improvements in the

CC signal-to-noise ratio. The present sequence is a flanking probe for a

CC probe set of the invention.

XX

SQ Sequence 45 BP; 11 A; 12 C; 11 G; 8 T; 0 U; 3 Other;

Query Match 50.0%; Score 15; DB 13; Length 45;

Best Local Similarity 78.3%; Pred. No. 9.6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGAATTGCGGAGCCAGCGCA 24

DB 21 GGAGTTGCGGGCTCCACAGGCA 43

RESULT 39

AAT62767

ID AAT62767 standard; DNA; 27 BP.

XX AC AAT62767;

XX 03-JUN-1997 (first entry)

DE Human bax gene forward primer.

XX

XX p53 responsive element; p53-REU; bax gene; apoptosis; cell death; stroke;

KW cancer; tumour suppressor; polymerase chain reaction; PCR; primer; ss.

XX OS Synthetic.

XX WO9519367-A1.

XX 20-JUL-1995.

XX 12-JAN-1995; 95WO-US0000710.

XX 14-JAN-1994; 94US-00182619.

XX 27-OCT-1994; 94US-00330535.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Reed JC, Miyashita T, Harigai M, Hanada M;

XX WPI; 1995-263824/34.

XX p53 responsive element(s) for down-regulation of bcl-2 gene and up-

FT regulation of bax gene - and identification of agent(s) useful to

XX modulate cell death, e.g. cancer or stroke.

XX Example ID; Page 24; 69pp; English.

XX A forward primer (AAT62767) including an EcoRI linker sequence and a

CC reverse primer (AAT62768) were used to amplify the entire open reading

CC frame of bax cDNA using RT-PCR. The PCR product was used as a bax-

CC specific hybridisation probe to detect Bax mRNA levels in murine myeloid

CC leukaemia M1 cells following transfection with a plasmid encoding a temp.

CC suppressor p53 tumour suppressor. The results indicated that p53 tumour

CC suppressor increases the expression of Bax mRNA. A p53 responsive

CC element, p53-REU, has been identified in the human bax promoter (see also

CC AAT62760)

XX

SQ Sequence 27 BP; 4 A; 5 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 49.3%; Score 14.8; DB 2; Length 27;

Best Local Similarity 73.1%; Pred. No. 1.1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTGCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTGCGGAGCCAGCGGCACTG 26
|||||

RESULT 40

AAT03167
ID AAT03167 standard; DNA; 27 BP.
XX
AC AAT03167;
XX
DT 05-JUN-1996 (first entry)
XX
DE Human Bax gene forward PCR primer.
XX
KW Mcl-1; Bax; apoptosis; cell death; regulation; Bcl-2; novel; detection;
KW ss.
XX
OS Synthetic.
XX
PN W09528497-A1.
XX
PD 26-OCT-1995.
XX
PF 12-APR-1995; 95WO-US004600.
XX
PR 13-APR-1994; 94US-00226876.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Reed JC, Sato T;
XX
DR WPI; 1995-373811/48.
XX

PT Detection of novel proteins involved in apoptosis - by interaction with
PT proteins involved in apoptosis.
XX

PS Example 1; Page 23; 62pp; English.

XX AAT03167 and AAT03168 are primers used for the amplification of the human
CC Bax gene. The Bax gene is used in a new method for identifying novel
CC proteins involved in apoptosis. The method involves contacting a suspect
CC protein with a protein known to be involved in apoptosis (excluding the
CC Bax protein). Proteins detected using this method can act as upstream
CC activators or downstream effectors of a cellular protein such as Bax
CC which induces apoptosis. If the protein is a Bcl-2 related protein
CC apoptosis levels are decreased due to the protein binding to and
CC inactivating Bax
XX

SQ Sequence 27 BP; 4 A; 5 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 49.3%; Score 14.8; DB 2; Length 27;
Best Local Similarity 73.1%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGAATTGCGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTGCGGAGCCAGCGGCACTG 26
|||||

Search completed: November 18, 2005, 11:52:31
Job time : 209.578 secs

This Page Blank (uspto)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	15.6	52.0	36	8	AZ788496	AZ788496 2M0035E09
2	15.6	52.0	40	8	AZ597065	AZ597065 1M0410N10
C 3	15.6	52.0	50	1	AU104279	AU104279 AU104279
4	14.8	49.3	50	1	AU108041	AU108041 AU108041
5	14.8	49.3	50	1	AU108042	AU108042 AU108042
6	14.8	49.3	50	1	AU108043	AU108043 AU108043
7	14.8	49.3	50	1	AU108044	AU108044 AU108044
C 8	14	46.7	40	1	AA887629	AA887629 nq6b05.s
C 9	14	46.7	48	8	AZ601433	AZ601433 1M0419N11
10	13.8	46.0	41	7	H84363	H84363 YV85C09.s1
C 11	13.6	45.3	26	8	AZ949204	AZ949204 2M0212M04
12	13.6	45.3	50	1	AA643428	AA643428 nu31c03.s
13	13.6	45.3	50	9	CR230947	CR230947 Reverse.s
14	13.4	44.7	48	6	C01535	C01535 HUMGS000853
15	13.4	44.7	50	1	AU102737	AU102737 AU102737
C 16	13.2	44.0	34	1	AG668097	AG668097 AJ668097
C 17	13.2	44.0	34	5	BQ594733	BQ594733 E012441-0
C 18	13.2	44.0	34	8	BZ764154	BZ764154 SALK_1240
C 19	13.2	44.0	34	8	BZ764155	BZ764155 SALK_1240
C 20	13.2	44.0	40	4	BG032379	BG032379 602301364
C 21	13.2	44.0	41	9	CG426236	CG426236 01S0576-0
C 22	13.2	44.0	42	9	HS4275866	AJ275866 Homo sapi
C 23	13.2	44.0	43	1	AA074398	AA074398 zml15f07.s
C 24	13.2	44.0	45	4	BI556158	BI556158 603237933

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 15.6; DB 8; Length 36;
Best Local Similarity 70.0%; Pred. No. 5.8e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGAATTCGCGAGCCAGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 5 GAGAATTGCGCGACCAAGGACATGAAG 34

RESULT 2

AZ597065

LOCUS

1M0410N10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0410N10 R, genomic survey sequence.

ACCESSION

AZ597065

VERSION

AZ597065.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 40)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0410 row: N column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1..40

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0410N10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 15.6; DB 8; Length 40;
Best Local Similarity 70.0%; Pred. No. 5.8e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCGAATTCGCGAGCCAGCGCACTGAAG 30
||||| ||||| ||||| ||||| |||||
Db 3 GCGAATTCAGTAACCCACGCTAGGGAG 32

RESULT 3

AUI04279/c

LOCUS

AUI04279 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HBP20593, mRNA sequence.

ACCESSION

AUI04279

VERSION

AUI04279.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

AUTHORS

Suzuki, Y., Taiba, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HEP20593"

/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 52.0%; Score 15.6; DB 1; Length 50;

Best Local Similarity 81.8%; Pred. No. 5.9e+04;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 GCGAGCCAGCGCGCACTGAAG 30

||||| ||||| ||||| ||||| |||||

Db 43 GCGAGCGCGAGGGCAGCTAAG 22

RESULT 4
 AUI08041
 LOCUS AUI08041 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION AUI08041 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV61366, mRNA sequence.

ACCESSION AUI08041
 VERSION AUI08041 GI:13557563
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.,

Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES Location/Qualifiers

source

1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV61366"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;

Best Local Similarity 88.9%; Pred. No. 1.3e+05;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 9 GCGGAGTCAGCGGCCT 26

RESULT 5

AUI08042

LOCUS AUI08042 50 bp mRNA linear EST 28-JAN-2004

DEFINITION AUI08042 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV61783, mRNA sequence.

ACCESSION AUI08042

VERSION AUI08042

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.,

Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

source

1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV61783"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;

Best Local Similarity 88.9%; Pred. No. 1.3e+05;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 9 GCGGAGTCAGCGGCCT 26

RESULT 6

AUI08043

LOCUS AUI08043 50 bp mRNA linear EST 28-JAN-2004

DEFINITION AUI08043 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 ZRV62110, mRNA sequence.

ACCESSION AUI08043

VERSION AUI08043

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.,

Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

source

1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRV62110"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 49.3%; Score 14.8; DB 1; Length 50;

Best Local Similarity 88.9%; Pred. No. 1.3e+05;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGGAGCCAGCGGCCT 26

DB 11 GCGGAGTCAGCGGCCT 28

RESULT 7

```

AUI08044
LOCUS      AUI08044      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI08044 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            ZRV6CS16, mRNA sequence.
ACCESSION  AUI08044
VERSION     AUI08044.1 GI:13557566
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL     21270072
MEDLINE     11375929
PUBMED      Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 88.9%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9  GCGGAGCCAGACGGCACT 26
        ||||| ||||| ||||| |||||
Db      11 GCGGAGTCAGACGGCGCT 28

RESULT 8
AA887629/c
LOCUS      AA887629      40 bp      mRNA      linear      EST 07-APR-1998
DEFINITION nq36b05.s1 NCI CGAP Col10 Homo sapiens cDNA clone IMAGE:1160145 3'
            similar to TR:Q62381 Q62381 TOLL01D-LIKE ;, mRNA sequence.
ACCESSION  AA887629
VERSION     AA887629.1 GI:3003304
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 40)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

```

```

www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 797 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source           1..40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="IMAGE:1160145"
                     /tissue_type="colon tumor RER+"
                     /lab_host="DH10B"
                     /clone_lib="NCI CGAP Col10"
                     /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     RER+ colon tumor, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector. Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo (N-Soares4)."
ORIGIN
Query Match      46.7%; Score 14; DB 1; Length 40;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1  GCGAATTCGCGAGCCAGACGGCACTGAAG 30
        ||||| ||||| ||||| ||||| |||||
Db      36 GGGTAGTTGAGGGCCAGCGCGGCTGTAG 7

RESULT 9
AZ601433/c
LOCUS      AZ601433      48 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION IM0419N1LR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0419N11 R, genomic survey sequence.
ACCESSION  AZ601433
VERSION     AZ601433.1 GI:11723623
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 48)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0419 row: N column: 11
            Seq primer: CACACAGGAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
     source           1..48
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"

```

```
/clone="UUGC1M0419N11"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

```
Query Match 46.7%; Score 14; DB 8; Length 48;
Best Local Similarity 77.3%; Pred. No. 2.8e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 GCGAATTCGGAGCCAGCAGCG 22
||||| | | | | | | | | |
Db 40 GCGAAGGCACACAGCAGCAGCG 19
```

RESULT 10

```
H84363
LOCUS
DEFINITION
H84363 41 bp mRNA linear EST 13-NOV-1995
IMAGE:249520 3' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12
(HUMAN); mRNA sequence.
```

```
ACCESSION H84363
VERSION H84363.1 GI:1063034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```

```
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lannon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
```

```
TITLE
JOURNAL
COMMENT High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
```

```
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: Pronega -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="mRNA"
```

FEATURES

source

```
/db_xref="GDB:3867236"
/db_xref="taxon:9606"
/clone="IMAGE:249520"
/sex="Male"
/tissue type="melanocyte"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares melanocyte 2NbHM"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGGAGCGCGCCAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
```

ORIGIN

```
Query Match 46.0%; Score 13.8; DB 7; Length 41;
Best Local Similarity 88.2%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 9 GCGGAGCCAGCAGCGCAC 25
||||| | | | | | | | | |
Db 1 GCAGAGGCGAGCAGCGCAC 17
```

RESULT 11

```
AZ949204/c
LOCUS
DEFINITION
AZ949204 26 bp DNA linear GSS 27-APR-2001
Clone UUGC2M0212M04 R, genomic survey sequence.
```

```
ACCESSION AZ949204
VERSION AZ949204.1 GI:13820431
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

```
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
```

```
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: M column: 04
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
```

JOURNAL

COMMENT

```
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212M04"
/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
```

FEATURES

source


```

RESULT 20
BG032379
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    BG032379
    602301364F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403174 5',
    mRNA sequence.
    BG032379
    BG032379.1 GI:12423624
    EST.
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 40)
    NIH-MGC http://mgs.nci.nih.gov/
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgabbs@mail.nih.gov
    Tissue Procurement: DCTD/DTF
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM1012 row: o column: 15
    High quality sequence stop: 40.
    Location/Qualifiers
    1..40
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:4403174"
    /tissue_type="mammary adenocarcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_87"
    /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
    Average insert size 1.383 kb. Library enriched for
    full-length clones and constructed by Life Technologies.
    Note: this is a NIH_MGC Library."

ORIGIN
Query Match 44.0%; Score 13.2; DB 4; Length 40;
Best Local Similarity 69.2%; Pred. No. 6e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 ATTCCGGAGCCAGCGGACCTGAAG 30
DB 3 ATTCCGAGATGACGGCGCTCGGATG 28

RESULT 21
CG426236/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    CG426236
    0150576-07C1-G08 UniformMu MutTail Library Zea mays genomic clone
    0150576-07C1-G08, genomic survey sequence.
    CG426236
    CG426236.1 GI:34734716
    GSS.
    Zea mays
    Zea mays
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
    1 (bases 1 to 41)
    Lathaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
    Sequence tagged transposon insertions from the UniformMu maize
    population
    Unpublished (2003)
    Contact: Donald R. McCarty

ORIGIN
Query Match 44.0%; Score 13.2; DB 9; Length 42;
Best Local Similarity 78.9%; Pred. No. 6e+05;

```

```

Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmu@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
0150576-07, Primer set: C
Class: transposon insertion site.
FEATURES
Location/Qualifiers
1..41
/organism="Zea mays"
/mol_type="genomic DNA"
/strains="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="0150576-07C1-G08"
/clone_lib="UniformMu MutTail Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match 44.0%; Score 13.2; DB 9; Length 41;
Best Local Similarity 83.3%; Pred. No. 6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ATTCCGGAGCCAGCGG 22
DB 38 AGTCGTGGAGCCAGACAG 21

RESULT 22
HSA275866
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
    HSA275866
    Homo sapiens DNA for trapped exon, clone j1A63F10, genomic survey
    sequence.
    AJ275866
    AJ275866.1 GI:6562523
    GSS; genome survey sequence.
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1
    Blouin,J.L., Duriaux Sail,G., Rossier,C. and Antonarakis,S.E.
    Isolation of portion of gene that map on chromosome 21q22 by exon
    trapping
    Unpublished
    2 (bases 1 to 42)
    Blouin,J.L.C.
    Direct Submission
    Submitted (07-DEC-1999) Blouin J.L.C., Medical Genetics, University
    Hospital and School of Medicine of Geneva, 1 rue Michel-Servet,
    1211 GENEVA, SWITZERLAND
    Location/Qualifiers
    1..42
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="21"
    /map="21q22"
    /clone="j1A63F10"
    /clone_lib="LL21NC02-Q"
    1..42
    /note="trapped"

ORIGIN
Query Match 44.0%; Score 13.2; DB 9; Length 42;
Best Local Similarity 78.9%; Pred. No. 6e+05;

```

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 CGGAGCCGAGCGGCACTGA 28
||||| ||||| |||||
Db 19 CGGAGACAGAGNTCACTGA 37

RESULT 23

AA074398/c

LOCUS

DEFINITION

AA074398 43 bp mRNA linear EST 23-DEC-1997
zmlf07.s1 Stragatene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:525829 3' similar to TR:G1136430 G1136430 KIAA0185 PROTEIN ; ,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AA074398.1 GI:1614329
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 43)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevasaki, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 1400 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3917258"
/db_xref="taxon:9606"
/clone="IMAGE:525829"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene pancreas (#937208)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTGTGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

0; Mismatches

8; Indels

0; Gaps

0;

Qy 2 GGAATTCGCGAGCGGCACTG 27
||||| ||||| ||||| |||||

Db

RESULT 24

BI556158

LOCUS

DEFINITION

BI556158 45 bp mRNA linear EST 05-SEP-2001
603237933F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5290664 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI556158.1 GI:15443472
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11735 row: b column: 09
High quality sequence stop: 45.
Location/Qualifiers

FEATURES

source

1. .45

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129.C57BL/6J.FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5290664"

/issue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

0; Mismatches

8; Indels

0; Gaps

0;

Qy 2 GGAATTCGCGAGCGGCACTG 27
||||| ||||| ||||| |||||

Db 18 GGTCCTCGCGAGCGGCGCTCG 43
||||| ||||| ||||| |||||

RESULT 25

AU107457

LOCUS

DEFINITION

AU107457 50 bp mRNA linear EST 28-JAN-2004
AU107457 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
NBLAN24NF, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AU107457.1 GI:13556978
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NBLAN24NF"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GAATTCGGGAGCCAGCGGCACTGA 28
|||||
Db 1 GAAGACGCCGCCAGACAGCACAGA 26
|||||

RESULT 26
AUI08040
LOCUS
DEFINITION
AUI08040 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNG09859, mRNA sequence.
ACCESSION
AUI08040
VERSION
AUI08040.1 GI:13557562
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG09859"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.0%; Score 13.2; DB 1; Length 50;

Best Local Similarity 83.3%; Pred. No. 6.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 GCGGAGCCAGACGGCACT 26
|||||
Db 11 GCGGAGTGAGACGGCGCT 28
|||||

RESULT 27
AZ666536
LOCUS
DEFINITION
AZ666536
VERSION
AZ666536.1 GI:11803682
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: D column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
FEATURES
source
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0548D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 44.0%; Score 13.2; DB 8; Length 50;

```

Best Local Similarity 69.2%; Pred. No. 6.1e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGGATTTCGGAGCGCAGCGCACT 26
Db 7 GGGTATTCATGAGCGCAGCAACT 32

RESULT 28
AA776443/c
LOCUS
DEFINITION
  36 bp mRNA linear EST 05-FEB-1998
  zj50h10.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
  clone IMAGE:453763 3' similar to gb|U28107|TRRRRH Trichoderma
  reesei 25S ribosomal (rRNA); mRNA sequence.
ACCESSION
  AA776443
VERSION
  AA776443.1 GI:2835777
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 36)
  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
  Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
  Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
  Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
  WashU-NCI human EST Project
  Unpublished (1997)
  Contact: wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Seq primer: -40m13 fwd ET from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..36
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:1390119"
      /db_xref="taxon:9606"
      /clone="IMAGE:453763"
      /sex="male"
      /dev_stage="20 week-post conception fetus"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares fetal liver spleen INFLS S1"
      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
      with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
      This is a subcloned version of the original Soares fetal
      liver spleen INFLS library. 1st strand cDNA was primed
      with a Pac I - oligo(dT) primer [5'
      AACTGGAGATTAATTAAGACTCTTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Pac I and cloned into the Pac I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization. Library
      constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
  Query Match 43.3%; Score 13; DB 1; Length 36;
  Best Local Similarity 65.5%; Pred. No. 7.3e+05;
  Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGGATTTCGGAGCGCAGCGCACTGAG 30
Db 31 GGGCTTCGGGAATACGCGGGGAAAGAG 3

RESULT 29
AU223982/c
LOCUS
DEFINITION
  38 bp mRNA linear EST 21-OCT-2002
  AU223982 Ipomoea trifida anther Ipomoea trifida cDNA clone
  IAM-0341, mRNA sequence.
ACCESSION
  AU223982
VERSION
  AU223982.1 GI:24206955
KEYWORDS
  EST.
SOURCE
  Ipomoea trifida
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.
  1 (bases 1 to 38)
  Tsuchiya,T., Ando,A., Ogawa,C., Futagami,K., Watase,T. and
  Kowayama,Y.
  Expressed Sequence Tags from Reproductive Organs of Ipomoea trifida
  cDNA Libraries
  Unpublished (2002)
  Contact: Tohru Tsuchiya
  Faculty of Bioreources
  Mie University
  1515 Kamihama, Tsu, Mie 514-8507, Japan
  Tel: 81-59-231-9515
  Fax: 81-59-231-9515
  Email: tsuchiya@bio.mie-u.ac.jp.
  Location/Qualifiers
    1..38
      /organism="Ipomoea trifida"
      /mol_type="mRNA"
      /db_xref="taxon:35884"
      /clone="IAM-0341"
      /tissue_type="anther"
      /dev_stage="tri-nucleate pollen stage"
      /clone_lib="Ipomoea trifida anther"
ORIGIN
  Query Match 43.3%; Score 13; DB 1; Length 38;
  Best Local Similarity 65.5%; Pred. No. 7.3e+05;
  Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGCGAGCCAGCGCACTGAA 29
Db 32 GCGAATTCGGCGCGCTAGCGCGCGGAA 4

RESULT 30
BX230810
LOCUS
DEFINITION
  46 bp DNA linear GSS 29-JAN-2003
  Danio rerio genomic clone DKEY-54G22, genomic survey sequence.
ACCESSION
  BX230810
VERSION
  BX230810.1 GI:28064960
KEYWORDS
  GSS.
SOURCE
  Danio rerio (zebrafish)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 46)
  Humphray,S.J., Huckle,E. and Durham,J.L.
  Direct Submission
  Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
  Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humphray@sanger.ac.uk Unpublished
  This sequence was generated from the SP6 end of BAC 54G22. 54G22 is
  part of the Daniokey BAC Library created by R. Plasterk and N.V.
  Keygene. Further details:
  http://www.sanger.ac.uk/Projects/D_rerio/.
  Location/Qualifiers
    1..46
      /organism="Danio rerio"
      /mol_type="genomic DNA"
      /db_xref="taxon:7955"
      /clone="DKEY-54G22"
      /tissue_type="Testis"

```

```

ORIGIN
Query Match      43.3%; Score 13; DB 9; Length 46;
Best Local Similarity 76.2%; Pred. No. 7.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 10 CGGAGCCAGCGGCACTGAAG 30
    |||||
Db 12 CGCCCCAGACTGCACAGAG 32

RESULT 31
AUI03141
LOCUS
DEFINITION
AUI03141 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT03715, mRNA sequence.
ACCESSION
AUI03141
VERSION
AUI03141.1 GI:13552662
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 65.5%; Pred. No. 7.4e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCGCACTGAAG 30
    |||||
Db 21 GGACTTCGAGTAGGACACAGGACGGAAG 49

RESULT 33
AUI06584/c
LOCUS
DEFINITION
AUI06584 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT03468, mRNA sequence.
ACCESSION
AUI06584
VERSION
AUI06584.1 GI:13556105
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 8 CGCGAGCCAGCGGCACTGA 28
    |||||
Db 13 CTCGAGCAGGACTGCACGGA 33

RESULT 32
AUI05783
LOCUS
DEFINITION
AUI05783 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP13475, mRNA sequence.
ACCESSION
AUI05783
VERSION
AUI05783.1 GI:13555304
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 50)

```

```

Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      5 ATTGCGGAGCGCAGCGGCAC 25
        |||||
Db      48 AATGCGGAGCCATCAGCTC 28

RESULT 34
AUI06592/c
LOCUS
DEFINITION AUI06592 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT07173, mRNA sequence.
ACCESSION AUI06592
VERSION AUI06592.1 GI:13556113
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
        Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
        Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
        mapping of mRNA start sites
JOURNAL ENBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
        Department of Virology
        Institute of Medical Science, University of Tokyo
        4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
        Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="KAT09005"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 GGAATTCGCGGAGCGCAGCGCTGAAG 30
        |||||
Db      14 GGCAGCCCCGAGCCCCAGCGCGTTAAG 42

RESULT 35
CG894749
LOCUS
DEFINITION CG894749 50 bp DNA linear GSS 08-DEC-2003
            03S4734-00A1-C06 UniformMu MUTAIL Library Zea mays genomic clone
            03S4734-00A1-C06, genomic survey sequence.
ACCESSION CG894749
VERSION CG894749.1 GI:39550244
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 50)
AUTHORS Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
        population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
        Plant Molecular and Cellular Biology Program
        University of Florida
        PO 110690 Gainesville, FL 32611-0690, USA
        Tel.: 352-392-1928 x322
        Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
03S4734-00, Primer set: A
Class: transposon insertion site.
FEATURES
source
1..50
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone_lib="03S4734-00A1-C06"
/clone_lib="UniformMu MUTAIL Library"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
        insertions in Mu inactive lines were extracted from the
        UniformMu maize population by the thermo asymmetric
        interlaced PCR (TAIL) protocol using primers specific for

```

```

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
ENBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
        Department of Virology
        Institute of Medical Science, University of Tokyo
        4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
        Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="KAT09005"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      43.3%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 GGAATTCGCGGAGCGCAGCGCTGAAG 30
        |||||
Db      14 GGCAGCCCCGAGCCCCAGCGCGTTAAG 42

RESULT 36
CG894749
LOCUS
DEFINITION CG894749 50 bp DNA linear GSS 08-DEC-2003
            03S4734-00A1-C06 UniformMu MUTAIL Library Zea mays genomic clone
            03S4734-00A1-C06, genomic survey sequence.
ACCESSION CG894749
VERSION CG894749.1 GI:39550244
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 50)
AUTHORS Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize
        population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
        Plant Molecular and Cellular Biology Program
        University of Florida
        PO 110690 Gainesville, FL 32611-0690, USA
        Tel.: 352-392-1928 x322
        Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
03S4734-00, Primer set: A
Class: transposon insertion site.
FEATURES
source
1..50
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone_lib="03S4734-00A1-C06"
/clone_lib="UniformMu MUTAIL Library"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
        insertions in Mu inactive lines were extracted from the
        UniformMu maize population by the thermo asymmetric
        interlaced PCR (TAIL) protocol using primers specific for

```


the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 43.3%; Score 13; DB 9; Length 50;
Best Local Similarity 76.2%; Pred. No. 7.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 AATTCGGAGCGCAGCGCA 24
|||||
Db 8 ACTTGTGGAGCAACGGTA 28
|||||

RESULT 37

AJ042471/c

LOCUS 33 bp mRNA linear EST 24-SEP-1998
DEFINITION oyl4d01.x1 Soares senescent_fibroblasts NbHSF Homo sapiens cDNA
clone IMAGE:1665793 3' similar to TR:Q99490 Q99490 KIAA0167
PROTEIN. [1] ; mRNA sequence.

ACCESSION AJ042471 GI:3281665

VERSION AJ042471.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 33)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1518 Std Error: 0.00

Seq primer: -40m13 fwd ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1..33

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1665793"

/tissue_type="senescent fibroblast"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares senescent fibroblasts NbHSF"

/note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCCATTTTTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 42.7%; Score 12.8; DB 1; Length 33;

Best Local Similarity 70.8%; Pred. No. 8.9e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTCGGAGCGCAGCGCACTG 27
|||||

31 AACTGCCAGCCATCTCGCGGTG 8
|||||

Db

RESULT 38

BT547045

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BT547045

VERSION

BT547045.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

(human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 38)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11659 row: i column: 18

High quality sequence stop: 38.

Location/Qualifiers

1..38

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5261657"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/notes="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTN-3', size-selected for average

insert size 2.5 kb and normalized to 10⁵. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIMH/NHGRI, National Institutes of Health). Note: this

is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity

Matches 14; Conservative

Mismatches 0; Gaps 0;

Qy 1 GGGAAATCGCGGAGCC 16
|||||

20 GGGAAATCGCGGAGCC 35
|||||

Db

RESULT 39

BT547045

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BT547045

VERSION

BT547045.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

(human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: L1A11575 Row: g Column: 05
High quality sequence stop: 41.
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5228572"
/lab_host="DH10B"
/clone_lib="NIH_MGC 120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.7%; Score 12.8; DB 4; Length 41;
Best Local Similarity 87.5%; Pred. No. 8.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 GCGGAGCGACGCGCA 24
| | | | | | | | | |
Db 18 GGGGAGCGACGCGCA 33

RESULT 40
BX121769
LOCUS BX121769 41 bp DNA linear GSS 28-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-59P11, genomic survey sequence.
ACCESSION BX121769
VERSION BX121769.1 GI:27952695
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 41)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 59P11. 59P11 is
part of the Daniokey BAC Library created by R. Piasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1..41
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-59P11"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"

FEATURES

source
1..41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5228572"
/lab_host="DH10B"
/clone_lib="NIH_MGC 120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

Query Match 42.7%; Score 12.8; DB 9; Length 41;
Best Local Similarity 70.8%; Pred. No. 8.9e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGAATTCGGGAGCCGACGCGCA 24
| | | | | | | | | |
Db 9 GAGAAAACGAAGAGCGCAGCCGCGCA 32

Search completed: November 18, 2005, 21:12:51
Job time : 1437.98 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 58.289 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: us-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATTCGGGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgm2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgm2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1	US-07-989-160-7
2	17.2	57.3	31	3	US-09-113-750A-46
3	16.2	54.0	23	2	US-08-479-614-20
4	16.2	54.0	23	2	US-09-159-385-5
5	16.2	54.0	23	3	US-09-186-277-5
6	16.2	54.0	38	2	US-08-403-852D-42
7	16.2	54.0	38	3	US-08-510-646B-44
8	16.2	54.0	38	3	US-09-231-818-42
9	16.2	54.0	38	4	US-09-635-359B-42
10	15.2	50.7	33	3	US-08-984-277-3
11	15.2	50.7	33	4	US-09-759-112A-3
12	15	50.0	31	1	US-08-368-803-26
13	15	50.0	31	2	US-08-578-096A-27
14	15	50.0	31	3	US-09-240-426-27
15	14.8	49.3	26	4	US-08-997-685A-26
16	14.8	49.3	27	1	US-08-182-619-8
17	14.8	49.3	27	1	US-08-330-535A-8
18	14.8	49.3	27	1	US-08-607-289-4
19	14.8	49.3	27	1	US-08-607-289-12
20	14.8	49.3	27	1	US-08-688-145-4
21	14.8	49.3	27	1	US-08-616-732A-1
22	14.8	49.3	27	2	US-08-838-844-8
23	14.8	49.3	27	3	US-09-037-742B-1
24	14.8	49.3	27	5	PCT-US95-04600-4
25	14.8	49.3	27	5	PCT-US95-04600-12
26	14.8	49.3	30	1	US-07-642-734C-25
27	14.8	49.3	30	3	US-08-439-009A-25

28	14.6	48.7	25	4	US-09-396-196G-68463	Sequence 68463, A
29	14.6	48.7	50	4	US-09-443-199C-940	Sequence 940, A
30	14.4	48.0	25	4	US-09-396-196G-68465	Sequence 68465, A
c 31	14.4	48.0	44	4	US-09-410-935B-15	Sequence 15, Appl
c 32	14.4	48.0	44	4	US-09-784-403A-15	Sequence 15, Appl
c 33	14.4	48.0	50	3	US-08-951-200A-3	Sequence 3, Appl
34	14.2	47.3	39	1	US-08-253-155A-88	Sequence 88, Appl
35	14.2	47.3	39	1	US-08-625-209A-17	Sequence 17, Appl
36	14.2	47.3	39	3	US-08-853-733B-17	Sequence 17, Appl
c 37	14.2	47.3	47	4	US-09-422-978-3058	Sequence 3058, Ap
38	14	46.7	30	2	US-08-821-782-8	Sequence 8, Appli
39	14	46.7	30	2	US-08-821-782-24	Sequence 24, Appl
40	14	46.7	30	3	US-09-292-435A-8	Sequence 8, Appli
41	14	46.7	30	3	US-09-292-435A-24	Sequence 24, Appl
c 42	14	46.7	33	1	US-08-170-290A-52	Sequence 52, Appl
c 43	14	46.7	33	3	US-09-198-723A-73	Sequence 73, Appl
c 44	14	46.7	33	3	US-09-198-723A-74	Sequence 74, Appl
c 45	14	46.7	33	4	US-09-684-881-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-07-989-160-7
; Sequence 7, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-07-989-160-7

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAAATTCGGGAGCCAGCGCACTGAAG 30
|||||

```
Db      1  GGGAAATTCGGAGCGCAGCGCACTGAAG 30

RESULT 2
US-09-113-750A-46
; Sequence 46, Application US/09113750A
; Patent No. 6294176
; GENERAL INFORMATION:
; APPLICANT: David E. Junker and Mark D. Cochran
; TITLE OF INVENTION: Recombinant Raccoonpox virus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,750A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 55744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)262-0400
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic
; US-09-113-750A-46

Query Match      57.3%; Score 17.2; DB 3; Length 31;
Best Local Similarity 73.3%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1  GGGAAATTCGGAGCGCAGCGCACTGAAG 30
        |||||
Db      2  GGGAAATTCCTATCGCGTACGCGCACTGAGG 31

RESULT 3
US-08-479-614-20
; Sequence 20, Application US/08479614
; Patent No. 5861294
; GENERAL INFORMATION:
; APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N.,
; APPLICANT: Kerwin, Jr., James F., McNally, Teresa
; TITLE OF INVENTION: Adenosine Kinase Polypeptides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: D-377 AP6D, 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System 7.1
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,614
; FILING DATE: June 7, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5749 US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-4884
; TELEFAX: (708) 938-2623
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-479-614-20

Query Match      54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  GAATTCGGAGCGCAGCAGCGC 23
        |||||
Db      1  GAATTCGTGGAGCCAAACCGC 21

RESULT 4
US-09-159-385-5
; Sequence 5, Application US/09159385
; Patent No. 5958748
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: PH-569
; CURRENT APPLICATION NUMBER: US/09/159,385
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotides
; US-09-159-385-5

Query Match      54.0%; Score 16.2; DB 2; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GGGAAATTCGGAGCGCAGCAGC 21
        |||||
Db      1  GGGAAATTCGGAGCGCAGCAGG 21

RESULT 5
US-09-186-277-5
; Sequence 5, Application US/09186277
```

; Patent No. 6171841
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: 081356/0128
; CURRENT APPLICATION NUMBER: US/09/186,277
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-186-277-5

Query Match 54.0%; Score 16.2; DB 3; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGC 21
Db 1 GGGAAATTCGGGAGCCAGGAGG 21

RESULT 6

US-08-403-852D-42
; Sequence 42, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,852D
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-00000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-852D-42

Query Match 54.0%; Score 16.2; DB 2; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGCAGC 27
Db 11 GSGAGTTTCGCGCGCTGGGAGCGCACCG 37

RESULT 7

US-08-510-646B-44
; Sequence 44, Application US/08510646B
; Patent No. 6077699
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03806.0054-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-510-646B-44

Query Match 54.0%; Score 16.2; DB 3; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37

RESULT 8

US-09-231-818-42
; Sequence 42, Application US/09231818
; Patent No. 6171846

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231.818
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403.852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PC7/FR 93/00923
FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-231-818-42

Query Match 54.0%; Score 16.2; DB 3; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37

RESULT 9

US-09-635-359B-42
; Sequence 42, Application US/09635359B
; Patent No. 6670157

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635.359B
FILING DATE: 09-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/231.818
FILING DATE: 15-JAN-1999
APPLICATION NUMBER: US 08/403.852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PC7/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-635-359B-42

Query Match 54.0%; Score 16.2; DB 4; Length 38;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGCACTG 27
|:|||||:|:|
Db 11 GSGAGTTCCGCGCGTGGGACGCGCACCG 37


```
; Patent No. 5980906
; GENERAL INFORMATION:
; APPLICANT: Avian herpesvirus-based live recombinant
; TITLE OF INVENTION: avian vaccine
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578.096A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-578-096A-27

Query Match 50.0%; Score 15; DB 2; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGAGCCAGCGGCAC 25
Db 6 GAATTCGGAGAGAGAGGAAC 28

RESULT 14
US-09-240-426-27
; Sequence 27, Application US/09240426
; Patent No. 6045803
; GENERAL INFORMATION:
; APPLICANT: Avian herpesvirus-based live recombinant
; TITLE OF INVENTION: avian vaccine
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,426
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,096
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-09-240-426-27

Query Match 50.0%; Score 15; DB 3; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GAATTCGGAGCCAGCGGCAC 25
Db 6 GAATTCGGAGAGAGAGGAAC 28

US-08-598-096A-26
; Patent No. 5980906
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 26
; TYPE: DNA
; ORGANISM: mouse;
; US-08-997-685A-26

Query Match 49.3%; Score 14.8; DB 4; Length 26;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ATTGCGGAGCCAGCGGCACCTGAAG 30
Db 1 ATGTTCCGAGCCAGAGCGGTGGAG 26

RESULT 16
US-08-182-619-8
; Sequence 8, Application US/08182619
; Patent No. 5484710
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN
; TITLE OF INVENTION: CELL DEATH
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,619
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9867
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-182-619-8

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```


Qy 2 GGAATTCGGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 17

US-08-330-535A-8
; Sequence 8, Application US/08330535A
; Patent No. 5659024
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Horigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
; TITLE OF INVENTION: DEATH
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; STREET: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330.535A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,619
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 18

US-08-607-269-4
; Sequence 4, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-607-269-4

Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCGGCACTG 27
|||||
Db 1 GGAATTCGGGTGATGGACGGGTCCG 26

RESULT 19

US-08-607-269-12
; Sequence 12, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:

```
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 9882
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-607-269-12
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 20
US-08-688-145-4
; Sequence 4, Application US/08688145
; Patent No. 5744310
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Promoter Sequence and Screening
; Patent No. 5744310
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,145
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-688-145-4
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 9882
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-607-269-12
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 21
US-08-616-732A-1
; Sequence 1, Application US/08616732A
; Patent No. 5770690
; GENERAL INFORMATION:
; APPLICANT: Bitler, Catherine Mastroni
; APPLICANT: Bowersox, Stephen Scott
; APPLICANT: Crea, Roberto
; APPLICANT: Demo, Susan Dunham
; APPLICANT: Horne, William A.
; APPLICANT: Zhou, Mei
; TITLE OF INVENTION: Bax Omega Protein and Methods
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,732A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/495,042
; FILING DATE: 27-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 5865-0017.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: PCR primer Bax F
US-08-616-732A-1
Query Match 49.3%; Score 14.8; DB 1; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGACGGCACTG 27
Db 1 GGAATTCGCGGTGATGGACGGGTCCG 26

RESULT 22
US-08-838-844-8
; Sequence 8, Application US/08838844
; Patent No. 5908750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
```

;; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
;; TITLE OF INVENTION: DEATH
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell & Flores LLP
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/838,844

;; FILING DATE: 11-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/182,619
;; FILING DATE: 14-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/330,535

;; FILING DATE: 27-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 2520
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)

US-08-838-844-8
Query Match 49.3%; Score 14.8; DB 2; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGGGAGCGGTCG 26

RESULT 23
US-09-037-742B-1
;; Sequence 1, Application US/09037742B
;; Patent No. 6140484
;; GENERAL INFORMATION:
;; APPLICANT: Bitler, Catherine Mastroni
;; APPLICANT: Bowersox, Stephen Scott
;; APPLICANT: Crea, Roberto
;; APPLICANT: Demo, Susan Dunham
;; APPLICANT: Horne, William A.
;; APPLICANT: Zhou, Mei

;; TITLE OF INVENTION: Bax Omega Protein and Methods
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04600
;; FILING DATE: 12-APR-1995

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Imbra, Richard J.
;; REGISTRATION NUMBER: 37,643
;; REFERENCE/DOCKET NUMBER: FP-LJ 1361
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid

;; MOLECULE TYPE: DNA (genomic)

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/037,742B
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/616,732
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sholtz, Charles K.
;; REGISTRATION NUMBER: 38,615
;; REFERENCE/DOCKET NUMBER: 5865-0017.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: PCR primer Bax F

US-09-037-742B-1
Query Match 49.3%; Score 14.8; DB 3; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCGGCACTG 27
Db 1 GGAATTCGGGAGCGGTCG 26

RESULT 24
PCT-US95-04600-4
;; Sequence 4, Application PC/TUS9504600
;; GENERAL INFORMATION:
;; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
;; TITLE OF INVENTION: Interaction of Proteins Involved in
;; TITLE OF INVENTION: a Cell Death Pathway
;; NUMBER OF SEQUENCES: 29
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04600
;; FILING DATE: 12-APR-1995

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Imbra, Richard J.
;; REGISTRATION NUMBER: 37,643
;; REFERENCE/DOCKET NUMBER: FP-LJ 1361
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid

;; MOLECULE TYPE: DNA (genomic)

```
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-04600-4

Query Match          49.3%; Score 14.8; DB 5; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCCGGAGCGACGACGCGACTG 27
    |||||
Db 1 GGAATTCGGGTGATGACGCGGTCG 26

RESULT 25
PCT-US95-04600-12
; Sequence 12, Application PC/TUS9504600
; GENERAL INFORMATION:
; APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
; TITLE OF INVENTION: Interaction of Proteins Involved in
; TITLE OF INVENTION: a Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04600
; FILING DATE: 12-APR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Imbra, Richard J.
; REGISTRATION NUMBER: 37,643
; REFERENCE/DOCKET NUMBER: FP-LJ 1361
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-04600-12

Query Match          49.3%; Score 14.8; DB 5; Length 27;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCGACGACGCGACTG 27
    |||||
Db 1 GGAATTCGGGTGATGACGCGGTCG 26

RESULT 26
US-07-642-734C-25
; Sequence 25, Application US/07642734C
; Patent No. 5824513
; GENERAL INFORMATION:
; APPLICANT: Katz, L
; APPLICANT: Donadio, S
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Recombinant DNA Method for Producing
; TITLE OF INVENTION: Erythromycin Analogs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstein
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
```

```
; ADDRESSEE: Edward H. Gorman
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,734C
; FILING DATE: 17-JAN-91
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M
; REGISTRATION NUMBER: 32652
; REFERENCE/DOCKET NUMBER: 4952.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-9396
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: PCR primer 10b
; US-07-642-734C-25

Query Match          49.3%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCGACGACGCGACTG 27
    |||||
Db 2 GGAATTCGGGTGATGACGCGGACTG 27

RESULT 27
US-08-439-009A-25
; Sequence 25, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polyketides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstein
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
```

REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.D1
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: PCR primer 10b
US-08-439-009A-25

Query Match 49.3%; Score 14.8; DB 3; Length 30;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GGAATTCGGGAGCCAGCAGCGCACTG 27
Db 2 GGAATTCGGTGTGATCGCGGCACTG 27

RESULT 28

US-09-396-196G-68463
Sequence 68463, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68463
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-68463

Query Match 48.7%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CGCGGAGCCAGCAGCGCACTGA 28
Db 1 CCCTTAGCTAGAGCGCACTGA 21

RESULT 29

US-09-443-199C-940
Sequence 940, Application US/09443199C
Patent No. 6670464
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Leach, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
FILE REFERENCE: 15966-534A
CURRENT APPLICATION NUMBER: US/09/443,199C
CURRENT FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/109,024
PRIOR FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 1272
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 940

LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (26)...(0)
NAME/KEY: misc feature
LOCATION: (25)...(26)
OTHER INFORMATION: nucleotide deleted between bases 25 and 26
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number cg43982025
US-09-443-199C-940

Query Match 48.7%; Score 14.6; DB 4; Length 50;
Best Local Similarity 69.0%; Pred. No. 3.9e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGCAGCGCACTGAA 29
Db 2 GGGAGGCGCATATCTTGGCGGACAGCA 30

RESULT 30

US-09-396-196G-68465
Sequence 68465, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68465
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-68465

Query Match 48.0%; Score 14.4; DB 4; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 AGCCAGCAGCGCACTGA 28
Db 4 AGCTAGAGCGCACTGA 19

RESULT 31

US-09-410-935B-15/c
Sequence 15, Application US/09410935B
Patent No. 6504083
GENERAL INFORMATION:
APPLICANT: Barbour, Eric
APPLICANT: EuClaire Meyer, Terry
APPLICANT: Eid Saad, Mohammed
TITLE OF INVENTION: No. 6504083el Maize Promoters
FILE REFERENCE: 5718-72
CURRENT APPLICATION NUMBER: US/09/410,935B
CURRENT FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: US 60/107,201
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/103,294
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 19

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-253-155A-88

Query Match 47.3%; Score 14.2; DB 1; Length 39;
Best Local Similarity 70.4%; Pred. No. 5.7e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCGGAGCGGCACTGA 28
||||| ||||| ||||| ||||| |||||
Db 9 GGAATTCAGGAGGAGCGGCGGCGGA 35

RESULT 35

US-08-625-209A-17
; Sequence 17, Application US/08625209A
; Patent No. 5756671
; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jen0
; APPLICANT: Lamphere, Lou
; TITLE OF INVENTION: Cdc37 Cell-Cycle Regulatory Protein,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,209A
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV048.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-625-209A-17

Query Match 47.3%; Score 14.2; DB 1; Length 39;
Best Local Similarity 70.4%; Pred. No. 5.7e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCGGAGCGGCACTGA 28
||||| ||||| ||||| ||||| |||||
Db 9 GGAATTCAGGAGGAGCGGCGGCGGA 35

RESULT 36

US-08-853-733B-17
; Sequence 17, Application US/08853733B
; Patent No. 6015692
; GENERAL INFORMATION:

; APPLICANT: Gyuris, Jen0

; APPLICANT: Lamphere, Lou
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Cdc37 Cell-Cycle Regulatory Protein,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,733B
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/625,209
; FILING DATE: 10-APRIL-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Paula A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: MIV-048.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)832-1000
; TELEFAX: (617)832-7000
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-853-733B-17

Query Match 47.3%; Score 14.2; DB 3; Length 39;
Best Local Similarity 70.4%; Pred. No. 5.7e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGGAGCGGAGCGGCACTGA 28
||||| ||||| ||||| ||||| |||||
Db 9 GGAATTCAGGAGGAGCGGCGGCGGA 35

RESULT 37

US-09-422-978-3058/c
; Sequence 3058, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Il'ya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CFI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3058
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele

```
; LOCATION: 24
; OTHER INFORMATION: 99-21916-359 : polymorphic base A or G
US-09-422-978-3058

Query Match      47.3%; Score 14.2; DB 4; Length 47;
Best Local Similarity 84.2%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGAGCCAGCGCACTGAA 29
    ||||| ||||| |||||
Db 43 GGAGCCATAGGCACTGCA 25

RESULT 38
US-08-821-782-8
; Sequence 8, Application US/08821782
; Patent No. 5981183
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 61601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,782
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ahern, Paul L.
; REGISTRATION NUMBER: 17020
; REFERENCE/DOCKET NUMBER: 66425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: (25)3533
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
US-08-821-782-8

Query Match      46.7%; Score 14; DB 2; Length 30;
Best Local Similarity 77.3%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TTCCGGAGCGCAGCGCACTG 27
    ||||| ||||| |||||
Db 2 TTGACGGAGCGGACGGCGCTG 23

RESULT 40
US-09-292-435A-8
; Sequence 8, Application US/09292435A
; Patent No. 6303306
; GENERAL INFORMATION:
; APPLICANT: Yutaka, Takarada
; APPLICANT: Hiroaki, Inoue
; APPLICANT: Shuji, Shibata
; APPLICANT: Yoshihisa, Kawamura
; TITLE OF INVENTION: METHOD FOR AMPLIFYING AND DETECTING
; TITLE OF INVENTION: OF TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING THERMOSTABLE ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
```


STATE: Illinois
COUNTRY: USA
ZIP: 61601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM PC
OPERATING SYSTEM: Dos 5.0
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,435A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ahern, Paul L.
REGISTRATION NUMBER: 17020
REFERENCE/DOCKET NUMBER: 66425
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (25)3533
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: Genomic DNA
US-09-292-435A-8

Query Match 46.7%; Score 14; DB 3; Length 30;
Best Local Similarity 77.3%; Pred. No. 6.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 6 TTCGGGAGCCAGCGGCACTG 27
||| ||||| ||||| |||||
Db 2 TTGACGGAGCGGCGGCTG 23

Search completed: November 18, 2005, 11:22:01
Job time : 59.289 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 403.232 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-7

Perfect score: 30

Sequence: 1 GGGAAATCGCGAGCCAGCGCACTGAAG 30

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:**

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-469-172-7	Sequence 7, Appli
2	30	100.0	30	US-10-788-779-7	Sequence 7, Appli
3	18.8	62.7	50	US-10-349-780A-28	Sequence 28, Appl
4	17	56.7	25	US-11-036-317-804897	Sequence 804897,
5	16.4	54.7	25	US-10-956-157-203038	Sequence 203038,

6	16.2	54.0	38	21	US-10-716-803-42	Sequence 42, Appl
7	16.2	54.0	39	15	US-10-123-036-15	Sequence 15, Appl
8	16.2	54.0	39	22	US-10-483-289A-3	Sequence 3, Appli
9	15.8	52.7	25	22	US-10-719-900-439430	Sequence 439430,
10	15.6	52.0	25	16	US-10-098-263B-97474	Sequence 97474, A
11	15.6	52.0	25	16	US-10-098-263B-128306	Sequence 128306,
12	15.6	52.0	25	24	US-10-719-956-258512	Sequence 258512,
13	15.6	52.0	25	24	US-10-719-956-258513	Sequence 258513,
14	15.6	52.0	25	26	US-11-036-317-21919	Sequence 21919, A
15	15.6	52.0	25	26	US-11-036-317-875174	Sequence 875174,
16	15.4	51.3	25	22	US-10-719-900-805772	Sequence 805772,
17	15.4	51.3	25	22	US-10-719-900-844398	Sequence 844398,
18	15.4	51.3	25	26	US-11-036-317-804896	Sequence 804896,
19	15.4	51.3	25	26	US-11-060-756-299133	Sequence 299133,
20	15.4	51.3	34	9	US-09-858-349-14	Sequence 14, Appl
21	15.4	51.3	41	19	US-10-035-833A-1888	Sequence 1888, Ap
22	15.4	51.3	41	19	US-10-035-833A-4483	Sequence 4483, Ap
23	15.2	50.7	24	20	US-10-667-891-24	Sequence 24, Appl
24	15.2	50.7	24	21	US-10-719-900-784963	Sequence 35, Appl
25	15.2	50.7	25	22	US-10-719-956-25613	Sequence 784963,
26	15.2	50.7	25	24	US-10-719-956-25613	Sequence 25613, A
27	15.2	50.7	25	26	US-11-036-317-503091	Sequence 503091,
28	15.2	50.7	25	26	US-11-036-317-61467	Sequence 61467,
29	15.2	50.7	25	26	US-11-060-756-148502	Sequence 148502,
30	15.2	50.7	25	26	US-11-060-756-255015	Sequence 255015,
31	15.2	50.7	33	10	US-09-759-112A-3	Sequence 3, Appli
32	15	50.0	25	22	US-10-719-900-169041	Sequence 169041,
33	15	50.0	25	22	US-10-956-157-231991	Sequence 231991,
34	15	50.0	25	22	US-10-956-157-285782	Sequence 285782,
35	15	50.0	25	26	US-11-036-317-142021	Sequence 142021,
36	15	50.0	25	26	US-11-036-317-561534	Sequence 561534,
37	15	50.0	25	26	US-11-036-317-674828	Sequence 674828,
38	15	50.0	25	26	US-11-036-317-708626	Sequence 708626,
39	15	50.0	25	26	US-11-036-317-794581	Sequence 794581,
40	15	50.0	25	26	US-11-036-317-830452	Sequence 830452,
41	15	50.0	25	26	US-11-036-317-965123	Sequence 965123,
42	15	50.0	28	20	US-10-802-441-10	Sequence 10, Appl
43	15	50.0	29	10	US-09-841-994-12	Sequence 12, Appl
44	14.8	49.3	25	22	US-10-956-157-161705	Sequence 161705,
45	14.8	49.3	25	22	US-10-956-157-177245	Sequence 177245,

ALIGNMENTS

RESULT 1
US-08-469-172-7
; Sequence 7, Application US/08469172
; Publication No. US20030054343A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-469-172-7

Query Match 100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGACGGCACTGAAG 30
| | | | | | | | | | | | | | | | | |
Db 1 GGGAAATTCGGGAGCCAGACGGCACTGAAG 30

RESULT 2
US-10-788-779-7
; Sequence 7, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: BOSTON
; STREET: 60 STATE STREET, Suite 510
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-788-779-7

Query Match 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGACGGCACTGAAG 30
| | | | | | | | | | | | | | | | | |
Db 1 GGGAAATTCGGGAGCCAGACGGCACTGAAG 30

RESULT 3
US-10-349-780A-28
; Sequence 28, Application US/10349780A
; Publication No. US20040146866A1
; GENERAL INFORMATION:
; APPLICANT: Fu, Guoliang
; TITLE OF INVENTION: QUANTITATIVE MULTIPLEX DETECTION OF NUCLEIC ACIDS
; FILE REFERENCE: patent1
; CURRENT APPLICATION NUMBER: US/10/349,780A
; CURRENT FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-780A-28

Query Match 62.7%; Score 18.8; DB 24; Length 50;
Best Local Similarity 76.7%; Pred. No. 2.2e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGGAGCCAGACGGCACTGAAG 30
| | | | | | | | | | | | | | | | | |
Db 14 GAGAAATTCGAGATCCAGGTGTCACTGAAG 43

RESULT 4
US-11-036-317-804897
; Sequence 804897, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 804897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-804897

Query Match 56.7%; Score 17; DB 26; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TTCCGGAGCCAGACGGCACTGAAG 30
| | | | | | | | | | | | | | | | | |
Db 1 TGCACGTAGCGAGACGGCCTGAAG 25

RESULT 5
US-10-956-157-203038
```

```

; REGISTRATION NUMBER: 46,063
; REFERENCE/DOCKET NUMBER: 03806.0054-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-716-803-42

Query Match 54.0%; Score 16.2; DB 21; Length 38;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGAAATTCGGGAGCCAGACGGCACTG 27
Db 11 GSGAGTTCGCGCGCTGGGACGGCACCG 37
; : ||| ||||| : ||||| |
; : ||| ||||| : ||||| |

RESULT 7
US-10-123-036-15/c
; Sequence 15, Application US/10123036
; Publication No. US20030073656A1
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
; FILE REFERENCE: 0010872/0483963
; CURRENT APPLICATION NUMBER: US/10/123,036
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/283,788
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-123-036-15

Query Match 54.0%; Score 16.2; DB 15; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CGCGGAGCCAGACGGCACTGA 28
Db 26 CGCGGAACCAAGACGCGCTGA 6
; ||||| ||||| |||||
; ||||| ||||| |||||

RESULT 8
US-10-483-289A-3
; Sequence 3, Application US/10483289A
; Publication No. US20050048466A1
; GENERAL INFORMATION:
; APPLICANT: Qian, Qijun
; TITLE OF INVENTION: A specific proliferation in tumour cell which can express
; FILE REFERENCE: IEC020038PUS
; CURRENT APPLICATION NUMBER: US/10/483,289A
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-10-483-289A-3

```

Query Match 54.0%; Score 16.2; DB 22; Length 39;
Best Local Similarity 72.4%; Pred. No. 3.2e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGCACTGAAG 30
|||||
Db 1 GGAATTCGCGCGCCGAGATCTCACAGACG 29

RESULT 9

US-10-719-900-439430
; Sequence 439430, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439430
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-719-900-439430

Query Match 52.7%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GGAGCCAGACGGCACTGAA 29
|||||
Db 5 GGAGCCAGAGGTACTGAA 23

RESULT 10

US-10-098-263B-97474
; Sequence 97474, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 97474
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-97474

Query Match 52.0%; Score 15.6; DB 16; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGCGC 23
|||||
Db 2 GGAATTCGCGAAGCAAGAGGCGC 23

RESULT 11

US-10-098-263B-128306/c
; Sequence 128306, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 128306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-128306

Query Match 52.0%; Score 15.6; DB 16; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGAGCCAGACGCGC 23
|||||
Db 24 GGAATTCGCGAAGCAAGAGGCGC 3

RESULT 12

US-10-719-956-258512
; Sequence 258512, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258512
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-258512

Query Match 52.0%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CGCGGAGCCAGACGCACTGAA 29
|||||
Db 1 CGCGGAGCCACAAAGGCCCGAA 22

RESULT 13

US-10-719-956-258513
; Sequence 258513, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258513
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-258513

Query Match 52.0%; Score 15.6; DB 24; Length 25;

Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 CGCGAGCCAGCGGCACTGAA 29
|||||
Db 1 CGCGAGCCACATGGCCCGGAA 22

RESULT 14

US-11-036-317-21919/c
; Sequence 21919, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-21919

Query Match 52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 CGCGAGCCAGCGGCACTGAAG 30
|||||
Db 23 GCAGAGCAAAAGGCACTGAAG 2

RESULT 15

US-11-036-317-875174
; Sequence 875174, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 875174
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-875174

Query Match 52.0%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGAATTCGCGGAGCCAGCGC 23
|||||
Db 2 GGAATTCGCGGAGCAAGACTGC 23

RESULT 16

US-10-719-900-805772/c
; Sequence 805772, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 805772
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-805772

Query Match 51.3%; Score 15.4; DB 22; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 AATTGGGAGCCAGCGGCACTGA 28
|||||
Db 25 AAGACCCGGATACCGGCACTGA 1

RESULT 17

US-10-719-900-844398/c
; Sequence 844398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 844398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-844398

Query Match 51.3%; Score 15.4; DB 22; Length 25;
Best Local Similarity 94.1%; Pred. No. 7.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 AGCCGAGCGGCACTGAA 29
|||||
Db 24 AGCCGAGCGGCACTGAA 8

RESULT 18

US-11-036-317-804896
; Sequence 804896, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 804896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-804896

```
Query Match      51.3%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 TTTCGGAGCCAGCAGCGGCACTGAAG 30
Db 1 TGCAGTGAGCAGCAGCGCCCTGAAG 25

RESULT 19
US-11-060-756-299133/C
; Sequence 299133, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-299133

Query Match      51.3%; Score 15.4; DB 26; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ATTCGGAGCCAGCAGCGCACTGAA 29
Db 25 ATTCAGAACCAATGTCACTGAA 1

RESULT 20
US-09-858-349-14
; Sequence 14, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 34
; TYPE: DNA
; ORGANISM: pET-21aVH3, XhoI
US-09-858-349-14

Query Match      51.3%; Score 15.4; DB 9; Length 34;
Best Local Similarity 76.0%; Pred. No. 7.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGAAATTCGGAGCCAGCGGCAC 25
Db 1 GGGAAATTCCTCGAGCTATGCGGCAC 25

RESULT 21
US-10-035-833A-1888/C
; Sequence 1888, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
```

```
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1888
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-1888

Query Match      51.3%; Score 15.4; DB 19; Length 41;
Best Local Similarity 70.4%; Pred. No. 7.1e+03;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTCGGAGCCAGCGGCACTGAAG 30
Db 41 AACTACAGAGCCAGCGCAGCRCTGCAG 15

RESULT 22
US-10-035-833A-4483/C
; Sequence 4483, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4483
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-4483

Query Match      51.3%; Score 15.4; DB 19; Length 41;
Best Local Similarity 70.4%; Pred. No. 7.1e+03;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AATTCGGAGCCAGCGGCACTGAAG 30
Db 41 AACTACAGAGCCAGCGCAGCRCTGCAG 15

RESULT 23
US-10-667-891-24
; Sequence 24, Application US/10667891
; Publication No. US20040171024A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: BREY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RZHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495.0294-00000
; CURRENT APPLICATION NUMBER: US/10/667,891
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
```



```
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-667-891-24

Query Match      50.7%; Score 15.2; DB 20; Length 24;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGAC 20
Db      1 GGGAAATTCGGTGGACAGAC 20

RESULT 24
US-10-807-466-35
; Sequence 35, Application US/10807466
; Publication No. US20040244066A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, CHARLES W.
; APPLICANT: BREY, PAUL T.
; APPLICANT: HOLM, INGE
; APPLICANT: GRAILLES, MARINE
; APPLICANT: RZHETSKY, ANDREY
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS IN DROSOPHILA AND
; FILE REFERENCE: 03495-0294-01000
; CURRENT APPLICATION NUMBER: US/10/807,466
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 10/667,891
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/413,469
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-807-466-35

Query Match      50.7%; Score 15.2; DB 21; Length 24;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGGGAGCCAGAC 20
Db      1 GGGAAATTCGGTGGACAGAC 20

RESULT 25
US-10-719-900-784963/c
; Sequence 784963, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 784963
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Mus musculus
US-10-719-900-784963

Query Match      50.7%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TCGCGAGCCAGCGGCACT 26
Db      25 TTGCAGAGTCAGACGGCACT 6

RESULT 26
US-10-719-956-25613
; Sequence 25613, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-25613

Query Match      50.7%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 CGGAGCCAGACGGCACTGAA 29
Db      4 CGGAGCGTGACGGCGCTGAA 23

RESULT 27
US-11-036-317-503091
; Sequence 503091, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 503091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-503091

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CGCGAGCCAGACGGCACTG 27
Db      3 CGTGGAGCCAGATGGCACAG 22

RESULT 28
US-11-036-317-611467
```

```
; Sequence 611467, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611467
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-611467

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TCGCGGAGCCAGCGGCACT 26
        ||| ||||| ||||| |||
Db      6 TCACGGAGCCAGACGGTAGT 25

RESULT 29
US-11-060-756-148502
; Sequence 148502, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-148502

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGAATTTCGCGGAGCCAGACG 21
        ||| ||||| ||||| |||
Db      4 GGAGTTTCGCGGAGCCAGAGG 23

RESULT 30
US-11-060-756-255015
; Sequence 255015, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255015
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-255015

Query Match      50.7%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GGAATTTCGCGGAGCCAGACG 21
        ||| ||||| ||||| |||
Db      1 GGAGTTTCGCGGAGCCAGAGG 20

RESULT 31
US-09-759-112A-3
; Sequence 3, Application US/09759112A
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1F7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112A
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)-(33)
; OTHER INFORMATION: 1F7 light chain 5' primer
US-09-759-112A-3

Query Match      50.7%; Score 15.2; DB 10; Length 33;
Best Local Similarity 85.0%; Pred. No. 8.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGCGGAGCCAGAC 20
        ||||| ||| ||||| |||
Db      1 GGGAAATTCATGGAGACAGAC 20

RESULT 32
US-10-719-900-169041/c
; Sequence 169041, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 169041
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-169041

Query Match      50.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GGGAAATTCGCGGAGCCAGCGGC 23
        ||| ||| ||| ||||| ||| |||
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 721.376 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_scs.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	26	100.0	26	6	112901	112901 Sequence 8
2	17.2	66.2	24	6	BD172395	BD172395 Secreted
3	17.2	66.2	24	6	BD172714	BD172714 Secreted
4	17.2	66.2	24	6	BD173033	BD173033 Secreted
5	17.2	66.2	24	6	BD173352	BD173352 Secreted
6	17.2	66.2	24	6	BD175386	BD175386 Secretory
7	17.2	66.2	24	6	AR410764	AR410764 Sequence
8	17.2	66.2	24	6	AR439128	AR439128 Sequence
9	17.2	66.2	24	6	AR473148	AR473148 Sequence
10	17.2	66.2	24	6	AR527134	AR527134 Sequence
11	17.2	66.2	24	6	AR566167	AR566167 Sequence
12	17.2	66.2	24	6	AX697613	AX697613 Sequence
13	17.2	66.2	24	6	BD075535	BD075535 Secretory
14	17	65.4	30	6	IB4403	IB4403 Sequence 4
15	17	65.4	30	6	AR202764	AR202764 Sequence
16	17	65.4	36	6	AP1851	AP1851 Sequence 10
17	17	65.4	39	6	IB4408	IB4408 Sequence 9
18	17	65.4	48	4	AB022055	AB022055 Canis fam
19	17	65.4	48	4	AB022058	AB022058 Canis fam

C 20	17	65.4	48	6	AR178317	AR178317 Sequence
C 21	17	65.4	48	6	AX323399	AX323399 Sequence
C 22	17	65.4	50	6	AS1711	AS1711 Sequence 17
C 23	17	65.4	50	6	AR167590	AR167590 Sequence
C 24	17	65.4	50	6	AR178300	AR178300 Sequence
C 25	17	65.4	50	6	BD223995	BD223995 Near infr
C 26	17	65.4	50	6	AR200395	AR200395 Sequence
C 27	17	65.4	50	6	AX323382	AX323382 Sequence
C 28	17	65.4	50	6	AX686852	AX686852 Sequence
C 29	16.6	63.8	25	6	CQ628816	CQ628816 Sequence
C 30	16.6	63.8	25	6	CQ628817	CQ628817 Sequence
C 31	16.6	63.8	25	6	CQ628818	CQ628818 Sequence
C 32	16.6	63.8	25	6	AR469879	AR469879 Sequence
C 33	16.6	63.8	25	6	AR469880	AR469880 Sequence
C 34	16.6	63.8	25	6	AR469881	AR469881 Sequence
C 35	16.6	63.8	42	6	AR031676	AR031676 Sequence
C 36	16.6	63.8	42	6	I90294	I90294 Sequence 36
C 37	16.6	63.8	48	6	AR111808	AR111808 Sequence
C 38	16.6	63.8	48	6	AR236256	AR236256 Sequence
C 39	16.6	63.8	48	6	AR275530	AR275530 Sequence
C 40	16.4	63.1	28	6	AR120088	AR120088 Sequence
C 41	16.4	63.1	28	6	AR120089	AR120089 Sequence
C 42	16.4	63.1	28	6	BD183077	BD183077 Novel ins
C 43	16.4	63.1	28	6	BD103248	BD103248 Novel ins
C 44	16.4	63.1	40	6	A35229	A35229 Synthetic p
C 45	16.4	63.1	40	6	AR012257	AR012257 Sequence

ALIGNMENTS

RESULT 1	112901	Sequence 8 from patent US 5429923.	26 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	112901	Sequence 8 from patent US 5429923.	26 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	112901	Sequence 8 from patent US 5429923.	26 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	112901	Sequence 8 from patent US 5429923.	26 bp	DNA	linear	PAT 26-JUL-1995
VERSION	112901.1	GI:910878	26 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 26)					
AUTHORS	Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.					
TITLE	Method for detecting hypertrophic cardiomyopathy associated mutations					
JOURNAL	Patent: US 5429923-A 8 04-JUL-1995;					
FEATURES	Location/Qualifiers					
source	1..26					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Query Match	100.0%;	Score 26;	DB 6;	Length 26;		
Best Local Similarity	100.0%;	Pred. No. 6.5;				
Matches	26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	CCCTCCTTCTGTACTCTCTCTGCTC	26			
Db	1					
	1	CCCTCCTTCTGTACTCTCTCTGCTC	26			
RESULT 2	BD172395/c	24 bp	DNA	linear	PAT 18-FEB-2003	
LOCUS	BD172395	24 bp	DNA	linear	PAT 18-FEB-2003	
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.					
ACCESSION	BD172395					
VERSION	BD172395.1	GI:28413695				
KEYWORDS	JP 200223786-A/168.					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1 (bases 1 to 24)					

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002223786-A 168 13-AUG-2002;

COMMENT GENENTECH INC

OS Artificial Sequence

PN JP 2002223786-A/168

PD 13-AUG-2002

PF 18-DEC-2001 JP 2001385135

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062285 PR

18-SEP-1997 US 60/062287, 17-OCT-1997 US 60/062286 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

21-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR

27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064103 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065186 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC (C12P21/02, C12R1:645), C12N15/00, C12N5/00

CC Description of Artificial Sequence: Synthetic FH Key

FT Location/Qualifiers

FT source 1. .24 /organism='Artificial Sequence'.

FEATURES

source 1. .24 Location/Qualifiers

1. .24 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTCTTGTACTCTCTCTGCTC 26

|||||

Db 24 CCTACTACTACTCTCTCTGCTC 3

|||||

RESULT 3

BD172714/c

LOCUS BD172714

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD172714

VERSION BD172714.1 GI:28414018

KEYWORDS JP 2002238586-A/168.

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

1 (bases 1 to 24)

Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002238586-A 168 27-AUG-2002;

COMMENT GENENTECH INC

OS Artificial Sequence

PN JP 2002238586-A/168

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

31-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR

07-NOV-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:645), PC (C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, C12N5/00, PC (C12N5/00, C12R1:91)

CC Description of Artificial Sequence: Synthetic FH Key

FT Location/Qualifiers

FT source 1. .24 /organism='Artificial Sequence'.

FEATURES

source 1. .24 Location/Qualifiers

1. .24 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTCTTGTACTCTCTCTGCTC 26

|||||

Db 24 CCTACTACTACTCTCTCTGCTC 3

|||||

RESULT 4

BD173033/c

LOCUS BD173033

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD173033

BD173033.1 GI:28414339
JP 2002238587-A/168.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: JP 2002238587-A 168 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238587-A/168
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-SEP-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR
28-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063341 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063564 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063435 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR
29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066511 PR
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
C12P21/02, C12P21/08, C12P21/02, C12R1:91, (C12P21/02, C12R1:19), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00, C12N15/00 CC
Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers 1. .24
FT source /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .24
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTTCTTGACTCCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCCTCTGCTC 3
|||||
RESULT 5
BD173352/c 24 bp DNA linear PAT 18-FEB-2003
LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding
DEFINITION

the same.
BD173352
BD173352.1 GI:28414663
JP 2002238588-A/168.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 24)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: JP 2002238588-A 168 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238588-A/168
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059263 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
21-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR
27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
28-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063435 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR
29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR
31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR
17-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR
21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/065693 PR
24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066364 PR
24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066511 PR
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
C12P21/02, C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, C12N5/00, C12R1:91) CC
Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers 1. .24
FT source /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .24
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTTCTTGACTCCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCCTCTGCTC 3
|||||
RESULT 6
BD175386/c 24 bp DNA linear PAT 18-MAR-2003
LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding

DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding the same.

ACCESSION BD175386
VERSION BD175386.1 GI:29121082
KEYWORDS JP 2002253280-A/168.
SOURCE synthetic construct
ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 24)

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and

Yuan, J.

TITLE Secretary and transmembrane polypeptide and nucleic acid encoding

the same

JOURNAL Patent: JP 2002253280-A 168 10-SEP-2002;

COMMENT GENETECH INC

OS Artificial Sequence

PN JP 2002253280-A/168

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR

27-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR

28-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR

31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC

A61P25/00,

PC A61P25/16, A61P25/28, A61P31/12, A61P35/00, C07K14/47, C07K16/18,

PC C07K19/00,

PC C12N1/19, C12N1/21, C12N5/10//A61K38/00, A61K39/395, A61K39/395,

PC A61P43/00,

PC C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,

PC C12R1:91),

PC C12N15/00, C12N5/00, A61K37/02, (C12N5/00, C12R1:91) CC

Description of Artificial Sequence: Synthetic FH Key

Location/Qualifiers

FT source

1. .24

/organism='Artificial Sequence'.

Location/Qualifiers

1. .24

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCTCTTGTACTCCTCTCTGCTC 26

||||| ||||| ||||| ||||| |||||

24 CCTACTACTACTCTCTCTGCTC 3

||||| ||||| ||||| ||||| |||||

RESULT 9

AR473148/c

Db 24 CCTACTACTACTCCTCTCTGCTC 3

RESULT 7

AR410764/c

LOCUS

DEFINITION

Sequence 204 from patent US 6635468.

ACCESSION

AR410764

VERSION

AR410764.1

GI:40162264

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 24)

AUTHORS

Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,

Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,

Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,

Kljasin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,

Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

JOURNAL

Patent: US 6635468-A 204 21-OCT-2003;

FEATURES

Location/Qualifiers

1. .24

/organism='unknown'

/mol_type='genomic DNA'

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCTCTTGTACTCCTCTCTGCTC 26

||||| ||||| ||||| ||||| |||||

24 CCTACTACTACTCCTCTCTGCTC 3

||||| ||||| ||||| ||||| |||||

RESULT 8

AR439128/c

LOCUS

DEFINITION

Sequence 204 from patent US 6664376.

ACCESSION

AR439128

VERSION

AR439128.1

GI:42664977

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 24)

AUTHORS

Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,

Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,

Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,

Kljasin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,

Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

JOURNAL

Patent: US 6664376-A 204 16-DEC-2003;

FEATURES

Location/Qualifiers

1. .24

/organism='unknown'

/mol_type='genomic DNA'

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.4e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCTCTTGTACTCCTCTCTGCTC 26

||||| ||||| ||||| ||||| |||||

24 CCTACTACTACTCCTCTCTGCTC 3

||||| ||||| ||||| ||||| |||||

LOCUS AR473148 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 204 from patent US 6686451.
ACCESSION AR473148
VERSION AR473148.1 GI:42708523
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Desnovers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6686451-A 204 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 10

AR527134/c
LOCUS AR527134 24 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 204 from patent US 6723535.
ACCESSION AR527134
VERSION AR527134.1 GI:53914051
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6723535-A 204 20-APR-2004;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 11

AR566167/c
LOCUS AR566167 24 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 204 from patent US 6767995.
ACCESSION AR566167
VERSION AR566167.1 GI:53983077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Desnovers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6767995-A 204 27-JUL-2004;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 12

AX697613/c
LOCUS AX697613 24 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 204 from Patent WO0104311.
ACCESSION AX697613
VERSION AX697613.1 GI:29498708
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ashkenazi, A.J., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0104311-A 204 18-JAN-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"

ORIGIN

Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
|||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 13

BD075535/c
LOCUS BD075535 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.
ACCESSION BD075535
VERSION BD075535.1 GI:22621138
KEYWORDS JP 2001516580-A/168.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 24)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL Patent: JP 2001516580-A 168 02-OCT-2001;

```
GENENTECH INC
OS Artificial Sequence
PN JP 2001516580-A/168
PD 02-OCT-2001
PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/06125 PR
17-SEP-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
21-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR
27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR
29-OCT-1997 US 60/064103, 31-OCT-1997 US 60/063870 PR
03-NOV-1997 US 60/065186, 17-NOV-1997 US 60/065846 PR
12-NOV-1997 US 60/065693, 21-NOV-1997 US 60/066120 PR
18-NOV-1997 US 60/066364, 24-NOV-1997 US 60/066772 PR
21-NOV-1997 US 60/066466, 24-NOV-1997 US 60/066770 PR
24-NOV-1997 US 60/066511, 24-NOV-1997 US 60/066453 PR
25-NOV-1997 US 60/066840
PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,
PC C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, C12P21/08, PC
C12R1/91,
PC C12N15/00, C12N5/00
CC Description of Artificial Sequence: Synthetic FH Key
Location/Qualifiers
FT source 1..24
FT Location/Qualifiers
FEATURES
source 1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 66.2%; Score 17.2; DB 6; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTCTCTGTACTCCTCCTGCTC 26
| | | | | | | | | | | | | | | |
Db 24 CCTACTACTCCTCCTGCTC 3
| | | | | | | | | | | | | | | |
RESULT 14
184403/c
LOCUS
DEFINITION Sequence 4 from patent US 5695933.
ACCESSION 184403
VERSION 184403.1 GI:3021923
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS Schalling, M., Hudson, T.J. and Housman, D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 4 09-DEC-1997;
FEATURES
Location/Qualifiers
source 1..36
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
repeat_region 1..36
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 36;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCTCTCTGTACTCCTCCTGCT 25
| | | | | | | | | | | | | | | |
Db 1 CCTCTCTGTACTCCTCCTGCT 25
| | | | | | | | | | | | | | | |
RESULT 15
AR202764
LOCUS
DEFINITION Sequence 12 from patent US 6365344.
ACCESSION AR202764
VERSION AR202764.1 GI:21498978
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS Nolan, G.P. and Rothenberg, S. Michael.
TITLE Methods for screening for transdominant effector peptides and RNA molecules
JOURNAL Patent: US 6365344-A 12 02-APR-2002;
FEATURES
Location/Qualifiers
source 1..30
/organism="unassigned DNA"
/mol_type="unassigned DNA"
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 30;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 CCTCTCTGTACTCCTCCTGCTC 26
| | | | | | | | | | | | | | | |
Db 1 CCTCTCTGTACTCCTCCTGCTC 25
| | | | | | | | | | | | | | | |
RESULT 16
A91851/c
LOCUS
DEFINITION Sequence 10 from Patent WO9823743.
ACCESSION A91851
VERSION A91851.1 GI:6740735
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 36)
AUTHORS Davies, K.E. and Theodosiou, A.
TITLE MURINE GUANINE NUCLEOTIDE EXCHANGE FACTOR - (MNGEF) AND HUMAN
HOMOLOGUES THEREOF
JOURNAL Patent: WO 9823743-A 10 04-JUN-1998;
MEDICAL RES COUNCIL (GB); DAVIES KAY ELIZABETH (GB)
FEATURES
Location/Qualifiers
source 1..36
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
repeat_region 1..36
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 36;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCTCTCTGTACTCCTCCTGCT 25
| | | | | | | | | | | | | | | |
```

Query Match 65.4%; Score 17; DB 4; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;

```
ORIGIN
/mol_type="unassigned DNA"

Query Match      65.4%; Score 17; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CCTCCTTCTTGTTACTCTCTCTCTGCTC 26
    ||||| || || || || || || || ||
Db  47  CCTCCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 21
AX323399/c
LOCUS      AX323399          48 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 34 from Patent WO0192511.
ACCESSION  AX323399
VERSION     AX323399.1  GI:18094161
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE      Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL    Patent: WO 0192511-A 34 06-DEC-2001;
            Aventis Pharma (FR)
FEATURES   Location/Qualifiers
            source
              1..48
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="synthetic oligonucleotide"

ORIGIN

Query Match      65.4%; Score 17; DB 6; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CCTCCTTCTTGTTACTCTCTCTCTGCTC 26
    ||||| || || || || || || || ||
Db  47  CCTCCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 22
A51711/c
LOCUS      A51711          50 bp      DNA      linear      PAT 10-MAR-1997
DEFINITION Sequence 17 from Patent WO9618744.
ACCESSION  A51711
VERSION     A51711.1  GI:2304515
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
            unclassified
REFERENCE  1 (bases 1 to 50)
AUTHORS    Crouzet,J., Scherman,D. and Wils,P.
TITLE      PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
            OLIGONUCLEOTIDE
JOURNAL    Patent: WO 9618744-A 17 20-JUN-1996;
            RHONE POULENC RORER SA (FR)
COMMENT    Other publication AU 4178996 960703
            Other publication FR 2728264 960621.
            Location/Qualifiers
            source
              1..50
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

ORIGIN

Query Match      65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CCTCCTTCTTGTTACTCTCTCTCTGCTC 26
    ||||| || || || || || || || ||
Db  49  CCTCCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 23
AR167590/c
LOCUS      AR167590          50 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6287762.
ACCESSION  AR167590
VERSION     AR167590.1  GI:17903379
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 50)
AUTHORS    Crouzet,J., Scherman,D. and Wils,P.
TITLE      Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL    Patent: US 6287762-A 17 11-SEP-2001;
            Location/Qualifiers
            source
              1..50
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

Query Match      65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CCTCCTTCTTGTTACTCTCTCTCTGCTC 26
    ||||| || || || || || || || ||
Db  49  CCTCCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 24
AR178300/c
LOCUS      AR178300          50 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 17 from patent US 6319672.
ACCESSION  AR178300
VERSION     AR178300.1  GI:20219438
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 50)
AUTHORS    Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
TITLE      Purification of a triple helix formation with an immobilized
            oligonucleotide
JOURNAL    Patent: US 6319672-A 17 20-NOV-2001;
            Location/Qualifiers
            source
              1..50
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

Query Match      65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CCTCCTTCTTGTTACTCTCTCTCTGCTC 26
    ||||| || || || || || || || ||
Db  49  CCTCCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 25
BD223995/c
LOCUS      BD223995          50 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Near infrared chemiluminescent acridinium compounds and uses
            thereof.
ACCESSION  BD223995
VERSION     BD223995.1  GI:33033765
KEYWORDS   .
SOURCE     BD223995.1  GI:33033765
```

KEYWORDS JP 2002522530-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 50)
JOURNAL Natrajan,A., Jiang,Q., Sharpe,D. and Law,S.-J.
COMMENT Near infrared chemiluminescent acridinium compounds and uses
thereof
PATENT: JP 2002522530-A 4 23-JUL-2002;
BAYER CORP
OS Homo sapiens (human)
PN JP 2002522530-A/4
PD 23-JUL-2002
PF 10-AUG-1999 JP 2000564941
PI 11-AUG-1998 US 60/096073
PR ANAND NATRAJAN QINGPING JIANG, DAVID SHARPE, SAY JONG LAW PC
C07D219/04, C07D401/12, C09K3/00, C09K11/07, C12N15/09, C12Q1/68, PC
G01N21/76,
PC G01N33/58//C07K14/765, C07K16/26, G01N33/532, C12N15/00 CC
VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16 FH Key
LOCATION/Qualifiers
FT misc feature (223).. (223).
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 26 CCTCTCTCTCTCTCTCTCTCTCTC 2
RESULT 26
AR200395/c
LOCUS AR200395 50 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6355803.
ACCESSION AR200395
VERSION AR200395.1 GI:20250469
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Natrajan,A., Jiang,Q., Sharpe,D. and Law,S.-J.
TITLE Near infrared chemiluminescent acridinium compounds and uses
thereof
JOURNAL Patent: US 6355803-A 4 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 26 CCTCTCTCTCTCTCTCTCTCTCTC 2
RESULT 27
AX323382/c
LOCUS AX323382 50 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 17 from Patent WO0192511.

AX323382
VERSION AX323382.1 GI:18094144
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Crouzet,J., Scherman,D., Wils,P., Blanche,P. and Cameron,B.
TITLE Purification of a triple helix formation with an immobilized
oligonucleotide
JOURNAL Patent: WO 0192511-A 17 06-DEC-2001;
FEATURES Aventis Pharma (FR)
source Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25
RESULT 28
AX686852/c
LOCUS AX686852 50 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 17 from Patent EP1281774.
ACCESSION AX686852
VERSION AX686852.1 GI:29372393
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Couzet,J., Scherman,D. and Wils,P.
TITLE Purification of a triple helix formation with an immobilized
oligonucleotide
JOURNAL Patent: EP 1281774-A 17 05-FEB-2003;
FEATURES Aventis Pharma S.A. (FR)
source Location/Qualifiers
1..50
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 65.4%; Score 17; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25
RESULT 29
CQ628816/c
LOCUS CQ628816 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13556 from Patent WO0192524.
ACCESSION CQ628816
VERSION CQ628816.1 GI:41679034
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13556 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 CTCCTTCTTGCTACTCCTCCTGCT 25
||||| ||||| ||||| ||||| |||||
Db 25 CTCCTTCTTGCTTCTCCTCCAGCT 3
RESULT 30
CQ628817/c
LOCUS CQ628817 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13557 from Patent WO0192524.
ACCESSION CQ628817
VERSION CQ628817.1 GI:41679035
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13557 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 CTCCTTCTTGCTACTCCTCCTGCT 25
||||| ||||| ||||| ||||| |||||
Db 24 CTCCTTCTTGCTTCTCCTCCAGCT 2
RESULT 31
CQ628818/c
LOCUS CQ628818 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13558 from Patent WO0192524.
ACCESSION CQ628818
VERSION CQ628818.1 GI:41679036
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13558 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 CTCCTTCTTGCTACTCCTCCTGCT 25
||||| ||||| ||||| ||||| |||||
Db 23 CTCCTTCTTGCTTCTCCTCCAGCT 1
RESULT 32
AR469879/c
LOCUS AR469879 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13556 from patent US 6686188.
ACCESSION AR469879
VERSION AR469879.1 GI:42704936
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13556 03-FEB-2004;
FEATURES
source 1. .25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 CTCCTTCTTGCTACTCCTCCTGCT 25
||||| ||||| ||||| ||||| |||||
Db 25 CTCCTTCTTGCTTCTCCTCCAGCT 3
RESULT 33
AR469880/c
LOCUS AR469880 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13557 from patent US 6686188.
ACCESSION AR469880
VERSION AR469880.1 GI:42704937
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13557 03-FEB-2004;
FEATURES
source 1. .25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 3 CTCCTTCTTGCTACTCCTCCTGCT 25
||||| ||||| ||||| ||||| |||||
Db 3 CTCCTTCTTGCTTCTCCTCCAGCT 25
||||| ||||| ||||| ||||| |||||

```

Db      24 CTCCTTCTTGCTCTCTCCAGCT 2
RESULT 34
LOCUS   AR469881/c          25 bp      DNA
DEFINITION   Sequence 13558 from patent US 6686188.
ACCESSION   AR469881
VERSION     AR469881.1   GI:42704938
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL     Patent: US 6686188-A 13558 03-FEB-2004;
FEATURES    Location/Qualifiers
            source          1..25
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Query Match      63.8%; Score 16.6; DB 6; Length 25;
Best Local Similarity 82.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      3 CTCCTTCTTGCTCTCTCTGCT 25
      ||||| ||||| ||||| |||||
Db      23 CTCCTTCTTGCTCTCTCCAGCT 1
RESULT 35
LOCUS   AR031676/c          42 bp      DNA
DEFINITION   Sequence 36 from patent US 5866394.
ACCESSION   AR031676
VERSION     AR031676.1   GI:5945965
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Houtz,R.L..
TITLE       Cloning and developmental expression of pea
            ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
            epsilon N-methyltransferase
JOURNAL     Patent: US 5866394-A 36 02-FEB-1999;
FEATURES    Location/Qualifiers
            source          1..42
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      63.8%; Score 16.6; DB 6; Length 42;
Best Local Similarity 82.6%; Pred. No. 3.9e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      4 TCCTTCTTGCTCTCTCTGCTC 26
      ||||| ||||| ||||| |||||
Db      33 TCCTTCTTGCTCTCTCTTCTC 11
RESULT 36
LOCUS   I90294              42 bp      DNA
DEFINITION   Sequence 36 from patent US 5723752.
ACCESSION   I90294
VERSION     I90294.1   GI:3410234
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 48)
AUTHORS     Berlin,V., Chiu,M.I., Cottarel,G. and Damagnez,V.
TITLE       Immunosuppressant target proteins
JOURNAL     Patent: US 6464974-A 7 15-OCT-2002;
FEATURES    Location/Qualifiers
            source          1..48
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Query Match      63.8%; Score 16.6; DB 6; Length 48;
Best Local Similarity 82.6%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      4 TCCTTCTTGCTCTCTCTGCTC 26
      ||||| ||||| ||||| |||||
Db      42 TTCTACTTGCTCTCTCCACCTC 20
RESULT 38
LOCUS   AR236256/c          48 bp      DNA
DEFINITION   Sequence 7 from patent US 6464974.
ACCESSION   AR236256
VERSION     AR236256.1   GI:27280077
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 48)
AUTHORS     Berlin,V., Chiu,M.I., Cottarel,G. and Damagnez,V.
TITLE       Immunosuppressant target proteins
JOURNAL     Patent: US 6464974-A 7 15-OCT-2002;
FEATURES    Location/Qualifiers
            source          1..48
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Query Match      63.8%; Score 16.6; DB 6; Length 48;
Best Local Similarity 82.6%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      4 TCCTTCTTGCTCTCTCTGCTC 26
      ||||| ||||| ||||| |||||
Db      42 TTCTACTTGCTCTCTCCACCTC 20
RESULT 37
LOCUS   AR111808/c          48 bp      DNA
DEFINITION   Sequence 7 from patent US 6127521.
ACCESSION   AR111808
VERSION     AR111808.1   GI:12828656
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 48)
AUTHORS     Berlin,V., Chiu,M.Isabel., Cottarel,G. and Damagnez,V.
TITLE       Immunosuppressant target proteins
JOURNAL     Patent: US 6127521-A 7 03-OCT-2000;
FEATURES    Location/Qualifiers
            source          1..48
                        /organism="unknown"
                        /mol_type="unassigned DNA"
ORIGIN
Query Match      63.8%; Score 16.6; DB 6; Length 48;
Best Local Similarity 82.6%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy      4 TCCTTCTTGCTCTCTCTGCTC 26
      ||||| ||||| ||||| |||||
Db      33 TCCTTCTTGCTCTCTCTTCTC 11

```

Best Local Similarity 82.6%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTTACTCTCTCCACCTC 20

RESULT 39
AR275530/c
LOCUS AR275530 48 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 7 from patent US 6509152.
ACCESSION AR275530
VERSION AR275530.1 GI:29708948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
Unclassified.
AUTHORS Berlin,V., Chiu,M.I., Cottarel,G. and Damagnez,V.
TITLE Immunosuppressant target proteins
JOURNAL Patent: US 6509152-A 7 21-JAN-2003;
FEATURES Location/Qualifiers
source 1..48
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 63.8%; Score 16.6; DB 6; Length 48;
Best Local Similarity 82.6%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTTACTCTCTCCACCTC 20

RESULT 40
AR120088/c
LOCUS AR120088 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6153596.
ACCESSION AR120088
VERSION AR120088.1 GI:14102787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
Unclassified.
AUTHORS Liotta,D.C., Petros,J.A., Wey,S.-J., Karr,J.F. and Pohl,J.
TITLE Polycationic oligomers
JOURNAL Patent: US 6153596-A 2 28-NOV-2000;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 63.1%; Score 16.4; DB 6; Length 28;
Best Local Similarity 76.9%; Pred. No. 4.9e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCTCTCTTCTTGTTACTCTCTCTGCTC 26
Db 28 CCTCTCTCTCTCCACCTCTCTCTCTC 3

Search completed: November 18, 2005, 17:43:00
Job time : 723.476 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 179.034 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167256

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	2	AAQ91128 Beta-card
2	26	100.0	26	9	ACA63118 Human bet
3	26	100.0	26	13	ADR05304 Human bet
4	18.6	71.5	50	10	ABZ22093 Polyanion
5	18.6	71.5	50	10	ABZ22129 Polyanion
6	18.4	70.8	32	3	AAA30793 Human Bip
7	17.2	66.2	24	2	AAx52400 Reverse P
8	17.2	66.2	24	3	ADC78524 Human PRO
9	17.2	66.2	24	4	AAf72558 Human PRO
10	17.2	66.2	24	8	ACA60167 Human sec
11	17.2	66.2	24	8	ACD07567 Novel hum
12	17.2	66.2	24	8	ABx71615 Human sec
13	17.2	66.2	24	8	ACH06947 Human sec
14	17.2	66.2	24	8	ABx96184 Human sec
15	17.2	66.2	24	8	ACA05505 Human sec
16	17.2	66.2	24	8	ACD20172 Human sec
17	17.2	66.2	24	8	ACA54975 Novel sec
18	17.2	66.2	24	9	ACD19810 Human sec
19	17.2	66.2	24	9	ADB29409 Human sec
20	17.2	66.2	24	9	ADA18265 Human sec

C 21	17.2	66.2	24	9	ACD66957	AcD66957 Human sec
C 22	17.2	66.2	24	9	ACD83118	AcD83118 Human PRO
C 23	17.2	66.2	24	9	ADA16240	Ada16240 Human sec
C 24	17.2	66.2	24	9	ADA42385	Ada42385 Human sec
C 25	17.2	66.2	24	9	ACD23296	AcD23296 Human PRO
C 26	17.2	66.2	24	9	ADA16664	Ada16664 Human sec
C 27	17.2	66.2	24	9	ADA13093	Ada13093 Human sec
C 28	17.2	66.2	24	9	ADA41961	Ada41961 Human sec
C 29	17.2	66.2	24	9	ADA17308	Ada17308 Human sec
C 30	17.2	66.2	24	9	ADA42811	Ada42811 Human sec
C 31	17.2	66.2	24	9	ACD23658	AcD23658 Human PRO
C 32	17.2	66.2	24	10	ADB77730	AdB77730 Human sec
C 33	17.2	66.2	24	10	ADB74866	AdB74866 Human sec
C 34	17.2	66.2	24	10	ADC28512	AdC28512 Human sec
C 35	17.2	66.2	24	10	ADC39712	AdC39712 Human sec
C 36	17.2	66.2	24	10	ADC40226	AdC40226 Human sec
C 37	17.2	66.2	24	10	ADC19050	AdC19050 Human sec
C 38	17.2	66.2	24	10	ADC34350	AdC34350 Human sec
C 39	17.2	66.2	24	10	ADC29405	AdC29405 Human sec
C 40	17.2	66.2	24	10	ADC28936	AdC28936 Human sec
C 41	17.2	66.2	24	10	ADC40821	AdC40821 Human sec
C 42	17.2	66.2	24	10	ADC19478	AdC19478 Human sec
C 43	17.2	66.2	24	10	ADC33926	AdC33926 Human sec
C 44	17.2	66.2	24	10	ADC12996	AdC12996 Human sec
C 45	17.2	66.2	24	10	ADC12448	AdC12448 Human sec

ALIGNMENTS

RESULT 1

AAQ91128
ID AAQ91128 standard; cDNA; 26 BP.

AC AAQ91128;

DT 19-FEB-1996 (first entry)

DE Beta-cardiac myosin heavy chain PCR primer D'.

KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;
diagnosis; primer; mutation; detection; ss.

OS Synthetic.

PN US5429923-A.

PD 04-JUL-1995.

PF 11-DEC-1992; 92US-00989160.

PR 11-DEC-1992; 92US-00989160.

PA (HARD) HARVARD COLLEGE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

DR Non-invasive method for diagnosis of hypertrophic cardio-myopathy -
useful for testing asymptomatic individual(s).

XX Example 1; Col 10; 22pp; English.

PS AAQ91121-Q91130 are nested PCR primers used for the amplification and
identification of beta-cardiac myosin heavy-chain RNA. They are used in a
new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),
the method involves detecting the presence or absence of specific HC-
associated mutations in the beta-cardiac myosin heavy-chain obtained from
a blood sample. The method may be used to diagnose familial or sporadic
HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

Db 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

RESULT 2

ACA63118

ID ACA63118 standard; DNA; 26 BP.

XX AC

XX ACA63118;

XX 28-AUG-2003 (first entry)

XX Human beta cardiac myosin heavy chain PCR primer D'.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;

XX familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;

XX sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;

XX Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;

XX phenylketonuria; cystic fibrosis.

XX Homo sapiens.

XX US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with

XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

XX hemophilia, by detecting a mutation in an amplified product of a beta

XX cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC

XX and FHC) comprises detecting a mutation associated with hypertrophic

XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy

XX chain DNA. The mutations associated with SHC/FHC are detected in the

XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-

XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect

XX sample). FHC associated point mutation can be classified and used to

XX determine life expectancy in affected individuals e.g. using a Kaplan-

XX Meier curve for the classified type of FHC causing point mutation. Also

XX included are an RNA probe comprising ribonucleotides arranged in a

XX sequence which is complementary to at least a portion of beta-cardiac

XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for

XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a nested PCR primer used to amplify a region of the beta cardiac
 CC myosin heavy chain cDNA containing an FHC-associated mutation

XX Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

Db 1 CCCTCCTTCTGTACTCTCTCTGCTC 26

RESULT 3

ADR05304

ID ADR05304 standard; DNA; 26 BP.

XX AC

XX ADR05304;

XX 21-OCT-2004 (first entry)

XX Human beta cardiac myosin heavy chain mutation detection primer D'A.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

XX familial hypertrophic cardiomyopathy;

XX sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to

XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

XX myosin heavy-chain DNA and detecting the mutation in the amplified

XX product.

XX Claim 18; SEQ ID NO 8; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,

XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,

XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an

XX amplified product, and detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy in the amplified product,

XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also

XX included are a set of DNA oligonucleotide primers for amplifying beta-

XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

CC Sequence 26 BP; 1 A; 13 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCTTCTGTACTCTCTCGTC 26
Db 1 CCCTCTTCTGTACTCTCTCGTC 26

RESULT 4

ABZ22093
ID ABZ22093 standard; DNA; 50 BP.

XX AC ABZ22093;

XX DT 11-MAR-2003 (first entry)

XX DE Polyanionic polymer related oligonucleotide #47.

XX KW Polyanionic polymer; bioactivity; water solubility; ss.

XX OS Synthetic.

XX PN WO200277036-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US008614.

XX PR 21-MAR-2001; 2001US-0277705P.

XX PA (LEUNG/) LEUNG D W.

XX XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;

PI Waggoner DW;

XX WPI; 2003-058367/05.

XX DR Producing monodispersed preparation of polyanionic polymer for therapy,
XX PT by expressing vector comprising ligation product of oligonucleotides
XX PT encoding glutamate/aspartate residues in host cell and isolating the
XX PT product.

XX PS Disclosure; Fig 5; 74pp; English.

CC The present invention describes a method (M) for producing a
CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
CC kD. (M) involves inserting into an expression vector (EV) a ligation
CC product formed by ligating together oligonucleotides that encode
CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
CC approximately of the same molecular weight. Also described: (1) a
CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
CC another polypeptide at either one end or at both ends of it; (2) a
CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
CC leucine, where the polyanionic polymer is polyglutamic acid or
CC polyaspartic acid; (3) a vector (III) comprising a cassette which
CC comprises a nucleotide sequence encoding a polyanionic polymer and at
CC least one other nucleotide sequence, where the polyanionic polymer is
CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
CC (IV) comprising (II) or a vector that comprises a nucleotide sequence
CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
CC recombinantly-produced polyanionic polymer (V) that is of any molecular
CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
CC is useful for treating a disease or ailment in an individual by
CC administering (I) to the individual. (I) is also useful for delivering an
CC effective amount of a pharmaceutically active agent, a therapeutic
CC protein or a drug to a patient in need of it, or for diagnostic and
CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to
CC ABP56400 represent sequences used in the exemplification of the present
CC invention

XX Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;

Query Match 71.5%; Score 18.6; DB 10; Length 50;
Best Local Similarity 84.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCTCTTCTGTACTCTCTCGTC 26
Db 21 CCTCTTCTGTACTCTCTCGTC 45

RESULT 5

ABZ22129
ID ABZ22129 standard; DNA; 50 BP.

XX AC ABZ22129;

XX DT 11-MAR-2003 (first entry)

XX DE Polyanionic polymer related oligonucleotide #83.

XX KW Polyanionic polymer; bioactivity; water solubility; ss.

XX OS Synthetic.

XX PN WO200277036-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US008614.

XX PR 21-MAR-2001; 2001US-0277705P.

XX PA (LEUNG/) LEUNG D W.

XX XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;

PI Waggoner DW;

XX WPI; 2003-058367/05.

XX DR Producing monodispersed preparation of polyanionic polymer for therapy,
XX PT by expressing vector comprising ligation product of oligonucleotides
XX PT encoding glutamate/aspartate residues in host cell and isolating the
XX PT product.

XX PS Example 7; Fig 8; 74pp; English.

XX The present invention describes a method (M) for producing a
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
 CC kD. (M) involves inserting into an expression vector (EV) a ligation
 CC product formed by ligating together oligonucleotides that encode
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
 CC approximately of the same molecular weight. Also described: (1) a
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
 CC another polypeptide at either one end or at both ends of it; (2) a
 CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
 CC leucine, where the polyanionic polymer is polyglutamic acid or
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at
 CC least one other nucleotide sequence, where the polyanionic polymer is
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
 CC (IV) comprising (III) or a vector that comprises a nucleotide sequence
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
 CC is useful for treating a disease or ailment in an individual by
 CC administering (I) to the individual. (I) is also useful for delivering an
 CC effective amount of a pharmaceutically active agent, a therapeutic
 CC protein or a drug to a patient in need of it, or for diagnostic and
 CC testing or research purposes. AB222045 to AB222131 and ABP56374 to
 CC ABP56400 represent sequences used in the exemplification of the present
 CC invention

SQ Sequence 50 BP; 1 A; 24 C; 1 G; 24 T; 0 U; 0 Other;

Query Match 71.5%; Score 18.6; DB 10; Length 50;
 Best Local Similarity 84.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 CCTCCTCTTGTACTCCCTGCTC 26
 |||||
 Db 21 CCTCCTCTTGTACTCCCTGCTC 45

RESULT 6

AAA30793/c
 ID AAA30793 standard; cDNA; 32 BP.
 XX
 AC AAA30793;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human BiP(78KD) forward PCR primer, derived from GenBank X87949.
 XX
 KW Immunoglobulin heavy chain binding protein; BiP(78KD); chondrocyte;
 KW autoantigen; rheumatoid arthritis; antiarthritic; antirheumatic; p78;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200021995-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-GB003316.
 XX
 PR 09-OCT-1998; 98GB-00022115.
 XX
 PA (UNLO) KINGS COLLEGE LONDON.
 XX
 PI Panayi GS, Corrigan VM, Bodman-Smith MD, Fife MS, Lanchbury JS;
 XX WPI; 2000-317942/27.
 DR
 XX New human immunoglobulin heavy chain binding protein and encoding
 XX polynucleotide, useful for diagnosis and treatment of rheumatoid
 XX arthritis.

PS Example 2; Page 8; 53pp; English.

XX The invention relates to a human immunoglobulin heavy chain binding
 CC protein, BiP(78KD) (Y90693), having a 639 amino acid sequence, and to the
 CC cDNA encoding it (A30792). The invention also encompasses a BiP(78KD)
 CC protein of 633 amino acids (Y90694). The cDNA encoding BiP(78KD), also
 CC referred to as p78 in the specification, was isolated from human
 CC chondrocytes (the specialised cells of articular cartilage) and human
 CC chondrosarcoma cell lines. The BiP(78KD) cDNA of this invention contains
 CC a number of differences compared with the published sequence (GenBank
 CC accession number X87949), and has therefore been deposited with
 CC GenBank with the accession number AF188611). These differences comprise 6
 CC single nucleotide substitutions and a codon insertion, and result in
 CC three amino acid substitutions and an arginine insertion at position 834-
 CC 836 of the protein. The BiP(78KD) proteins react with antibodies present
 CC in the serum of rheumatoid arthritis patients, and is therefore a
 CC putative autoantigen for this autoimmune disease. BiP(78KD) is also able
 CC to selectively proliferate synovial T-cells from patients with rheumatoid
 CC arthritis. BiP(78KD) or peptides derived from the protein are useful as
 CC reagents to indicate the presence of rheumatoid arthritis, and can be
 CC used in prognostic or diagnostic tests of body fluids for rheumatoid
 CC arthritis by ELISA (enzyme linked immunosorbent assay) or Western
 CC blotting. The protein or the cDNA encoding it can also be used to test
 CC for rheumatoid arthritis by detecting antibodies to the protein.
 CC BiP(78KD), its peptides and polynucleotides are also useful
 CC therapeutically. Sequences A30743-A30794 represent human BiP(78KD) PCR
 CC primers used in an exemplification of the invention for subcloning into a
 CC bacterial expression vector. The sequence of the primers are based on the
 CC previously published BiP(78KD) sequence (GenBank X87949)

SQ Sequence 32 BP; 13 A; 3 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 70.8%; Score 18.4; DB 3; Length 32;
 Best Local Similarity 95.0%; Pred. No. 1.7e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CCTCCTCTTGTACTCCCTCC 21
 |||||
 Db 29 CCTCCTCTTGTACTCCCTCC 10

RESULT 7

AA52400/c
 ID AA52400 standard; DNA; 24 BP.
 XX
 AC AA52400;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Reverse PCR primer used to amplify cDNA encoding PRO263.
 XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9914328-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063328P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064424P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PA (GETH) GENENTECH INC.
XX
XX Wood WI, Gurney AL, Pennica D, Chen J, Yuan J;
XX WPI; 1999-229533/19.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
XX gastrointestinal ulceration.
XX
XX Example 33; Page 140; 320pp; English.
XX
XX Oligonucleotides AAX52276-532 represent PCR primers and probes used to
XX isolate and amplify cDNA encoding secreted and transmembrane human
XX proteins (see AAX52213-74 and AAX1344-403). The cDNA sequences are
XX obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
XX fetal brain, fetal liver and fetal retina. The encoded polypeptides have
XX specific uses based on their homology to known polypeptides, e.g. PRO211
XX and PRO217 can be used for disorders associated with the preservation and
XX maintenance of gastrointestinal mucosa and the repair of acute and
XX chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
XX gastrointestinal ulceration and congenital microvillus atrophy), skin
XX diseases associated with abnormal keratinocyte differentiation (e.g.
XX psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
XX vulva and gliomas), potent effects on cell growth and development,
XX diseases related to growth or survival of nerve cells including
XX Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
XX PRO265 can be used as for fibromodulin, e.g. for reducing dermal
XX scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may

CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
CC have therapeutic applications in wound healing and tissue repair; PRO317
CC can be used for treating problems of the kidney, uterus, endometrium,
CC blood vessels, or related tissue, e.g. in the heart of genital tract
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 2; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCCTCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTCCTCTGCTC 3

RESULT 8

ADC78524/c

ID ADC78524 standard; DNA; 24 BP.

XX AC ADC78524;

XX DT 01-JAN-2004 (first entry)

XX Human PRO protein-related reverse PCR primer SEQ ID 204.

XX antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
XX neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
XX neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
XX antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
XX thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
XX gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
XX Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
XX nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
XX asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
XX atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
XX diabetes; stroke; gene therapy; transgenic; PRO; human; ss; primer; PCR.

XX Homo sapiens.

XX WO200015796-A2.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US021090.

XX 16-SEP-1998; 98WO-US019330.

XX (GETH) GENENTECH INC.

XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
XX Yuan J;

XX WPI; 2000-271434/23.

XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
XX homology, e.g. to growth and cancer-associated antigens.

XX Example 33; SEQ ID NO 204; 355pp; English.

XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
XX The polypeptides and polynucleotides of the invention may be useful as
XX research tools and as therapeutics for treating enterocolitis, Zollinger-
XX Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
XX Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
XX scarring and wound healing, nerve repair, thrombosis, bone and/or
XX cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
XX sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
XX infertility, premature aging, AIDS, diabetes complications and stroke.
XX The molecules may also be utilised during gene therapy procedures and
XX transgenic animal production. The current sequence is that of the PCR
XX primer of the invention which was used to analyse the human PRO DNA of

```
CC the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
      66.2%; Score 17.2; DB 3; Length 24;
      Best Local Similarity 86.4%; Pred. No. 4.7e+03;
      Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAATCTCTCTGCTC 26
    ||| || ||||| |||||
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 9
ID AAF72558 standard; DNA; 24 BP.
XX
AC AAF72558;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO polypeptide gene PCR primer SEQ ID NO: 204.
XX
KW Human; PRO: dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiac;
KW angiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2001-081051/09.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
XX treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
XX cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
XX disease).
XX
XX Example 33; Page 178; 393pp; English.
XX
XX The present sequence is a primer which was used in the isolation of one
XX
```

```
CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful for treating skin diseases
CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosa. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
      66.2%; Score 17.2; DB 4; Length 24;
      Best Local Similarity 86.4%; Pred. No. 4.7e+03;
      Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAATCTCTCTGCTC 26
    ||| || ||||| |||||
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 10
ID ACA60167 standard; DNA; 24 BP.
XX
AC ACA60167;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO263 PCR primer #3.
XX
KW Human; ss; PCR; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker; primer.
XX
OS Homo sapiens.
XX
PN US2003003530-A1.
XX
PD 02-JAN-2003.
XX
PF 11-JUL-2001; 2001US-00904011.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
```

29-OCT-1997; 97US-00634335P.
29-OCT-1997; 97US-00637046P.
29-OCT-1997; 97US-00637332P.
29-OCT-1997; 97US-00637334P.
29-OCT-1997; 97US-00637335P.
29-OCT-1997; 97US-00637338P.
31-OCT-1997; 97US-00642115P.
31-OCT-1997; 97US-00638706P.
31-OCT-1997; 97US-00641033P.
03-NOV-1997; 97US-00642488P.
07-NOV-1997; 97US-00648089P.
12-NOV-1997; 97US-00651868P.
17-NOV-1997; 97US-00658466P.
18-NOV-1997; 97US-00658466P.
21-NOV-1997; 97US-00656933P.
21-NOV-1997; 97US-00661206P.
21-NOV-1997; 97US-00663646P.
24-NOV-1997; 97US-00664533P.
24-NOV-1997; 97US-00664533P.
24-NOV-1997; 97US-00664668P.
24-NOV-1997; 97US-00665111P.
24-NOV-1997; 97US-00667702P.
24-NOV-1997; 97US-00667722P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
01-DEC-1998; 98WO-US025108.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003585.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2003-329602/31.
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, in generating probes and in tissue typing.
XX Example 33; Page 109; 484pp; English.
XX The invention relates to an isolated nucleic acid with at least 80%
XX nucleic acid sequence identity to a nucleotide sequence encoding one of
XX 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
XX PRO protein extracellular domain. Also included are a vector comprising
XX the PRO nucleic acid, a host cell comprising the vector, producing a PRO

polypeptide (by culturing the host cell for the expression of the PRO
polypeptide, and recovering the PRO polypeptide from the cell culture),
an isolated PRO polypeptide (having at least 80% sequence identity to:
(a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
acid sequence encoded by a nucleic acid molecule deposited with an ATCC
number (detailed in the specification); or (c) an extracellular domain of
a PRO polypeptide or to a PRO polypeptide lacking its associated signal
peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
heterologous amino acid sequence, an anti-PRO antibody, detecting a
PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
modulating at least one biological activity of a cell expressing a PRO245
or PRO1868. Nucleic acids which encode PRO can be used to generate either
transgenic animals or knock-out animals which may be used in the
development and screening of therapeutically useful reagents. The nucleic
acids may also be used in gene therapy, in chromosome identification, as
chromosome markers, or in generating probes. The PRO polypeptides are
useful as molecular markers for protein electrophoresis, and the isolated
nucleic acids may be used for recombinantly expressing those markers. The
PRO polypeptides and nucleic acids may also be used in tissue typing.
Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
affinity purification of PRO from recombinant cell culture or natural
sources. The present sequence is a PCR primer used to isolate a cDNA
encoding a PRO protein

Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CCTTCTTGACTCTCTCTGCTC 26
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 11
ACD07567/c
ID ACD07567 standard; DNA; 24 BP.
XX AC ACD07567;
XX AC ACD07567;
DT 07-AUG-2003 (first entry)
XX Novel human secreted and transmembrane protein PCR primer #77.
XX Human; secreted and transmembrane protein; PRO; pharmaceutical;
XX diagnostic; biosensor; bioreactor; Parkinson's disease;
XX Alzheimer's disease; inflammation; nephritis; wound healing;
XX nerve repair; collateral blood vessel formation; cancer;
XX colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
XX cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
XX scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
XX infertility; gene therapy; PCR; primer; ss.
XX Homo sapiens.
XX OS
XX US2002197671-A1.
XX PD
XX 26-DEC-2002.
XX 17-JUL-2001; 2001US-00907824.
XX 17-SEP-1997; 97US-00591133P.
XX 17-SEP-1997; 97US-00591135P.
XX 17-SEP-1997; 97US-00591176P.
XX 17-SEP-1997; 97US-00591199P.
XX 17-SEP-1997; 97US-00591212P.
XX 17-SEP-1997; 97US-00591222P.
XX 17-SEP-1997; 97US-00591846P.
XX 18-SEP-1997; 97US-00592633P.
XX 18-SEP-1997; 97US-00592666P.
XX 15-OCT-1997; 97US-00621255P.

```

PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 29-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000WO-US0665350.
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Deanoyers L, Eaton DL, Ferrara N;
PI
```

```

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-370793/35.
XX
XX New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
XX PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
XX cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
XX or strokes.
XX
XX Example 33; Page 100; 482pp; English.
XX
XX The invention describes a new isolated nucleic acid molecule comprising
XX the full length coding sequence of the DNA deposited with the American
XX Type Culture Collection (e.g. ATCC Deposit No. 209258) or a sequence
XX with at least 80% identity to a DNA encoding a PRO polypeptide comprising
XX any of 61 sequences having 164-1119 amino acids fully defined in the
XX specification. The PRO polypeptides or polynucleotides are useful as
XX pharmaceuticals, diagnostics, biosensors or bioreactors. These are
XX particularly useful for detecting or treating e.g. Parkinson's disease,
XX Alzheimer's disease, inflammations, nephritis, wound healing, nerve
XX repair, collateral blood vessel formation, cancers (e.g. colorectal
XX cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
XX arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
XX ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
XX infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
XX pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
XX therapeutic intervention in these diseases, and diagnostic determination
XX of the presence of these diseases. The PRO polypeptides are also useful
XX as molecular weight markers, or for chromosome identification. The PRO
XX genes are useful as hybridisation probes, or for screening libraries of
XX human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
XX therapy, particularly for replacing a defective gene. This sequence
XX represents a novel human secreted and transmembrane PRO polypeptide
XX associated primer
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 66.2%; Score 17.2; DB 8; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 4.7e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 5 CCTTTGTTACTCTCTCTGCTC 26
XX ||| || ||||| |||||
XX Db 24 CCTACTACTACTCTCTCTGCTC 3
XX
XX RESULT 12
XX ABX71615/c
XX ID ABX71615 standard; DNA; 24 BP.
XX
XX XX ABX71615;
XX AC ABX71615;
XX
XX DT 10-MAR-2003 (first entry)
XX XX
XX Human secreted/transmembrane protein PRO263 PCR primer #3.
XX
XX Human; PRO; secreted protein; transmembrane protein; enterocolitis;
XX gastrointestinal ulceration; skin disease; ss; PCR; primer;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; inflammatory disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
XX atherosclerosis; cardiac injury, infertility; birth defect;
XX premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
XX diabetic complication; wound repair.
XX
XX OS Homo sapiens.
XX
XX US2002132240-A1.
XX
```



```
XX 19-SEP-2002.
PD 18-JUL-2001; 2001US-00909320.
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059123P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063322P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 01-DEC-1998; 98WO-US025108.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 06-JAN-2000; 2000WO-US000219.

11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000WO-US026350.
XX (GETH ) GENENTECH INC.
XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2003-147434/14.
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
XX treating inflammatory diseases, organ failure, atherosclerosis, cardiac
XX injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
XX disease.
XX Example 33; Page 99; 473pp; English.
XX The invention relates to an isolated PRO polypeptide having at least 80%
XX amino acid sequence identity to: (a) any one of 61 fully defined amino
XX acid sequences given in the specification (appearing as ABUS4347-
XX ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence
XX deposited under American Type Culture Collection (accession numbers
XX listed in the specification); (c) any one of the PRO sequences which
XX lacks its associated signal peptide; (d) an extracellular domain of the
XX PRO polypeptide with its associated signal peptide; or (e) an
XX extracellular domain of the PRO polypeptide which lacks its associated
XX signal peptide. Also include are the nucleic acids encoding the PRO
XX polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
XX polypeptides and nucleic acids are useful in diagnosing or treating
XX enterocolitis, gastrointestinal ulceration, skin diseases associated with
XX abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
XX cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's
XX disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
XX rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
XX atherosclerosis, cardiac injury, infertility, birth defects, premature
XX aging, AIDS, cancer, diabetic complications, or mutations in general. The
XX polypeptides are also useful for wound repair and associated therapies
XX concerned with re-growth of tissue. The nucleotide sequences may be used
XX as hybridisation probes in chromosome and gene mapping, or in generating
XX antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
XX polypeptides, in assays to identify other proteins or molecules involved
XX in binding reaction, to generate transgenic animals or knockout animals,
XX which in turn are useful in the development and screening of
XX therapeutically useful reagents, for chromosome identification, and
XX tissue typing. The PRO polypeptides and nucleic acid molecules are also
XX useful in gene therapy, and as molecular weight markers for protein
XX electrophoresis purposes. The anti-PRO antibodies may be used in
XX diagnostic assays for PRO, or for the affinity purification of PRO from
XX recombinant cell culture or natural sources. The present sequence is a
XX PCR primer used to isolate a cDNA encoding a PRO polypeptide
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTTGTTACTCTCTGCTC 26
Db 24 CCTACTACTACTCTCTGCTC 3
```


CC PRO187 polypeptide is useful for treating Parkinson's disease,
 CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies
 CC and disease related to uncontrolled cell growth, e.g. cancer. PRO219
 CC polypeptide plays a regulatory role in the blood coagulation cascade.
 CC PRO246 polypeptides which serves as tumour specific antigens may be
 CC exploited as therapeutic targets for anti-tumour drugs. PRO269
 CC haemorrhage is useful as an antithrombotic agent with reduced risk for
 CC treatment of endometrial bleeding angiogenesis. PRO317 polypeptide is useful in
 CC treating endometrial bleeding angiogenesis. PRO387 polypeptides and
 CC portion have therapeutic applications in wound healing and tissue repair.
 CC PRO234 polypeptides are useful for treating asthma, rheumatoid arthritis,
 CC psoriasis and multiple sclerosis. The polypeptide and its nucleic acid
 CC are useful for tissue typing. PRO antibodies are useful for
 CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
 CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
 CC expression in specific cells, tissues or serum and for affinity
 CC purification of PRO from recombinant cell culture or natural sources. The
 CC present sequence represents a human secreted/transmembrane PRO
 CC polypeptide PCR primer

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 8; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTCTGCTACTCCCTGCTC 26
 ||||| ||||| ||||| |||||
 Db 24 CCTACTACTCTCCCTGCTC 3

RESULT 14

ABX96184/c

ID ABX96184 standard; DNA; 24 BP.

AC ABX96184;

DT 13-MAY-2003 (first entry)

DE Human secreted/transmembrane protein, #38, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
 KW endometriosis; cancer; tumour; ischaemia; coronary arterial disease;
 KW polycystic kidney disease; renal failure; inflammatory response; asthma;
 KW rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
 KW cytostatic; gynecological; cardiant; nephrotropic; hepatotropic;
 KW antiinflammatory.

XX Homo sapiens.

XX US2002160374-A1.

PN 31-OCT-2002.

PD 12-JUL-2001; 2001US-00905291.

PF 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0065120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 97US-0065722P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 02-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 XX Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
 XX Williams PM, Wood WI;
 XX WPI; 2003-288105/28.


```
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
XX 18-SEP-2000; 2000US-00665350.
PA (G8TH ) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams FW, Wood WI;
XX
XX WPI; 2003-331485/31.
XX
XX Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245
PT or PRO1868, useful in chromosome and gene mapping, in generating
PT antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
XX
XX Example 33; Page 107; 48lp; English.
XX
XX The invention relates to sixty one nucleic acids encoding PRO
CC polypeptides (secreted and transmembrane). The polynucleotide is useful
CC in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA, and in
CC gene therapy. The polynucleotide may also be used in preparing PRO
CC polypeptides by recombinant techniques, and in generating either
CC transgenic animals or knock-out animals which, in turn, are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptide or the antibody is used in preparing a medicament for
CC treating a condition responsive to the polypeptide or antibody, such as
CC mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
CC psoriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
CC e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
CC atrophica areata, angiogenesis, inflammatory disease e.g. asthma and
CC rheumatoid arthritis, ischaemia, and in various diagnostic assays. The
CC present sequence represents an PCR primer used in isolating a PRO
CC polypeptide
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. NO. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTCTACTCTCTCGTCTC 26
Db 24 CCTACTACTACTCTCTCGTCTC 3
RESULT 16
ACD20172/C
ID ACD20172 standard; DNA; 24 BP.
XX
XX ACD20172;
XX
XX 25-AUG-2003 (first entry)
DT
XX Human secreted / transmembrane polypeptide PRO263 reverse primer.
DE
XX Human; ss; PCR; primer; gene therapy; tumour; tissue typing; obesity;
XX diabetes; hypoinsulinaemia; hyperinsulinaemia; vascular permeability;
XX cardiac insufficiency disorder; immune response; regeneration; cartilage;
XX auditory hair cell; hearing loss; bone disorder; sports injury;
XX arthritis.
XX
XX Homo sapiens.
XX
XX US2003036060-A1.
XX
XX 20-FEB-2003.
XX
XX 12-JUL-2001; 2001US-00904859.
XX
XX
```

```
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063584P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0098026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR
```


18-NOV-1997; 97US-0065693P.
21-NOV-1997; 97US-0066120P.
21-NOV-1997; 97US-0066364P.
24-NOV-1997; 97US-0068453P.
24-NOV-1997; 97US-0068466P.
24-NOV-1997; 97US-0068511P.
24-NOV-1997; 97US-0066770P.
24-NOV-1997; 97US-0066772P.
25-NOV-1997; 97US-0066840P.
12-DEC-1997; 97US-0069425P.
04-JUN-1998; 98US-0080282P.
10-SEP-1998; 98US-0099803P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98US-0100262P.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
13-OCT-1998; 98US-0104080P.
20-NOV-1998; 98US-0109304P.
01-DEC-1998; 98WO-US025108.
22-DEC-1998; 98US-0113298P.
07-JUL-1999; 99US-0143048P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0146222P.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028584.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003585.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015284.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
(GETH) GENENTECH INC.
PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PW, Wood WI;
XX WPI; 2003-341586/32.
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
XX treating inflammatory diseases, organ failure, atherosclerosis, cardiac
XX injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
XX disease.
XX Example 33; Page 99; 473pp; English.
XX The invention describes sixty one nucleic acids encoding PRO polypeptides
XX (secreted and transmembrane). The PRO polypeptides and nucleic acids are
XX useful in diagnosing or treating enterocolitis, gastrointestinal
XX ulceration, skin diseases associated with abnormal keratinocyte
XX differentiation, e.g. psoriasis or epithelial cancers such as squamous

cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic
lateral sclerosis, inflammatory diseases, e.g. rheumatoid arthritis,
asthma or multiple sclerosis, organ failure, atherosclerosis, cardiac
injury, infertility, birth defects, premature aging, AIDS, cancer,
diabetic complications, or mutations in general. The polypeptides are
also useful for wound repair and associated therapies concerned with re-
growth of tissue. The PRO polypeptides and nucleic acid molecules are
also useful in gene therapy, and as molecular weight markers for protein
electrophoresis purposes. The anti-PRO antibodies may be used in
diagnostic assays for PRO, or for the affinity purification of PRO from
recombinant cell culture or natural sources. This sequence represents a
novel human PRO polypeptide associated primer
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 8; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 5 CCTTCTTGTTACTCCTCCTGCTC 26
Db 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 18
ACD19810/c
ID ACD19810 standard; DNA; 24 BP.
XX
AC ACD19810;
XX
DT 22-AUG-2003 (first entry)
XX
DE Human secreted / transmembrane polypeptide PRO263 reverse primer.
XX
KW Human; ss; PCR; primer; gene therapy; apoptosis; bleeding; tumour; ALS;
KW gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer;
KW coronary ischaemic condition; gastrointestinal mucosa disorder; asthma;
KW mucosal lesion repair; keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;
KW neurodegenerative disease; endometrial bleeding; wound healing;
KW tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
OS Homo sapiens.
XX
XX US2003027143-A1.
XX
XX 06-FEB-2003.
XX
XX 16-JUL-2001; 2001US-00906838.
XX
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.

PR	28-OCT-1997;	97US-0063541P.	PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PR	28-OCT-1997;	97US-0063544P.	PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU, Kljavin IJ;
PR	28-OCT-1997;	97US-0063544P.	PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PR	28-OCT-1997;	97US-0063550P.	XX	Williams PM, Wood WI;
PR	28-OCT-1997;	97US-0063556P.	DR	WPI; 2003-417249/39.
PR	29-OCT-1997;	97US-0063435P.	XX	Novel secreted and transmembrane polypeptides and polynucleotides
PR	29-OCT-1997;	97US-0063704P.	PT	encoding them useful for treating abnormal bleeding involved in
PR	29-OCT-1997;	97US-0063732P.	PT	gynecological diseases, skin diseases and neurodegenerative diseases.
PR	29-OCT-1997;	97US-0063734P.	XX	Example 33; Page 98; 467pp; English.
PR	29-OCT-1997;	97US-0063735P.	XX	The invention relates to an isolated secreted and transmembrane PRO
PR	29-OCT-1997;	97US-0063738P.	CC	polypeptide. The PRO polypeptides are useful for modulating biological
PR	31-OCT-1997;	97US-0064215P.	CC	activity of a cell, in diagnosing or treating abnormal bleeding involved
PR	31-OCT-1997;	97US-0063870P.	CC	in gynaecological diseases e.g. to avoid or lessen the need for
PR	31-OCT-1997;	97US-0064103P.	CC	hysterectomy, for treating angiogenesis, tumour, coronary ischaemic
PR	07-NOV-1997;	97US-0064248P.	CC	condition, disorders associated with the preservation and maintenance of
PR	07-NOV-1997;	97US-0064809P.	CC	gastrointestinal mucosa and the repair of acute and chronic mucosal
PR	12-NOV-1997;	97US-0065186P.	CC	lesions, skin diseases associated with abnormal keratinocyte
PR	17-NOV-1997;	97US-0065846P.	CC	differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
PR	18-NOV-1997;	97US-0065693P.	CC	disease, amyotrophic lateral sclerosis (ALS), neuropathies, disease
PR	21-NOV-1997;	97US-0066120P.	CC	related to uncontrolled cell growth (e.g. cancer), blood coagulation
PR	21-NOV-1997;	97US-0066364P.	CC	endometrial bleeding, wound healing, tissue repair, asthma, rheumatoid
PR	24-NOV-1997;	97US-0066453P.	CC	arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are
PR	24-NOV-1997;	97US-0066466P.	CC	useful in molecular biology including uses as hybridisation probes and in
PR	24-NOV-1997;	97US-0066511P.	CC	the generation of antisense RNA and DNA, for preparing PRO polypeptides,
PR	24-NOV-1997;	97US-0066770P.	CC	for generating transgenic animals or knockout animals. The PRO
PR	10-SEP-1998;	98US-0098003P.	CC	polypeptides and their nucleic acids are useful for tissue typing. PRO
PR	14-SEP-1998;	98WO-US018824.	CC	antibodies are useful for immunohistochemical staining and/or assay of
PR	14-SEP-1998;	98US-0100262P.	CC	sample fluids. Anti-PRO antibodies are useful in diagnostic assays for
PR	14-SEP-1998;	98WO-US019177.	CC	PRO e.g. detecting its expression in specific cells, tissues or serum and
PR	16-SEP-1998;	98WO-US019330.	CC	for affinity purification of PRO from recombinant cell culture or natural
PR	17-SEP-1998;	98US-0100859P.	CC	sources. The present sequence represents a human secreted and
PR	17-SEP-1998;	98WO-US019437.	CC	transmembrane PRO polypeptide PCR primer
PR	13-OCT-1998;	98US-0104080P.	XX	Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
PR	20-NOV-1998;	98US-0109304P.	SO	Quality Match 66.2%; Score 17.2; DB 9; Length 24;
PR	01-DEC-1998;	98WO-US025108.		Best Local Similarity 86.4%; Pred. No. 4.7e+03;
PR	01-DEC-1998;	98US-0113296P.		Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
PR	07-JUL-1999;	99US-0143048P.		
PR	26-JUL-1999;	99US-0145698P.		
PR	28-JUL-1999;	99US-0146222P.		
PR	08-SEP-1999;	99WO-US020594.	Qy	5 CCTTCTGTGTACTCCTCTGCTC 26
PR	13-SEP-1999;	99WO-US020944.	Db	24 CCTACTACTACTCCTCTGCTC 3
PR	15-SEP-1999;	99WO-US021090.		
PR	15-SEP-1999;	99WO-US021547.		
PR	05-OCT-1999;	99WO-US023089.		
PR	29-NOV-1999;	99WO-US028214.		
PR	30-NOV-1999;	99WO-US028313.	RESULT 19	
PR	01-DEC-1999;	99WO-US028301.	ADE29409/c	
PR	02-DEC-1999;	99WO-US028564.	ID	ADB29409 standard; DNA; 24 BP.
PR	02-DEC-1999;	99WO-US030095.	XX	
PR	16-DEC-1999;	99WO-US030095.	AC	ADB29409;
PR	20-DEC-1999;	99WO-US030911.	XX	
PR	20-DEC-1999;	99WO-US030999.	DT	20-NOV-2003 (first entry)
PR	05-JAN-2000;	2000WO-US000219.	XX	
PR	11-FEB-2000;	2000WO-US003565.	XX	Human secreted/transmembrane protein, #40, PCR primer #3.
PR	22-FEB-2000;	2000WO-US004414.	DE	
PR	24-FEB-2000;	2000WO-US005004.	KW	Human; PCR; primer; ss; PRO; secreted; transmembrane;
PR	02-MAR-2000;	2000WO-US005841.	KW	gastrointestinal mucosa; mucosal lesion; skin disease;
PR	30-MAR-2000;	2000WO-US007377.	KW	keratinocyte differentiation; psoriasis; Parkinson's disease;
PR	30-MAR-2000;	2000WO-US008439.	KW	Alzheimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy;
PR	02-MAY-2000;	2000WO-US014042.	KW	cell growth; cancer; tumour; viral infection; neurodegenerative disease;
PR	02-JUN-2000;	2000WO-US015264.	KW	antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
PR	28-JUL-2000;	2000WO-US020710.	KW	kidney tissue; apoptosis; therapeutic; tissue typing;
PR	24-AUG-2000;	2000WO-US023328.	KW	immunohistochemical staining; gene therapy; nontropic; neuroprotective;
PR	18-SEP-2000;	2000WO-US026350.	KW	cytostatic; virucide; anticoagulant.
XX			OS	
XX			XX	Homo sapiens.
XX			XX	
XX			PN	US2003092002-A1.
XX			XX	

(GETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;

CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTGTTGTAAGTCTCTGCTC 26

Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 20

ADA18265/c

ID ADA18265 standard; DNA; 24 BP.

XX AC ADA18265;

XX DT 20-NOV-2003 (first entry)

DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted; transmembrane;

XX gastrointestinal mucosa; mucosal lesion; skin disease;

XX keratinocyte differentiation; psoriasis; Parkinson's disease;

XX Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;

XX cell growth; cancer; tumour; viral infection; neurodegenerative disease;

XX antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

XX kidney tissue; apoptosis; therapeutic; tissue typing;

XX immunohistochemical staining; gene therapy; neuroprotective;

XX cytosolic; virucide; anticoagulant.

XX OS Homo sapiens.

XX FN US2003039971-A1.

XX PD 27-FEB-2003.

XX PF 16-JUL-2001; 2001US-00906646.

XX PR 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 17-SEP-1997; 97US-0059117P.

XX PR 17-SEP-1997; 97US-0059119P.

XX PR 17-SEP-1997; 97US-0059121P.

XX PR 17-SEP-1997; 97US-0059122P.

XX PR 18-SEP-1997; 97US-0059184P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 15-OCT-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 17-OCT-1997; 97US-0062287P.

XX PR 21-OCT-1997; 97US-0063486P.

XX PR 24-OCT-1997; 97US-0062814P.

XX PR 24-OCT-1997; 97US-0062816P.

XX PR 24-OCT-1997; 97US-0063045P.

XX PR 24-OCT-1997; 97US-0063120P.

XX PR 24-OCT-1997; 97US-0063121P.

XX PR 24-OCT-1997; 97US-0063127P.

XX PR 24-OCT-1997; 97US-0063128P.

XX PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066456P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-008026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 02-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PA XX

XX XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, KJavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams FM, Wood WI;
XX WPI; 2003-503392/47.
DR
XX
XX
PT New secreted and transmembrane polypeptides useful for treating skin,
PT neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and
PT multiple sclerosis.
XX
XX Example 33; SEQ ID NO 204; 471pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serve as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX
XX Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. NO. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 5 CCTTCTTACTCTCTCTGCTC 26
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 21
ACD66957/c

ID ACD66957 standard; DNA; 24 BP.
XX
AC ACD66957;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO263 PCR primer #3.
XX
KW Human; ss; PRO; secreted and transmembrane protein; inflammation;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; atherosclerosis;
KW infertility; birth defect; premature aging; malignancy; cancer; stroke;
KW heart attack; hypertension; gastrointestinal ulceration;
KW Parkinson's disease; Alzheimer's disease; AIDS; cholesterol uptake;
KW wound healing; tissue repair; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003045693-A1.
XX
PD 06-MAR-2003.
XX
PF 11-JUL-2001; 2001US-00903749.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063554P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 03-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.

PI 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088028P.
PR 10-SEP-1998; 98US-0098030P.
PR 14-SEP-1998; 98US-0098030P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0101917P.
PR 17-SEP-1998; 98US-0101917P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0143048P.
PR 08-SEP-1999; 98US-0146222P.
PR 13-SEP-1999; 98US-0146222P.
PR 13-SEP-1999; 98US-0146222P.
PR 15-SEP-1999; 98US-0146222P.
PR 15-SEP-1999; 98US-0146222P.
PR 05-OCT-1999; 98US-0146222P.
PR 29-NOV-1999; 98US-0146222P.
PR 30-NOV-1999; 98US-0146222P.
PR 01-DEC-1999; 98US-0146222P.
PR 02-DEC-1999; 98US-0146222P.
PR 16-DEC-1999; 98US-0146222P.
PR 20-DEC-1999; 98US-0146222P.
PR 20-DEC-1999; 98US-0146222P.
PR 20-DEC-1999; 98US-0146222P.
PR 05-JAN-2000; 2000US-0000219P.
PR 11-FEB-2000; 2000US-0000219P.
PR 22-FEB-2000; 2000US-0000219P.
PR 24-FEB-2000; 2000US-0000219P.
PR 02-MAR-2000; 2000US-0000219P.
PR 20-MAR-2000; 2000US-0000219P.
PR 30-MAR-2000; 2000US-0000219P.
PR 22-MAY-2000; 2000US-0000219P.
PR 02-JUN-2000; 2000US-0000219P.
PR 28-JUL-2000; 2000US-0000219P.
PR 24-AUG-2000; 2000US-0000219P.
PR 18-SEP-2000; 2000US-0000219P.
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-512316/48.
XX
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO1868), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in
PT mammals.
XX
XX
FS Example 33; Page 100; 476pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 61 PRO (secreted and transmembrane protein) polypeptides appearing as
CC ABO32756-ABO32816, or (b) any of 61 nucleotide sequences having 50-4053bp
CC fully defined in the specification; or the full length coding sequence of
CC any these 61 nucleotide sequences. Also included are the isolated PRO
CC polypeptide (lacking its associated signal peptide or an extracellular
CC domain of the PRO polypeptide, with or lacking its associated signal
CC peptide), a vector comprising the nucleic acid molecule, a host cell
CC comprising the vector fused to produce the PRO polypeptide, a chimaeric
CC molecule comprising the PRO polypeptide fused to a heterologous amino
CC acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868
CC polypeptide in a sample suspected of containing any of these PRO
CC polypeptides, linking a bioactive molecule to a cell expressing a PRO245

```
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0095803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

PA (GETH ) GENENTECH INC.
XX Ashkenazi A, Botstein D, Deanovors L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPT; 2003-492256/46.
XX Novel secreted and transmembrane PRO polypeptides and polynucleotides
PT encoding them, useful for treating abnormal bleeding involved in
PT gynecological diseases, skin diseases and neurodegenerative diseases.
XX Example 33; Page 100; 475pp; English.
XX The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides can be used in diagnosing or
CC treating abnormal bleeding involved in gynaecological diseases e.g. to
CC avoid or lessen the need for hysterectomy. They can also be used in
CC treating coronary ischaemic conditions, disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair of
CC acute and chronic mucosal lesions, skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis), Parkinson's disease,
CC Alzheimer's disease, asthma, rheumatoid arthritis, multiple sclerosis,
CC amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to
CC uncontrolled cell growth, such as cancer. This sequence represents a PCR
CC primer used to isolate a human PRO polynucleotide of the invention
XX SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Ov 5 CCTCTTGTACTCCTCCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 23
ADAL6240/C
ID ADAL6240 standard; DNA; 24 BP.
XX ADAL6240;
XX 06-NOV-2003 (first entry)
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabete; hyperinsulinaemia;
KW hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
KW arthritis; cardiant; vulnerary; cytostatic; ophthalmological;
osteopathic; antiarthritic; anorectic.
XX Homo sapiens.
XX US2003049621-A1.
XX 13-MAR-2003.
XX 11-JUL-2001; 2001US-00904119.
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
```


CC PRO genes may also be used in gene therapy, particularly for replacing a
 CC defective gene. The sequence presented is a PCR primer which was used to
 CC amplify a PRO polynucleotide of the invention.

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 9; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTCTGCTACTCCCTCTGCTC 26
 |||||
 Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 24

ADA42385/c

ID ADA42385 standard; DNA; 24 BP.

XX

AC ADA42385;

XX 20-NOV-2003 (first entry)

DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX

KW Human; PCR; primer; ss; PRO; secreted; transmembrane;

KW Gastrointestinal mucosa; mucosal lesion; skin disease;

KW keratinocyte differentiation; psoriasis; Parkinson's disease;

KW Alzheimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy;

KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;

KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

KW kidney tissue; apoptosis; therapeutic; tissue typing;

KW immunohistochemical staining; gene therapy; neurotropic; neuroprotective;

KW cytosolic; virucide; anticoagulant.

XX Homo sapiens.

OS

XX US2003054401-A1.

PN

XX 20-MAR-2003.

PD

XX 11-JUL-2001; 2001US-00903520.

PF 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062815P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 28-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98US-0100262P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-0113296P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 08-DEC-1999; 99WO-US020594.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.

(SETH) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tunas D;
 Williams PM, Wood WI;

WPI; 2003-755054/71.

Novel PRO polypeptides useful for treating Parkinson's disease,

PT

PT Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome,
PT psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological
XX diseases.
XX
PS Example 33; SEQ ID NO 204; 479pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTC 26
Db 24 CCTACTACTCTCTCGTC 3
RESULT 25
ACD23296/c
ID ACD23296 standard; DNA; 24 BP.
XX
AC ACD23296;
XX
DT 26-AUG-2003 (first entry)
XX
DE Human PRO PCR primer #83.
XX

KW Human; PRO; primer; ss; Parkinson's disease; Alzheimer's disease; ALS;
KW amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; AIDS;
KW Usher's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; congenital microvillus atrophy; psoriasis;
KW skin disease; endometrial bleeding; angiogenesis; ischaemic condition;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disease;
KW atherosclerosis; infertility; birth defect; premature aging; stroke; PCR;
KW diabetic complication.
XX Homo sapiens.
XX US2003064367-A1.
PN 03-APR-2003.
PD 13-JUL-2001; 2001US-00904485.
PF 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
XX 24-NOV-1997; 97US-0066772P.
XX 25-NOV-1997; 97US-0066840P.
XX 12-DEC-1997; 97US-0069425P.
XX 04-JUN-1998; 98US-0088026P.
XX 10-SEP-1998; 98US-0099803P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98US-0100262P.
XX 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-0113296P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000WO-US0665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-567176/53.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for
 PT treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
 PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
 XX
 PS Example 33; Page 101; 477pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are used for treating
 CC diseases related to growth or survival of nerve cells such as Parkinson's
 CC disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and
 CC neuropathies, diseases related to uncontrolled cell growth such as
 CC cancer, viral infections, Usher's syndrome, haemorrhage, enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration, congenital
 CC microvillus atrophy, skin diseases such as psoriasis and epithelial
 CC cancers, endometrial bleeding, angiogenesis, ischaemic conditions,
 CC asthma, rheumatoid arthritis, multiple sclerosis, inflammatory diseases,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, stroke and diabetic complications. The polynucleotides are
 CC also useful in chromosome and gene mapping. This sequence represents a
 CC PCR primer used in isolation of a human PRO polynucleotide of the
 CC invention
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 9; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTTCTTGTACTCTCTCTGCTC 26
 |||||
 Db 24 CCTACTACTACTCTCTCTGCTC 3
 RESULT 26
 ADA16664/c
 ID ADA16664 standard; DNA; 24 BP.
 XX ADA16664;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein, #40, PCR primer #3.
 XX
 KW Human; PCR; primer; ss; PRO; secreted; transmembrane;
 KW gastrointestinal mucosa; mucosal lesion; skin disease;
 KW keratinocyte differentiation; psoriasis; Parkinson's disease;
 KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
 KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
 KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
 KW kidney tissue; apoptosis; therapeutic; tissue typing;
 KW immunohistochemical staining; gene therapy; nootropic; neuroprotective;
 KW cytosstatic; virucide; anticoagulant.
 XX
 OS Homo sapiens.
 XX
 XX US2003039969-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 12-JUL-2001; 2001US-00904786.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.

```
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0100262P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 05-OCT-1999; 99US-0146222P.
PR 29-NOV-1999; 99US-0146222P.
PR 30-NOV-1999; 99US-0146222P.
PR 01-DEC-1999; 99US-0146222P.
PR 02-DEC-1999; 99US-0146222P.
PR 02-DEC-1999; 99US-0146222P.
PR 16-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 05-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-00003565.
PR 22-FEB-2000; 2000US-0000414.
PR 24-FEB-2000; 2000US-0000414.
PR 02-MAR-2000; 2000US-00005841.
PR 30-MAR-2000; 2000US-00007377.
PR 30-MAR-2000; 2000US-00008439.
PR 22-MAY-2000; 2000US-014042.
PR 02-JUN-2000; 2000US-015264.
PR 28-JUL-2000; 2000US-015264.
PR 24-AUG-2000; 2000US-023328.
PR 18-SEP-2000; 2000US-00665350.
PA (GETH ) GENENTECH INC.
XX
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX
XX WPI; 2003-503391/47.
XX
XX
XX New secreted and transmembrane PRO polypeptides e.g. PRO187, which is a
XX member of the epidermal growth factor-8 (EGF-8) family of proteins,
XX useful for treating cancer.
XX
XX Example 33; SEQ ID NO 204; 471pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
```

OS Homo sapiens.
XX US2003049622-A1.
XX 13-MAR-2003.
XX PF 14-JUL-2001; 2001US-00904956.
XX 17-SEP-1997; 97US-00591113P.
PR 17-SEP-1997; 97US-00591115P.
PR 17-SEP-1997; 97US-00591117P.
PR 17-SEP-1997; 97US-00591119P.
PR 17-SEP-1997; 97US-00591212P.
PR 17-SEP-1997; 97US-00591222P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062123P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066849P.
PR 12-DEC-1997; 97US-0069423P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX AShtenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AJ, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-521802/49.
XX New secreted and transmembrane PRO polypeptides, useful for treating the
PT cancer, skin disorders, neurodegenerative diseases, and for lessening the
PT effects of viral infection.
XX Example 33; SEQ ID NO 204; 473pp; English.
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of

therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.

Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTTCTGCTACTCTCTCGTC 26
||| || ||||| |||||
Db 24 CCTACTACTCTCTCGTC 3

RESULT 28

ADA41961/c
ID ADA41961 standard; DNA; 24 BP.
XX ADA41961;
AC
XX
XX 20-NOV-2003 (first entry)
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane;
KW gastrointestinal mucosa; mucosal lesion; skin disease;
KW keratinocyte differentiation; psoriasis; Parkinson's disease;
KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
KW kidney tissue; apoptosis; therapeutic; tissue typing;
KW immunohistochemical staining; gene therapy; nootropic; neuroprotective;
KW cytostatic; virucide; anticoagulant.
XX
OS Homo sapiens.
XX
XX US2003082540-A1.
PN
XX 01-MAY-2003.
PD
XX
XX 10-JUL-2001; 2001US-00902634.
PF
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059128P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063122P.
PR 24-OCT-1997; 97US-0063123P.
PR 24-OCT-1997; 97US-0063124P.
PR 24-OCT-1997; 97US-0063125P.
PR 24-OCT-1997; 97US-0063126P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-00633541P.
PR 28-OCT-1997; 97US-00633542P.
PR 28-OCT-1997; 97US-00633544P.
PR 28-OCT-1997; 97US-00633549P.
PR 28-OCT-1997; 97US-00633550P.
PR 28-OCT-1997; 97US-00633564P.
PR 29-OCT-1997; 97US-00633704P.
PR 29-OCT-1997; 97US-00633732P.
PR 29-OCT-1997; 97US-00633734P.
PR 29-OCT-1997; 97US-00633735P.
PR 29-OCT-1997; 97US-00633738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065593P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WT;

XX WPI; 2003-755103/71.

XX New PRO polypeptides useful for treating Parkinson's disease,

PT enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration,

PT Alzheimer's disease, amyotrophic lateral sclerosis and Usher syndrome.

XX Example 33; SEQ ID NO 204; 469pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides

CC and the nucleic acid encoding them. The polypeptides can be used to raise

CC antibodies that specifically bind to the PRO polypeptide, for linking a

CC bioactive molecule to a cell expressing a PRO protein and for modulating

CC at least one biological activity of a cell. PRO polypeptides are useful

CC for detecting other PRO polypeptides in a sample and for linking a

CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO

CC polypeptide antibodies are useful for modulating the biological activity

CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful

CC for treating disorders associated with the preservation and maintenance

CC of gastrointestinal mucosa and the repair of acute and chronic mucosal

CC lesions, skin diseases associated with abnormal keratinocyte

CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's

CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and

CC additionally, disease related to uncontrolled cell growth, e.g. cancer.

CC PRO polypeptides also serves as tumour specific antigens which may be

CC exploited as therapeutic targets for anti-tumour drugs, and are also

CC employed therapeutically in vivo for lessening the effects of viral

CC infection. The PRO polypeptides can be also used in assays to determine

CC if it has a role in neurodegenerative diseases or their reversal, as an

CC antithrombotic agent with reduced risk for haemorrhage as compared with

CC heparin, in treating other PRO-associated disorders, in modulating

CC endometrial bleeding angiogenesis, and may also have an effect on kidney

CC tissue. PRO polypeptides and their portions affect the expression of

CC genes which have a role in apoptosis. The polynucleotides are useful in

CC molecular biology including uses as hybridisation probes for cDNA library

CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in

CC chromosome and gene mapping, in the generation of antisense RNA and DNA,

CC for preparing PRO polypeptides, for generating transgenic animals or

CC knockout animals which are useful in the development and screening of

CC therapeutically useful reagents, as probes and for the genetic analysis

CC of individuals with genetic disorders as well as for recombinantly

CC expressing the protein and for chromosome identification. The proteins

CC are useful as molecular marker for protein electrophoresis purposes, as

CC therapeutic agents, for screening compounds to identify those that mimic

CC the PRO polypeptide (agonists) or prevent the effect of the PRO

CC polypeptide (antagonists). The polynucleotides and proteins are useful

CC for tissue typing. PRO antibodies are useful for immunohistochemical

CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in

CC diagnostic assays for PRO e.g. detecting its expression in specific

CC cells, tissues or serum and for affinity purification of PRO from

CC recombinant cell culture or natural sources. The PRO genes may also be

CC used in gene therapy, particularly for replacing a defective gene. The

CC sequence presented is a PCR primer which was used to amplify a PRO

CC polynucleotide of the invention.

XX

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 9; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTGATCTCTCTGTC 26

Db 24 CCTACTACTACTCTCTGTC 3

RESULT 29

ADA17308/c

ID ADA17308 standard; DNA; 24 BP.

XX

AC ADA17308;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX

KW Human; PCR; primer; ss; PRO; secreted; transmembrane;

KW gastrointestinal mucosa; mucosal lesion; skin disease;

KW keratinocyte differentiation; psoriasis; Parkinson's disease;

KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;

KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;

KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;

KW kidney tissue; apoptosis; therapeutic; tissue typing;

KW immunohistochemical staining; gene therapy; nontropic; neuroprotective;

KW cytostatic; virucide; anticoagulant.

XX

OS Homo sapiens.

XX

US2003017498-A1.

XX

PD 23-JAN-2003.

XX

PF 17-JUL-2001; 2001US-00908093.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 04-JUN-1998; 98US-0088036P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98US-0100262P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-0113296P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 PI Fliviaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI: 2003-531434/50.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Example 33; SEQ ID NO 204; 475pp; English.
 XX
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC and the nucleic acid encoding them. The polypeptides can be used to raise
 CC antibodies that specifically bind to the PRO polypeptide, for linking a
 CC bioactive molecule to a cell expressing a PRO protein and for modulating
 CC at least one biological activity of a cell. PRO polypeptides are useful
 CC for detecting other PRO polypeptides in a sample and for linking a
 CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
 CC polypeptide antibodies are useful for modulating the biological activity
 CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful

CC for treating disorders associated with the preservation and maintenance
 CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
 CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
 CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
 CC PRO polypeptides also serves as tumour specific antigens which may be
 CC exploited as therapeutic targets for anti-tumour drugs, and are also
 CC employed therapeutically in vivo for lessening the effects of viral
 CC infection. The PRO polypeptides can be also used in assays to determine
 CC if it has a role in neurodegenerative diseases or their reversal, as an
 CC antithrombotic agent with reduced risk for haemorrhage as compared with
 CC heparin, in treating other PRO-associated disorders, in modulating
 CC endometrial bleeding angiogenesis, and may also have an effect on kidney
 CC tissue. PRO polypeptides and their portions affect the expression of
 CC genes which have a role in apoptosis. The polynucleotides are useful in
 CC molecular biology including uses as hybridisation probes for cDNA library
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC for preparing PRO polypeptides, for generating transgenic animals or
 CC knockout animals which are useful in the development and screening of
 CC therapeutically useful reagents, as probes and for the genetic analysis
 CC of individuals with genetic disorders as well as for recombinantly
 CC expressing the protein and for chromosome identification. The proteins
 CC are useful as molecular marker for protein electrophoresis purposes, as
 CC therapeutic agents, for screening compounds to identify those that mimic
 CC the PRO polypeptide (agonists) or prevent the effect of the PRO
 CC polypeptide (antagonists). The polynucleotides and proteins are useful
 CC for tissue typing. PRO antibodies are useful for immunohistochemical
 CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
 CC diagnostic assays for PRO e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. The PRO genes may also be
 CC used in gene therapy, particularly for replacing a defective gene. The
 CC sequence presented is a PCR primer which was used to amplify a PRO
 CC polynucleotide of the invention.
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
 Query Match 66.2%; Score 17.2; DB 9; Length 24;
 Best Local Similarity 86.4%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 CCTCTGTGTACTCTCTCTGCTC 26
 Db 24 CCTACTACTACTCTCTGCTC 3
 RESULT 30
 ADA42811/c
 ID ADA42811 standard; DNA; 24 BP.
 XX
 AC ADA42811;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein, #40, PCR primer #3.
 XX
 KW Human; PCR; primer; ss; PRO; secreted; transmembrane;
 KW gastrointestinal mucosa; mucosal lesion; skin disease;
 KW keratinocyte differentiation; psoriasis; Parkinson's disease;
 KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
 KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
 KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
 KW kidney tissue; apoptosis; therapeutic; tissue typing;
 KW immunohistochemical staining; gene therapy; neurotropic; neuroprotective;
 KW cytosstatic; virucide; anticoagulant.
 XX
 OS Homo sapiens.
 XX
 PN US2003054351-A1.
 XX
 PD 20-MAR-2003.

XX 13-JUL-2001; 2001US-00904462.
PF 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063323P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065693P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-755052/71.
XX Novel isolated secreted and transmembrane PRO polypeptide, useful for
XX tissue typing, treating Parkinson's disease, Alzheimer's disease, birth
XX defects, cancer.
XX Example 33; SEQ ID NO 204; 464pp; English.
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
XX at least one biological activity of a cell. PRO polypeptides are useful
XX for detecting other PRO polypeptides in a sample and for linking a
XX bioactive molecule to a cell expressing a PRO polypeptide. The PRO
XX polypeptide antibodies are useful for modulating the biological activity
XX of a cell expressing PRO polypeptides. PRO polypeptides are also useful
XX for treating disorders associated with the preservation and maintenance
XX of gastrointestinal mucosa and the repair of acute and chronic mucosal
XX lesions, skin diseases associated with abnormal keratinocyte
XX differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
XX diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
XX additionally, disease related to uncontrolled cell growth, e.g. cancer.
XX PRO polypeptides also serves as tumour specific antigens which may be
XX exploited as therapeutic targets for anti-tumour drugs, and are also
XX employed therapeutically in vivo for lessening the effects of viral
XX infection. The PRO polypeptides can be also used in assays to determine
XX if it has a role in neurodegenerative diseases or their reversal, as an
XX antithrombotic agent with reduced risk for haemorrhage as compared with
XX heparin, in treating other PRO-associated disorders, in modulating
XX endometrial bleeding angiogenesis, and may also have an effect on kidney
XX tissue. PRO polypeptides and their portions affect the expression of
XX genes which have a role in apoptosis. The polynucleotides are useful in
XX molecular biology including uses as hybridisation probes for cDNA library
XX to isolate the full-length PRO cDNA or to isolate other cDNAs, in
XX chromosome and gene mapping, in the generation of antisense RNA and DNA,
XX for preparing PRO polypeptides, for generating transgenic animals or
XX knockout animals which are useful in the development and screening of
XX therapeutically useful reagents, as probes and for the genetic analysis
XX of individuals with genetic disorders as well as for recombinantly
XX expressing the protein and for chromosome identification. The proteins
XX are useful as molecular marker for protein electrophoresis purposes, as
XX therapeutic agents, for screening compounds to identify those that mimic

PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-765399/72.
XX
XX New isolated secreted and transmembrane polypeptide, useful for treating
PT diseases, e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
XX
XX Example 33; Page 96; 467pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serves as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX

SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTCTCTGTACTCCTCCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 33
ADB74866/c
ID ADB74866 standard; DNA; 24 BP.
XX
XX ADB74866;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane;
KW Gastrointestinal mucoas; mucosal lesion; skin disease;
KW keratinocyte differentiation; psoriasis; Parkinson's disease;
KW Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy;
KW cell growth; cancer; tumour; viral infection; neurodegenerative disease;
KW antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis;
KW kidney tissue; apoptosis; therapeutic; tissue typing;
KW immunohistochemical staining; gene therapy; nontropic; neuroprotective;
KW cytosstatic; virucide; anticoagulant.
XX
XX Homo sapiens.
OS
XX US2003082542-A1.
PN
XX
XX 01-MAY-2003.
PD
XX
XX 17-JUL-2001; 2001US-00907979.
PF
XX
XX 17-SEP-1997; 97US-0059113P.
PR
XX 17-SEP-1997; 97US-0059115P.
PR
XX 17-SEP-1997; 97US-0059117P.
PR
XX 17-SEP-1997; 97US-0059119P.
PR
XX 17-SEP-1997; 97US-0059121P.
PR
XX 17-SEP-1997; 97US-0059122P.
PR
XX 18-SEP-1997; 97US-0059184P.
PR
XX 18-SEP-1997; 97US-0059263P.
PR
XX 15-OCT-1997; 97US-0062125P.
PR
XX 17-OCT-1997; 97US-0062285P.
PR
XX 17-OCT-1997; 97US-0062287P.
PR
XX 21-OCT-1997; 97US-0063486P.
PR
XX 24-OCT-1997; 97US-0062814P.
PR
XX 24-OCT-1997; 97US-0062816P.
PR
XX 24-OCT-1997; 97US-0063045P.
PR
XX 24-OCT-1997; 97US-0063120P.
PR
XX 24-OCT-1997; 97US-0063121P.
PR
XX 24-OCT-1997; 97US-0063128P.
PR
XX 27-OCT-1997; 97US-0063327P.
PR
XX 27-OCT-1997; 97US-0063329P.
PR
XX 28-OCT-1997; 97US-0063541P.
PR
XX 28-OCT-1997; 97US-0063542P.
PR
XX 28-OCT-1997; 97US-0063544P.
PR
XX 28-OCT-1997; 97US-0063549P.
PR
XX 28-OCT-1997; 97US-0063550P.
PR
XX 28-OCT-1997; 97US-0063564P.
PR
XX 29-OCT-1997; 97US-0063435P.
PR
XX 29-OCT-1997; 97US-0063704P.
PR
XX 29-OCT-1997; 97US-0063732P.
PR
XX 29-OCT-1997; 97US-0063734P.
PR
XX 29-OCT-1997; 97US-0063735P.
PR
XX 29-OCT-1997; 97US-0063738P.
PR

PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 18-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088028P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0100262P.
PR 17-SEP-1998; 98US-0100262P.
PR 17-SEP-1998; 98US-0100262P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113298P.
PR 07-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 08-SEP-1999; 98US-0146222P.
PR 13-SEP-1999; 98US-0146222P.
PR 15-SEP-1999; 98US-0146222P.
PR 05-OCT-1999; 98US-0146222P.
PR 29-NOV-1999; 98US-0146222P.
PR 30-NOV-1999; 98US-0146222P.
PR 01-DEC-1999; 98US-0146222P.
PR 02-DEC-1999; 98US-0146222P.
PR 16-DEC-1999; 98US-0146222P.
PR 20-DEC-1999; 98US-0146222P.
PR 20-DEC-1999; 98US-0146222P.
PR 05-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-0000355.
PR 22-FEB-2000; 2000US-0000444.
PR 24-FEB-2000; 2000US-0000504.
PR 02-MAR-2000; 2000US-0005841.
PR 20-MAR-2000; 2000US-0007377.
PR 30-MAR-2000; 2000US-0008439.
PR 22-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0020710.
PR 18-SEP-2000; 2000US-00665350.
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams FM, Wood WI;
XX
XX WPI; 2003-765412/72.
XX
XX Novel isolated native PRO polypeptide useful for tissue typing,
PT modulating biological activity of cell, as molecular weight markers in
PT protein electrophoresis, for treating enterocolitis, Zollinger-Ellison
PT syndrome.
XX

PS Example 33; Page 101; 475pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful
CC for treating disorders associated with the preservation and maintenance
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and
CC additionally, disease related to uncontrolled cell growth, e.g. cancer.
CC PRO polypeptides also serve as tumour specific antigens which may be
CC exploited as therapeutic targets for anti-tumour drugs, and are also
CC employed therapeutically in vivo for lessening the effects of viral
CC infection. The PRO polypeptides can be also used in assays to determine
CC if it has a role in neurodegenerative diseases or their reversal, as an
CC antithrombotic agent with reduced risk for haemorrhage as compared with
CC heparin, in treating other PRO-associated disorders, in modulating
CC endometrial bleeding angiogenesis, and may also have an effect on kidney
CC tissue. PRO polypeptides and their portions affect the expression of
CC genes which have a role in apoptosis. The polynucleotides are useful in
CC molecular biology including uses as hybridisation probes for cDNA library
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC for preparing PRO polypeptides, for generating transgenic animals or
CC knockout animals which are useful in the development and screening of
CC therapeutically useful reagents, as probes and for the genetic analysis
CC of individuals with genetic disorders as well as for recombinantly
CC expressing the protein and for chromosome identification. The proteins
CC are useful as molecular marker for protein electrophoresis purposes, as
CC therapeutic agents, for screening compounds to identify those that mimic
CC the PRO polypeptide (agonists) or prevent the effect of the PRO
CC polypeptide (antagonists). The polynucleotides and proteins are useful
CC for tissue typing. PRO antibodies are useful for immunohistochemical
CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in
CC diagnostic assays for PRO e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO from
CC recombinant cell culture or natural sources. The PRO genes may also be
CC used in gene therapy, particularly for replacing a defective gene. The
CC sequence presented is a PCR primer which was used to amplify a PRO
CC polynucleotide of the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTTCTGTACTCCTCCTGCTC 26
||| || ||||| |||||
DB 24 CCTACTACTACTCCTCCTGCTC 3
RESULT 34
ADC28512/C
ID ADC28512 standard; DNA; 24 BP.
XX
XX
AC ADC28512;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;

rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
retinitis pigmentosa; obesity; diabete; hyperinsulinaemia;
hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
arthritis; cardiant; vulnerary; cytostatic; ophthalmological;
osteopathic; antiarthritic; anorectic.

Homo sapiens.

US2003059772-A1.

27-MAR-2003.

18-JUL-2001; 2001US-00909064.

17-SEP-1997; 97US-0059113P.

17-SEP-1997; 97US-0059115P.

17-SEP-1997; 97US-0059117P.

17-SEP-1997; 97US-0059119P.

17-SEP-1997; 97US-0059121P.

17-SEP-1997; 97US-0059122P.

17-SEP-1997; 97US-0059184P.

18-SEP-1997; 97US-0059263P.

18-SEP-1997; 97US-0059266P.

15-OCT-1997; 97US-0062125P.

17-OCT-1997; 97US-0062285P.

17-OCT-1997; 97US-0062287P.

21-OCT-1997; 97US-0063486P.

24-OCT-1997; 97US-0062814P.

24-OCT-1997; 97US-0062816P.

24-OCT-1997; 97US-0063045P.

24-OCT-1997; 97US-0063120P.

24-OCT-1997; 97US-0063121P.

24-OCT-1997; 97US-0063127P.

24-OCT-1997; 97US-0063128P.

27-OCT-1997; 97US-0063327P.

27-OCT-1997; 97US-0063329P.

28-OCT-1997; 97US-0063541P.

28-OCT-1997; 97US-0063542P.

28-OCT-1997; 97US-0063544P.

28-OCT-1997; 97US-0063549P.

28-OCT-1997; 97US-0063550P.

28-OCT-1997; 97US-0063564P.

28-OCT-1997; 97US-0063435P.

29-OCT-1997; 97US-0063704P.

29-OCT-1997; 97US-0063732P.

29-OCT-1997; 97US-0063734P.

29-OCT-1997; 97US-0063735P.

29-OCT-1997; 97US-0063738P.

29-OCT-1997; 97US-0064215P.

31-OCT-1997; 97US-0063870P.

31-OCT-1997; 97US-0064103P.

03-NOV-1997; 97US-0064248P.

07-NOV-1997; 97US-0064809P.

12-NOV-1997; 97US-0065186P.

17-NOV-1997; 97US-0065846P.

18-NOV-1997; 97US-0065693P.

21-NOV-1997; 97US-0066120P.

21-NOV-1997; 97US-0066364P.

24-NOV-1997; 97US-0066453P.

24-NOV-1997; 97US-0066466P.

24-NOV-1997; 97US-0066511P.

24-NOV-1997; 97US-0066770P.

24-NOV-1997; 97US-0066772P.

25-NOV-1997; 97US-0066840P.

12-DEC-1997; 97US-0069425P.

04-JUN-1998; 98US-0088026P.

10-SEP-1998; 98US-0098030P.

10-SEP-1998; 98WO-US018824.

14-SEP-1998; 98US-0100262P.

14-SEP-1998; 98WO-US019177.

16-SEP-1998; 98WO-US019330.

17-SEP-1998; 98US-0100858P.

17-SEP-1998; 98WO-US019437.

13-OCT-1998; 98US-0104080P.

20-NOV-1998; 98US-0109304P.

01-DEC-1998; 98WO-US025108.

22-DEC-1998; 98US-0113296P.

07-JUL-1999; 99US-0143048P.

26-JUL-1999; 99US-0145698P.

28-JUL-1999; 99US-0146222P.

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020944.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-NOV-1999; 99WO-US028214.

30-NOV-1999; 99WO-US028313.

01-DEC-1999; 99WO-US028301.

02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030911.

20-DEC-1999; 99WO-US030999.

05-JAN-2000; 2000WO-US000219.

11-FEB-2000; 2000WO-US003565.

22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US005004.

02-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US007377.

30-MAR-2000; 2000WO-US008439.

22-MAY-2000; 2000WO-US014042.

02-JUN-2000; 2000WO-US015264.

28-JUL-2000; 2000WO-US020710.

24-AUG-2000; 2000WO-US023328.

18-SEP-2000; 2000WO-US0665350.

(GETH) GENENTECH INC.

Aehkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;

Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

Williams PM, Wood WI;

WPI; 2003-540670/51.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.

Example 33; SEQ ID NO 204; 470pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonatal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated proliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial cells, modulating glucose or FFA uptake, inducing proliferation and/or re-differentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia, hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polynucleotides

CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
CC useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a PCR primer which was used to
CC amplify a PRO polynucleotide of the invention.

XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 10; Length 24;

Best Local Similarity 86.4%; Pred. No. 4.7e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTGTGACTCCCTGCTC 26

Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 35

ID ADC39712/c
ID ADC39712 standard; DNA; 24 BP.

XX AC ADC39712;

XX DT 18-DEC-2003 (first entry)

XX DE Human secreted/transmembrane protein, #40, PCR primer #3.

XX Human; PCR; primer; ss; PRO; secreted, transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
KW hypotension; bone disorder; cartilage disorder; sport injury;
KW arthritis; cardiac; vulnary; cytostatic; ophthalmological;
KW osteopathic; antiarthritic; anorectic.

XX OS Homo sapiens.

XX PN US2003059828-A1.

XX PD 27-MAR-2003.

XX PF 13-JUL-2001; 2001US-00904553.

XX PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-009803P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.

PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 08-SEP-1999; 99WO-US020534.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000WO-US0665350.
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Fan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPT; 2003-540676/51.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PI encoding them useful for treating skin, neurodegenerative diseases, as an
PT antithrombotic agent and for inducing endothelial cell apoptosis.
XX
XX Example 33; SEQ ID NO 204; 473pp; English.
PS
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating

at least one biological activity of a cell. PRO polypeptides are useful
for detecting other PRO polypeptides in a sample and for linking a
bioactive molecule to a cell expressing a PRO polypeptide. The PRO
polypeptide antibodies are useful for modulating the biological activity
of a cell expressing PRO polypeptides. The PRO polypeptides or
polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
bioreactors. These are useful for stimulating hypertrophy of neonatal
heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
proliferation of endothelial cells, modulating the proliferation of
stimulated T-lymphocytes, enhancing the survival or proliferation of
retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
cells, modulating glucose or FFA uptake, inducing proliferation and/or re
differentiation of chondrocytes. In particular, these are useful for
detecting or treating cardiac insufficiency disorders, wounds, cancerous
tumours, retinal disorders or injuries (e.g. loss of sight due to
retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
hypopinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
arthritis) in mammals. PRO polypeptides and their portions affect the
expression of genes which have a role in cell death. The polynucleotides
are useful in molecular biology including uses as hybridisation probes
for cDNA library to isolate the full-length PRO cDNA or to isolate other
cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
and DNA, for preparing PRO polypeptides, for generating transgenic
animals or knockout animals which are useful in the development and
screening of therapeutically useful reagents, as probes and for the
genetic analysis of individuals with genetic disorders as well as for
recombinantly expressing the protein and for chromosome identification.
The proteins are useful as molecular marker for protein electrophoresis
purposes, as therapeutic agents, for screening compounds to identify
those that mimic the PRO polypeptide (agonists) or prevent the effect of
the PRO polypeptide (antagonists). The polynucleotides and proteins are
useful for tissue typing. PRO antibodies are useful for
immunohistochemical staining and/or assay of sample fluids. Anti-PRO
antibodies are useful in diagnostic assays for PRO e.g. detecting its
expression in specific cells, tissues or serum and for affinity
purification of PRO from recombinant cell culture or natural sources. The
PRO genes may also be used in gene therapy, particularly for replacing a
defective gene. The sequence presented is a PCR primer which was used to
amplify a PRO polynucleotide of the invention.

Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTTGTACTCTCTGCTC 26
||| || ||||| |||||
Db 24 CCTACTACTCTCTGCTC 3
RESULT 37
ADC19050/c
ID ADC19050 standard; DNA; 24 BP.
XX
XX ADC19050;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy; proliferation;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
KW hypopinsulinaemia; bone disorder; cartilage disorder; sport injury;
KW osteopathic; cardiac; vulnery; cytostatic; ophthalmological;
XX
XX antiarthritic; anorectic.
OS Homo sapiens.

XX US2003036061-A1.
PN 20-FEB-2003.
XX 18-JUL-2001; 2001US-00909204.
XX 17-SEP-1997; 97US-00591133P.
PR 17-SEP-1997; 97US-00591151P.
XX 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-00592263P.
XX 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
XX 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062287P.
XX 17-OCT-1997; 97US-0063486P.
PR 21-OCT-1997; 97US-0062844P.
XX 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063550P.
PR 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
PR 03-NOV-1997; 97US-0064103P.
XX 07-NOV-1997; 97US-0064284P.
PR 12-NOV-1997; 97US-0064809P.
XX 17-NOV-1997; 97US-0065186P.
PR 18-NOV-1997; 97US-0065846P.
XX 21-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
XX 24-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066770P.
PR 25-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
XX 04-JUN-1998; 98US-0069425P.
PR 10-SEP-1998; 98US-009803P.
XX 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
XX 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
XX 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
XX 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
XX 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.

PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
XX 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
XX 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
XX 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
XX 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
XX 18-SEP-2000; 2000WO-US023328.
XX 18-SEP-2000; 2000US-00665350.
PA (GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvarozoff E, Fong S, Gao W, Gerber H, Hillan KJ, Kljavin IJ;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI William PM, Wood WI;
XX WPI; 2003-615762/58.
DR Novel secreted and transmembrane polypeptide for modulating biological
XX activity of cell expressing the polypeptide, identifying agonists or
XX antagonists of polypeptide, and as molecular weight markers.
XX Example 33; SEQ ID NO 204; 476pp; English.
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX and the nucleic acid encoding them. The polypeptides can be used to raise
XX antibodies that specifically bind to the PRO polypeptide, for linking a
XX bioactive molecule to a cell expressing a PRO protein and for modulating
XX at least one biological activity of a cell. PRO polypeptides are useful
XX for detecting other PRO polypeptides in a sample and for linking a
XX bioactive molecule to a cell expressing a PRO polypeptide. The PRO
XX polypeptide antibodies are useful for modulating the biological activity
XX of a cell expressing PRO polypeptides. The PRO polypeptides or
XX polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
XX bioreactors. These are useful for stimulating hypertrophy of neonatal
XX heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
XX proliferation of endothelial cells, modulating the proliferation of
XX stimulated T-lymphocytes, enhancing the survival or proliferation of
XX retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
XX cells, modulating glucose or FFA uptake, inducing proliferation and/or re
XX differentiation of chondrocytes. In particular, these are useful for
XX detecting or treating cardiac insufficiency disorders, wounds, cancerous
XX tumours, retinal disorders or injuries (e.g. loss of sight due to
XX retinitis pigmentosa), obesity, diabetes, hyperinsulinemia,
XX hypoparathyroidism, or bone or cartilage disorders (e.g. sports injuries or
XX arthritis) in mammals. PRO polypeptides and their portions affect the
XX expression of genes which have a role in cell death. The polynucleotides
XX are useful in molecular biology including uses as hybridisation probes
XX for cDNA library to isolate the full-length PRO cDNA or to isolate other
XX cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
XX and DNA, for preparing PRO polypeptides, for generating transgenic
XX animals or knockout animals which are useful in the development and
XX screening of therapeutically useful reagents, as probes and for the
XX genetic analysis of individuals with genetic disorders as well as for
XX recombinantly expressing the protein and for chromosome identification.

The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to amplify a PRO polynucleotide of the invention.

24-NOV-1997; 97US-0066770P.
25-NOV-1997; 97US-0066772P.
25-NOV-1997; 97US-0066840P.
12-DEC-1997; 97US-0069425P.
14-JUN-1998; 98US-0088026P.
10-SEP-1998; 98US-0098803P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98US-0100262P.
16-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
13-OCT-1998; 98US-0104080P.
20-NOV-1998; 98US-0109304P.
01-DEC-1998; 98WO-US025108.
22-DEC-1998; 98US-0113296P.
07-JUL-1999; 98US-0143048P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0146222P.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028564.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Ann Roy M, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-585107/55.
XX
PT Novel isolated PRO polypeptides e.g. PRO234 (useful for treating
PT rheumatoid arthritis, psoriasis and multiple sclerosis) and PRO187
PT (useful for treating Alzheimer's disease, cancer).
XX
XX Example 33; SEQ ID NO 204; 45ipp; English.
PS
PS The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. The PRO polypeptides or
CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are useful for stimulating hypertrophy of neonatal
CC heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
CC proliferation of endothelial cells, modulating the proliferation of
CC stimulated T-lymphocytes, enhancing the survival or proliferation of
CC retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial
CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
CC differentiation of chondrocytes. In particular, these are useful for
CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
CC tumours, retinal disorders or injuries (e.g. loss of sight due to
CC retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
CC hypoparathyroidism, or bone or cartilage disorders (e.g. sports injuries or
CC arthritis) in mammals. PRO polypeptides and their portions affect the
CC expression of genes which have a role in cell death. The polynucleotides
CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
CC useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a PCR primer which was used to
CC amplify a PRO polynucleotide of the invention.
XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 CCTCTGTGTACTCTCTCTGTC 26
Db 24 CCTACTACTACTCTCTGTC 3
RESULT 40
ADC28936/c
ID ADC28936 standard; DNA; 24 BP.
XX
XX AC ADC28936;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #40, PCR primer #3.
XX
XX Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic;
KW tissue typing; immunohistochemical staining; gene therapy; proliferation;
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;
KW retinitis pigmentosa; obesity; diabetes; hyperinsulinaemia;
KW hypoparathyroidism; bone disorder; cartilage disorder; sport injury;
KW arthritis; cardant; vulnary; cytostatic; ophthalmological;
KW osteopathic; antiarthritic; anorectic.
XX
XX Homo sapiens.
OS
XX US2003049677-A1.
PN
PD 13-MAR-2003.
XX
XX 17-JUL-2001; 2001US-00907794.
XX
XX 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062123P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100859P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 27-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028219.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-615797/58.
DR
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating skin, neurodegenerative diseases, as an
PT antithrombotic agent and for inducing endothelial cell apoptosis.
XX
PS Example 33; SEQ ID NO 204; 470pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC and the nucleic acid encoding them. The polypeptides can be used to raise
CC antibodies that specifically bind to the PRO polypeptide, for linking a
CC bioactive molecule to a cell expressing a PRO protein and for modulating
CC at least one biological activity of a cell. PRO polypeptides are useful
CC for detecting other PRO polypeptides in a sample and for linking a
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO
CC polypeptide antibodies are useful for modulating the biological activity
CC of a cell expressing PRO polypeptides. The PRO polypeptides or
CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are useful for stimulating hypertrophy of neonatal
CC heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated
CC proliferation of endothelial cells, modulating the proliferation of
CC stimulated T-lymphocytes, enhancing the survival or proliferation of
CC retinal neurons or rod photoreceptor cells, inducing C-fos in endothelial
CC cells, modulating glucose or FFA uptake, inducing proliferation and/or re
CC differentiation of chondrocytes. In particular, these are useful for
CC detecting or treating cardiac insufficiency disorders, wounds, cancerous
CC tumours, retinal disorders or injuries (e.g. loss of sight due to
CC retinitis pigmentosa), obesity, diabetes, hyperinsulinaemia,
CC hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or
CC arthritis) in mammals. PRO polypeptides and their portions affect the
CC expression of genes which have a role in cell death. The polynucleotides
CC are useful in molecular biology including uses as hybridisation probes
CC for cDNA library to isolate the full-length PRO cDNA or to isolate other
CC cDNAs, in chromosome and gene mapping, in the generation of antisense RNA
CC and DNA, for preparing PRO polypeptides, for generating transgenic
CC animals or knockout animals which are useful in the development and
CC screening of therapeutically useful reagents, as probes and for the
CC genetic analysis of individuals with genetic disorders as well as for
CC recombinantly expressing the protein and for chromosome identification.
CC The proteins are useful as molecular marker for protein electrophoresis
CC purposes, as therapeutic agents, for screening compounds to identify
CC those that mimic the PRO polypeptide (agonists) or prevent the effect of
CC the PRO polypeptide (antagonists). The polynucleotides and proteins are
CC useful for tissue typing. PRO antibodies are useful for
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its
CC expression in specific cells, tissues or serum and for affinity

CC purification of PRO from recombinant cell culture or natural sources. The
CC PRO genes may also be used in gene therapy, particularly for replacing a
CC defective gene. The sequence presented is a PCR primer which was used to
CC amplify a PRO polynucleotide of the invention.

XX
SQ Sequence 24 BP; 7 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 4.7e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTGTACTCTCTCTGCTC 26
||| || |||||
Db 24 CCTACTACTCTCTCTGCTC 3

Search completed: November 18, 2005, 11:52:33
Job time : 181.034 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1243.65 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTGTGACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsal:*
9: gb_gser2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	71.5	49	8	AZ407440 1M0178H15
2	18	69.2	27	8	AZ345323 1M0079M16
3	17	65.4	33	8	AZ435186 1M0222E03
4	17	65.4	35	8	AZ421500 1M0199J13
5	17	65.4	36	8	AZ479840 1M0300P16
6	17	65.4	37	8	AZ623276 1M0460M16
7	17	65.4	44	8	AZ968544 2M0240J20
8	17	65.4	45	8	AZ843544 2M0142Q22
9	17	65.4	50	8	AZ397298 1M0162A13
10	16.6	63.8	41	1	AU256766 AU256766
11	16.4	63.1	41	8	AZ450486 1M0249D13
12	16.2	62.3	27	8	AZ835139 2M0129P09
13	16.2	62.3	37	1	AI966611 sc53c11.y
14	16	61.5	50	9	CR235166 Forward s
15	15.6	60.0	43	1	AI570014 tr91a09.x
16	15.4	59.2	32	8	AZ500072 1M0338A14
17	15.4	59.2	31	8	AZ792853 2M0045C07
18	15.4	59.2	33	8	AZ783357 2M0025B05
19	15.4	59.2	34	1	AV847122 AV847122
20	15.4	59.2	37	8	AZ392980 1M0155F13
21	15.4	59.2	37	8	AZ761912 1M0356B02
22	15.4	59.2	40	8	AZ345503 1M0080G05
23	15.4	59.2	46	1	AI088341 qb07a07.x
24	15.4	59.2	49	1	AA388129 vc86f05.r

c 25	15.4	59.2	50	1	AU102295
c 26	15	57.7	29	8	AZ854411 2M0158B05
c 27	15	57.7	40	8	AZ537227 AST-2P030
c 28	15	57.7	45	5	BQ590260 E012843-0
c 29	14.8	56.9	26	8	AZ942099 2M0202C09
c 30	14.8	56.9	44	8	AZ456843 1M0259J24
c 31	14.8	56.9	50	8	AZ767297 1M0566G21
c 32	14.6	56.2	39	1	AJ794161 AJ794161
c 33	14.6	56.2	50	7	CF329688 NACL-05-
c 34	14.4	55.4	38	2	BE736376 601306S13
c 35	14.4	55.4	40	7	CF319095 HD--09-H1
c 36	14.4	55.4	43	7	CF292564 30DGS--01
c 37	14.4	55.4	48	8	AZ443723 1M0238D11
c 38	14.4	55.4	50	9	AL943250 Arabidops
c 39	14.2	54.6	21	8	AZ645664 1M0511C13
c 40	14.2	54.6	39	7	CO783803 BL279A.AO
c 41	14.2	54.6	42	7	R39311 yd01c07.s1
c 42	14.2	54.6	43	7	W86565 zh63h03.r1
c 43	14.2	54.6	46	1	AI124130 SMOVL3CAN
c 44	14.2	54.6	48	8	BH629491 1007073A0
c 45	14.2	54.6	49	1	AA719607 zh37a05.s

ALIGNMENTS

RESULT 1
AZ407440
LOCUS
DEFINITION 1M0178H15F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0178H15 F, genomic survey sequence.
ACCESSION AZ407440
VERSION AZ407440.1 GI:10531549
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0178 row: H column: 15
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 49.
Location/Qualifiers
1. 49
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUC1M0178H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 71.5%; Score 18.6; DB 8; Length 49;
Best Local Similarity 84.0%; Pred. No. 1.1e+04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 24 CCTCTCTCTCTCTCTCTCTCTGCTC 48

RESULT 2
AZ345323/c
LOCUS
DEFINITION
1M0079M16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0079M16 R, genomic survey sequence.

ACCESSION
AZ345323
VERSION
AZ345323.1 GI:10424560
GSS.
SOURCE
Mus musculus
(house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: M column: 16
Seq primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1..27

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0079M16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 69.2%; Score 18; DB 8; Length 27;
Best Local Similarity 80.8%; Pred. No. 1.8e+04;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCTCTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 27 CCTCTCTCTCTCTCTCTCTCTGCTC 2

RESULT 3
AZ435186/c

LOCUS
DEFINITION
1M0222E03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0222E03 F, genomic survey sequence.

ACCESSION
AZ435186
VERSION
AZ435186.1 GI:10559199
GSS.
SOURCE
Mus musculus
(house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: E column: 03
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..33

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 36;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 34 CCTCTCTCTCTCTCTCTCTCTC 10

RESULT 6

AZ623276/c
LOCUS
DEFINITION
1M0460M16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460M16 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ623276
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37)

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: M column: 16

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 37.

FEATURES

source

Location/Qualifiers
1..37

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460M16"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 37;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 35 CCTCTCTCTCTCTCTCTCTCTC 11

RESULT 7

AZ968544/c
LOCUS
DEFINITION
2M0240J20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0240J20 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ968544
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 44)

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0240 row: J column: 20

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 44.

FEATURES

source

Location/Qualifiers
1..44

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0240J20"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 65.4%; Score 17; DB 8; Length 50;
Best Local Similarity 80.0%; Pred. No. 4.4e+04;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCCTTCTTGTTACTCCTCCTGCTC 26
|||||||
Db 26 CCTCCTTCACATCCCTCCTCCCTC 50

RESULT 10

AU256766/c
AU256766 41 bp mRNA linear EST 25-APR-2002
LOCUS AU256766 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0008949 3', mRNA sequence.

ACCESSION

AU256766

VERSION

AU256766.1 GI:20320746

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@nara.ac.jp,
URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

source

1..41
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0008949"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 63.8%; Score 16.6; DB 1; Length 41;
Best Local Similarity 82.6%; Pred. No. 6.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCTCCTTCTTGTTACTCCTCCTGCTC 24
|||||||
Db 40 CCTCCTTCTTCTCCTCCTCCCGC 18

RESULT 11

AZ450486
LOCUS AZ450486 41 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0249D13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0249D13 F, genomic survey sequence.

AZ450486

VERSION AZ450486.1 GI:10605322

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0249 row: D column: 13

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 41.

FEATURES

source

1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0249D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 63.1%; Score 16.4; DB 8; Length 41;
Best Local Similarity 76.9%; Pred. No. 7.2e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCCTTCTTGTTACTCCTCCTGCTC 26
|||||||
Db 2 CCTCCTCCTCCTCCTCCTCCTCCTC 27

RESULT 12

AZ835139
LOCUS AZ835139 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0129P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0129P09 F, genomic survey sequence.

ACCESSION
AZ835139
VERSION
AZ835139.1
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM

GI:13005047

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

REFERENCE
AUTHORS

1 (bases 1 to 27)

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: P column: 09

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1..27

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0129P09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW42 [GI4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.3%; Score 16.2; DB 8; Length 27;

Best Local Similarity 85.7%; Pred. No. 8.2e+04;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCTCCTCTTGTACTCCTCT 22

|||||

Db 7 CCTCCTCTTGTACTCCTCT 27

|||||

RESULT 13

AI966611/c

LOCUS

sc53c11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

37 bp mRNA linear EST 12-JUL-2004

CR235166

50 bp DNA linear GSS 06-JUL-2004

CR235166

LOCUS

ACCESSION
AI966611
VERSION
AI966611.1
KEYWORDS
GSS.
SOURCE
Glycine max (soybean)
ORGANISM

GI:5761248

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Mammalia; Eutheria; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 37)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Fape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

REFERENCE
AUTHORS

1 (bases 1 to 37)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams 82"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-1293"

/tissue type="Mature flowers, field grown plants"

/lab_host="XL10-Gold"

/clone_lib="Gm-c1015"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR cDNA library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adaptors
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."

ORIGIN

Query Match 62.3%; Score 16.2; DB 1; Length 37;

Best Local Similarity 85.7%; Pred. No. 8.4e+04;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCTCCTCTTGTACTCCTCT 22

|||||

Db 35 CCTCCTCTTGTACTCCTCT 15

|||||

RESULT 14

CR235166

LOCUS

CR235166

50 bp DNA linear GSS 06-JUL-2004

CR235166

LOCUS

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 31;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 CCTCTTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 25 CCTCTCTCATCTCTCTCTCTC 1

RESULT 17
AZ792853/c

LOCUS AZ792853 32 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0045C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045C07 R, genomic survey sequence.

ACCESSION AZ792853

VERSION AZ792853.1 GI:12937209

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: C column: 07

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

source

1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045C07"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 32;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 CCTCTTCTTGTACTCTCTCTGCTC 26
||||| ||| ||||| |||||
Db 32 CCTCTCTCTCTCTCTCTCTCTC 8

RESULT 18
AZ783357

LOCUS AZ783357 33 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0025B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0025B05 F, genomic survey sequence.

ACCESSION AZ783357

VERSION AZ783357.1 GI:12918011

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: B column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

FEATURES

source

1..33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0025B05"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 33;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTCTGTACTCCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 3 CCTCCTCTCTCTCTCTCTCTCTCTCTC 27

RESULT 19

AV847122 34 bp mRNA linear EST 08-NOV-2001
LOCUS
DEFINITION AV847122 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone rcieg9fi4 3', mRNA sequence.
ACCESSION AV847122
VERSION
KEYWORDS
SOURCE
ORGANISM

Ciona intestinalis
Ciona intestinalis
Ciona intestinalis

REFERENCE

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 34)
Sathou, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sathousacidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 34
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcieg9fi4"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

FEATURES

source

ORIGIN

Query Match 59.2%; Score 15.4; DB 1; Length 34;
Best Local Similarity 76.0%; Pred. No. 1.6e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTCTGTACTCCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 8 CTTCCTCTCTGTCTCTCTCTCTGATC 32

RESULT 20

AZ392980/C
LOCUS
DEFINITION AZ392980 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0155P13 R, genomic survey sequence.
ACCESSION AZ392980
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

REFERENCE

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Kelly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0155 row: P column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
1. 37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0155P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMP42 (Gill4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 37;
Best Local Similarity 76.0%; Pred. No. 1.7e+05;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCCTCTCTGTACTCCTCTCTCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 26 CCTCCTCTCTCTCTCTCTCTCTCTC 2

RESULT 21

AZ761912/C
LOCUS
DEFINITION AZ761912 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0556D02 R, genomic survey sequence.
ACCESSION AZ761912
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

REFERENCE

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0556 row: D column: 02
 Seq primer: CACACAGGAAAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers
 1. .37

FEATURES source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0556D02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 37;
 Best Local Similarity 76.0%; Pred. No. 1.7e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTCTCTC 26

Db 37 CCTCTCTCTCTCTCTCTCTCTCTC 13

RESULT 22
 AZ345503
 LOCUS
 DEFINITION 1M0080C05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G05 F, genomic survey sequence.
 ACCESSION AZ345503
 VERSION AZ345503.1 GI:10424740
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 40)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE JOURNAL COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: G column: 05
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 40.
 Location/Qualifiers
 1. 40

FEATURES source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080G05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.2%; Score 15.4; DB 8; Length 40;
 Best Local Similarity 76.0%; Pred. No. 1.7e+05;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTCTGTACTCTCTCTCTGCT 25

Db 8 CCTCTCTCTCTCTCTCTCTCTCT 32

RESULT 23
 AI088341
 LOCUS
 DEFINITION qb07a07.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:1695540 3' similar to TR:Q19985 Q19985 F40E10.6 ;, mRNA sequence.
 ACCESSION AI088341
 VERSION AI088341
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46)
 REFERENCE

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG04811"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 59.2%; Score 15.4; DB 1; Length 50;
Best Local Similarity 94.1%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGCTACTCC 18
||||| ||||| |||||
Db 34 CCTCTCTCTGCTACTCC 18

RESULT 26
AZ854411 29 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0158B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0158B05 F, genomic survey sequence.

ACCESSION AZ854411
VERSION AZ854411.1 GI:13043500
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0158 row: B column: 05

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 29.

FEATURES

Location/Qualifiers

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0158B05"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 57.7%; Score 15; DB 8; Length 29;
Best Local Similarity 78.3%; Pred. No. 2.3e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TCCTCTCTGTACTCTCTCTGCTC 26
||||| ||||| ||||| |||||
Db 5 TCCTCTCTGTACTCTCTCTGCTC 27

RESULT 27

AZ537227/c

LOCUS

DEFINITION AST-2P03013 Genetrap PC-3 Human Prostatic Carcinoma Library Homo
sapiens genomic 5', genomic survey sequence.

ACCESSION AZ537227

VERSION AZ537227.1 GI:11114155

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)

REFERENCE

AUTHORS Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M.,
Bernardino, A., Durick, K. and Pollok, B.
Exon-trap tags from a PC-3 GenomeScreen(TM) Library
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Greg Henkel

Gene Expression

Aurora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA

Tel: 8584048436

Fax: 8584046719

Email: henkel@aurorabio.com

Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
preceded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAmp-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.

FEATURES

Location/Qualifiers

1..40
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Adenocarcinoma"
/cell_type="Epithelial"
/clone_lib="PC-3"
/clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
Library"

/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total
RNA from genetrap pools; shotgun clone in pAmp-1 and used
to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 57.7%; Score 15; DB 8; Length 40;
Best Local Similarity 78.3%; Pred. No. 2.3e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25
||||| ||||| ||||| |||||
Db 30 CTCCTCTCTGTCTCCACTCTCTGCT 8


```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0259 row: J column: 24
            Seq primer: CACACAGGAAACAGTATGACC
            Class: plasmid ends
            High quality sequence stop: 44.
FEATURES
source      Location/Qualifiers
            1..44
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0259J24"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
ORIGIN
Query Match      56.9%; Score 14.8; DB 8; Length 44;
Best Local Similarity 73.1%; Pred. NO. 2.8e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCCTCCTCTTGTACTCTCTGCTC 26
Db 41 CCCTCCTCTTGTACTCTCTGCTC 16

RESULT 31
AZ767297
LOCUS      AZ767297          50 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION  IM056621F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0566G21 F, genomic survey sequence.
ACCESSION  AZ767297
VERSION    AZ767297.1  GI:12885248

```

```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0566 row: G column: 21
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 50.
FEATURES
source      Location/Qualifiers
            1..50
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0566G21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
ORIGIN
Query Match      56.9%; Score 14.8; DB 8; Length 50;
Best Local Similarity 73.1%; Pred. NO. 2.8e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCCTCCTCTTGTACTCTCTGCTC 26
Db 7 CTCCCTCTTGTACCTCTCTCCCTC 32

RESULT 32
AJ794161/c
LOCUS      AJ794161          39 bp      mRNA      linear      EST 11-AUG-2004
DEFINITION  AJ794161 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.3.04 h20, mRNA sequence.
ACCESSION  AJ794161
VERSION    AJ794161.1  GI:51109489

```

```

KEYWORDS EST
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 39)
AUTHORS Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
TITLE Antirrhinum EST collection
JOURNAL Unpublished (2003)
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
1..39
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="019.3.04.h20"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
ORIGIN
Query Match 56.2%; Score 14.6; DB 1; Length 39;
Best Local Similarity 81.0%; Pred. No. 3.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CCTCTCTTCTGTACTCTCTCT 22
| | | | | | | | | | | | | |
Db 37 CCTCTCTCTTGTACCTCTCT 17

RESULT 33
LOCUS CF329688 50 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-B16.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-B16, mRNA
sequence.
ACCESSION CF329688.1 GI:33807590
VERSION CF329688
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 50)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..50
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-B16"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

```

```

RT-PCR."
ORIGIN
Query Match 56.2%; Score 14.6; DB 7; Length 50;
Best Local Similarity 81.0%; Pred. No. 3.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTCTCTTCTGTACTCTCTCC 21
| | | | | | | | | | | | | |
Db 30 CTCCCTTCTCTCTCTCTCTCC 50

RESULT 34
LOCUS BE736376/c 38 bp mRNA linear EST 15-SEP-2000
DEFINITION 601306513F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640802 5',
mRNA sequence.
ACCESSION BE736376.1 GI:10150368
VERSION BE736376
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM345 row: j column: 03
High quality sequence stop: 38.
FEATURES
source
1..38
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3640802"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
```

```

ORIGIN
Query Match 55.4%; Score 14.4; DB 2; Length 38;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCTCTCTTGTGTACTCTCTCTGCT 25
| | | | | | | | | | | | | |
Db 38 CCGCGTTCTCTCTCTCTCTCCAGCT 15

RESULT 35
LOCUS CF319095 40 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-H17.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H17, mRNA sequence.

```

```

ACCESSION   CF319095
VERSION     CF319095.1  GI:33690856
KEYWORDS
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..40
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD-09-H17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

ORIGIN
Query Match      55.4%; Score 14.4; DB 7; Length 40;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTTCTGCTACTCTCTCTCC 24
    ||||| ||||| ||||| |||||
Db 32 CCTCTCTCTGCTGCTCTCGCTCC 9

RESULT 36
CF292564/c
LOCUS         CF292564
DEFINITION   30DGS--01-G23.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-G23, mRNA
            sequence.
ACCESSION     CF292564
VERSION       CF292564.1  GI:33661597
KEYWORDS
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 43)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355

CF292564
LOCUS         CF292564/c
DEFINITION   30DGS--01-G23.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-G23, mRNA
            sequence.
ACCESSION     CF292564
VERSION       CF292564.1  GI:33661597
KEYWORDS
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 43)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355

CF319095
LOCUS         CF319095
DEFINITION   30DGS--01-G23.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--01-G23, mRNA
            sequence.
ACCESSION     CF319095
VERSION       CF319095.1  GI:33690856
KEYWORDS
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 43)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..43
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--01-G23"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

ORIGIN
Query Match      55.4%; Score 14.4; DB 7; Length 43;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGCTACTCTCTCTCTC 26
    ||||| ||||| ||||| |||||
Db 43 CTCCTCTCTCTCTCTCTCTCTCTC 20

RESULT 37
AZ443723/c
LOCUS         AZ443723
DEFINITION   IM0238D11F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
            clone UUCG1M0238D11 F, genomic survey sequence.
ACCESSION     AZ443723
VERSION       AZ443723.1  GI:10591984
KEYWORDS
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 48)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,I.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0238 row: D column: 11
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.

JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: dunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0238 row: D column: 11
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.

FEATURES             Location/Qualifiers
     source           1..48
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUCG1M0238D11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUCG1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.4%; Score 14.4; DB 8; Length 48;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTCCTCTCTGTGACTCCCTGCT 25
||||| ||| | ||||| |||
Db 46 CTCCTCTCTCTCTCTCTCTCT 23

RESULT 38
AL943250 50 bp DNA linear GSS 31-MAR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-272H06-015096,
DEFINITION genomic survey sequence.
ACCESSION AL943250
VERSION AL943250.1 GI:24399848
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse Genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4

AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
PUBMED Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

Location/Qualifiers
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-272H06-015096"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (Ti) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 55.4%; Score 14.4; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 3.9e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTGACTCCCTGCTC 26
||||| ||| | ||||| |||
Db 24 CTCCTCTATGTACCACTCCTGCTC 47

RESULT 39
AZ645664 21 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0511C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0511C13 F, genomic survey sequence.
ACCESSION AZ645664
VERSION AZ645664.1 GI:11775376
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 13
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.6%; Score 14.2; DB 8; Length 21;
 Best Local Similarity 84.2%; Fred. No. 4.3e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTACTCTCTCT 22
 ||||| || ||||| |||||
 Db 1 TCCTCTATTACTCTCTCT 19

RESULT 40
CO783803/c

LOCUS

DEFINITION BL279A_A01 6-Day Axolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
 CDNA 5' similar to hypothetical protein, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ambystoma mexicanum (axolotl)
 Ambystoma mexicanum
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 Ambystoma.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 39)
 Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
 Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M.
 An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
 expressed sequence tags from embryonic and regenerating blastema
 cDNA libraries

JOURNAL

COMMENT

Genome Biol. (2004) In press
 Contact: Elly M. Tanaka
 Tanaka Lab
 Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden

Pfotenhauerstrasse 108, 01307 Dresden, Germany

Tel.: 0049 351 210 2620

Fax: 0049 351 210 1489

Email: tanaka@mpi-cbg.de

Plate: BL279A row: 01 column: A

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES

source

1..39
 /organism="Ambystoma mexicanum"

/mol_type="mRNA"

/db_xref="taxon:8296"

/tissue_type="Tail Blastema"

/cell_type="regenerating tail blastema"

/clone.lib="6-Day Axolotl Tail Blastema (6DaxBL)"

/note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;

Unnormalized cDNA plasmid library prepared by Invitrogen.

Size fractionated mRNA was polydT primed and cloned into

NotI-SalI site of pCMVSPORT6. Bacterial host is

EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DaxBL"

ORIGIN

Query Match 54.6%; Score 14.2; DB 7; Length 39;
 Best Local Similarity 84.2%; Fred. No. 4.6e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCCTTCTTGTACTCTCTCC 21
 ||||| || ||||| |||||
 Db 20 CTTCTTCTTATGCTCTCTCC 2

Search completed: November 18, 2005, 21:12:54
 Job time : 1246.65 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 50.5171 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTCTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	1	US-07-989-160-8
2	17.2	66.2	24	4	US-09-907-794A-204
3	17.2	66.2	24	4	US-09-905-125A-204
4	17.2	66.2	24	4	US-09-902-775A-204
5	17.2	66.2	24	4	US-09-906-700-204
6	17.2	66.2	24	4	US-09-903-603A-204
7	17.2	66.2	24	4	US-09-904-920A-204
8	17.2	66.2	24	4	US-09-909-064-204
9	17.2	66.2	24	4	US-09-905-381A-204
10	17.2	66.2	24	4	US-09-906-618-204
11	17	65.4	30	1	US-08-068-747-4
12	17	65.4	30	3	US-08-589-109A-12
13	17	65.4	39	1	US-08-068-747-9
14	17	65.4	48	3	US-09-580-923-34
15	17	65.4	50	3	US-08-860-038-17
16	17	65.4	50	3	US-09-580-923-17
17	17	65.4	50	3	US-09-371-489-4
18	16.6	63.8	25	4	US-09-866-108A-13556
19	16.6	63.8	25	4	US-09-866-108A-13557
20	16.6	63.8	25	4	US-09-866-108A-13558
21	16.6	63.8	42	1	US-08-391-000-36
22	16.6	63.8	42	1	US-08-741-931-36
23	16.6	63.8	48	3	US-09-012-515A-7
24	16.6	63.8	48	3	US-08-360-144A-7
25	16.6	63.8	48	3	US-09-012-504A-7
26	16.6	63.8	48	4	US-09-012-399A-7
27	16.6	63.8	48	5	PCT-US95-06722-7

Sequence 2, Appli
Sequence 3, Appli
Sequence 41, Appli
Sequence 52, Appli
Sequence 41, Appli
Sequence 52, Appli
Sequence 41, Appli
Sequence 52, Appli
Sequence 19, Appli
Sequence 20, Appli
Sequence 10, Appli
Sequence 38, Appli
Sequence 11, Appli
Sequence 13555, A
Sequence 13559, A
Sequence 62750, A
Sequence 10, Appli
Sequence 22, Appli

US-07-989-160-8
Sequence 8, Application US/07989160
Patent No. 5429923
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07989,160
FILING DATE: 11-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-989-160-8

ALIGNMENTS

RESULT 1
US-07-989-160-8
Sequence 8, Application US/07989160
Patent No. 5429923
GENERAL INFORMATION:
APPLICANT: SEIDMAN, CHRISTINE
APPLICANT: SEIDMAN, JOHN
APPLICANT: WATKINS, HUGH
APPLICANT: ROSENZWEIG, ANTHONY
TITLE OF INVENTION: A METHOD FOR DETECTING
TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07989,160
FILING DATE: 11-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY, ELIZABETH A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: GWL-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-989-160-8

Query Match 100.0%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTCTCTTCTGTACTCTCTCTGCTC 26
|||||

Db 1 CCTCTTCTTTGTACTCTCTCTGCTC 26

RESULT 2

US-09-907-794A-204/c

; Sequence 204, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 204

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide probe

US-09-907-794A-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;

Best Local Similarity 86.4%; Pred. No. 9.1e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCTGCTC 26

Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 3

US-09-905-125A-204/c

; Sequence 204, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-125A-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;
Best Local Similarity 86.4%; Pred. No. 9.1e+02;
Matches 19%; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCTGCTC 26
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 4

US-09-902-775A-204/c
; Sequence 204, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIORITY FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;
Best Local Similarity 86.4%; Pred. No. 9.1e+02;
Matches 19%; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCTGCTC 26
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 5

US-09-906-700-204/c
; Sequence 204, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Genetech, Inc.	US 60/145,698
APPLICANT: Ashkenazi, Avi	US 60/145,698
APPLICANT: Botstein, David	US 60/145,698
APPLICANT: Desnoyers, Luc	US 60/145,698
APPLICANT: Eaton, Dan L.	US 60/145,698
APPLICANT: Ferrara, Napoleone	US 60/145,698
APPLICANT: Filvaroff, Ellen	US 60/145,698
APPLICANT: Fong, Sherman	US 60/145,698
APPLICANT: Gao, Wei-Qiang	US 60/145,698
APPLICANT: Gerber, Hanspeter	US 60/145,698
APPLICANT: Gerritsen, Mary E.	US 60/145,698
APPLICANT: Goddard, A.	US 60/145,698
APPLICANT: Godowski, Paul J.	US 60/145,698
APPLICANT: Grimaldi, Christopher J.	US 60/145,698
APPLICANT: Gurney, Austin L.	US 60/145,698
APPLICANT: Hillan, Kenneth, J.	US 60/145,698
APPLICANT: Klijavin, Ivar J.	US 60/145,698
APPLICANT: Mather, Jennie P.	US 60/145,698
APPLICANT: Pan, James	US 60/145,698
APPLICANT: Paoni, Nicholas F.	US 60/145,698
APPLICANT: ROY, Margaret Ann	US 60/145,698
APPLICANT: Stewart, Timothy A.	US 60/145,698
APPLICANT: Tumas, Daniel	US 60/145,698
APPLICANT: Williams, P. Mickey	US 60/145,698
APPLICANT: Wood, William, I.	US 60/145,698
TITLE OF INVENTION: Secreted and Transmitted	US 60/145,698
TITLE OF INVENTION: Acids Encoding the	US 60/145,698
FILE REFERENCE: 10466-14	US 60/145,698
CURRENT APPLICATION NUMBER: US/09/904,92	US 60/145,698
CURRENT FILING DATE: 2001-07-13	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US00/04414	US 60/145,698
PRIOR FILING DATE: 2000-02-22	US 60/145,698
PRIOR APPLICATION NUMBER: US 60/143,048	US 60/145,698
PRIOR FILING DATE: 1999-07-07	US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698	US 60/145,698
PRIOR FILING DATE: 1999-07-26	US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222	US 60/145,698
PRIOR FILING DATE: 1999-07-28	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/20594	US 60/145,698
PRIOR FILING DATE: 1999-09-08	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/20944	US 60/145,698
PRIOR FILING DATE: 1999-09-13	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/21090	US 60/145,698
PRIOR FILING DATE: 1999-09-15	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/21547	US 60/145,698
PRIOR FILING DATE: 1999-09-15	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/23089	US 60/145,698
PRIOR FILING DATE: 1999-10-05	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/28214	US 60/145,698
PRIOR FILING DATE: 1999-11-29	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/28313	US 60/145,698
PRIOR FILING DATE: 1999-11-30	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/28564	US 60/145,698
PRIOR FILING DATE: 1999-12-02	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/28565	US 60/145,698
PRIOR FILING DATE: 1999-12-02	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/30095	US 60/145,698
PRIOR FILING DATE: 1999-12-16	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/30911	US 60/145,698
PRIOR FILING DATE: 1999-12-20	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US99/30999	US 60/145,698
PRIOR FILING DATE: 1999-12-20	US 60/145,698
PRIOR APPLICATION NUMBER: PCT/US00/00219	US 60/145,698

; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-064-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;
Best Local Similarity 86.4%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTC 26
||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCGTC 3

RESULT 9
US-09-905-381A-204/c
; Sequence 204, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-381A-204

Query Match 66.2%; Score 17.2; DB 4; Length 24;
Best Local Similarity 86.4%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCGTC 26
||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCGTC 3

RESULT 10
US-09-906-618-204/c
; Sequence 204, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.


```

; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
;
US-08-068-747-4

Query Match 65.4%; Score 17; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.le+03;
Matches 20; Conservative 0; Mismatches 5; Indels

Qy 2 CCTCCTCTCTGTGACTCTCTCTGCTC 26
    ||||| || | ||||| |||
Db 30 CCTCCTCTCTCTCTCTCTCTCTCTC 6

RESULT 12
US-08-589-109A-12
; Sequence 12, Application US/08:589109A
; Patent No. 6365344
; GENERAL INFORMATION:
; APPLICANT: No. 6365344an, Garry P.
; APPLICANT: Rothenberg, Michael S.
; TITLE OF INVENTION: Methods for Screening for Transdominant
; TITLE OF INVENTION: Effector Peptides and RNA Molecules
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,109A
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.

```

REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cdna
US-08-589-109A-12

Query Match 65.4%; Score 17; DB 3; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 13

US-08-068-747-9
Sequence 9, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-9

Query Match 65.4%; Score 17; DB 1; Length 39;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

Db 1 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 14

US-09-580-923-34/c
Sequence 34, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
APPLICANT: Crouzet, Joel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligonucleotide
US-09-580-923-34

Query Match 65.4%; Score 17; DB 3; Length 48;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTTCTTGTACTCTCTCGTGC 26
Db 47 CCTCTCTCTCTCTCTCTCTCTCTC 23

RESULT 15

US-08-860-038-17/c
Sequence 17, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/860,038
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICANT: SCHERMAN, Daniel
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-17

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTGCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 16
US-09-580-923-17/c

; Sequence 17, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wills, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-580-923-17

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTGCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 49 CCTCTCTCTCTCTCTCTCTCTCTC 25

RESULT 17
US-09-371-489-4/c
; Sequence 4, Application US/09371489
; Patent No. 6355803
; GENERAL INFORMATION:
; APPLICANT: Anand Natrajan

; APPLICANT: Qingping Jiang
; APPLICANT: David Sharpe
; APPLICANT: Say-Jong Law
; TITLE OF INVENTION: NEAR INFRARED CHEMILUMINESCENT
; FILE REFERENCE: CCDDT-258XX
; CURRENT APPLICATION NUMBER: US/09/371,489
; CURRENT FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: 60/096,073
; EARLIER FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (223)...(223)
; OTHER INFORMATION: VANCO B PMP-PROBE 496.20 (ON PMP) IN EXAMPLE 16
US-09-371-489-4

Query Match 65.4%; Score 17; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCTCTCTCTGTACTCTCTCTGCTC 26
||||| ||| ||| ||| ||| ||| |||
Db 26 CCTCTCTCTCTCTCTCTCTCTCTC 2

RESULT 18

US-09-866-108A-13556/c
; Sequence 13556, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13556
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13556

Query Match 63.8%; Score 16.6; DB 4; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25
|||||
Db 25 CTCCTCTCTGTCTCTCTCCAGCT 3

RESULT 19

US-09-866-108A-13557/c
; Sequence 13557, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 13557

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-13557

Query Match 63.8%; Score 16.6; DB 4; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25
|||||
Db 24 CTCCTCTCTGTCTCTCTCCAGCT 2

RESULT 20

US-09-866-108A-13558/c

; Sequence 13558, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 13558

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-13558

Query Match 63.8%; Score 16.6; DB 4; Length 25;

Best Local Similarity 82.6%; Pred. No. 1.5e+03;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CTCCTCTCTGTACTCTCTCTGCT 25

|||||

Db 23 CTCCTCTCTGTCTCTCCAGCT 1

RESULT 21

US-08-391-000-36/c

; Sequence 36, Application US/08391000

; Patent No. 5723752

; GENERAL INFORMATION:

; APPLICANT: HOUTZ, Robert L.

; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF

; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/391,000
FILING DATE: 21-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-391-000-36

Query Match 63.8%; Score 16.6; DB 1; Length 42;
Best Local Similarity 82.6%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||||| | ||||| |||
Db 33 TCCTTCTTGTTACTCTCTCTGCTC 11

RESULT 22

US-08-741-931-36/c
Sequence 36, Application US/08741931
Patent No. 5866394
GENERAL INFORMATION:
APPLICANT: HOUTZ, Robert L.
TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
SUBUNIT N-METHYLTRANSFERASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,931
FILING DATE: 31-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-741-931-36

Query Match 63.8%; Score 16.6; DB 2; Length 42;
Best Local Similarity 82.6%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||||| | ||||| |||
Db 33 TCCTTCTTGTTACTCTCTCTGCTC 11

RESULT 23

US-09-012-515A-7/c
Sequence 7, Application US/09012515A
Patent No. 6127521
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/360,144
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-012-515A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTTGTTACTCTCTCTGCTC 26
||||||| | ||||| |||
Db 42 TTCTACTTGTTACTCTCTCACCTC 20

RESULT 24

US-08-360-144A-7/c
Sequence 7, Application US/08360144A
Patent No. 6150137
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique

;; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
;; STREET: One Post Office Square
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109-2170
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/360,144A
;; FILING DATE: 20-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: APV-036.02
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-832-1000
;; TELEFAX: 617-832-7000
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 48 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-360-144A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 25
US-09-012-504A-7/c
; Sequence 7, Application US/09012504A
; Patent No. 6464974
; GENERAL INFORMATION:
; APPLICANT: Berlin, V.
; APPLICANT: Chiu, I.
; APPLICANT: Cottarel, G.
; APPLICANT: Damagnez, V.
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; FILE REFERENCE: APBI-P05-036
; CURRENT APPLICATION NUMBER: US/09/012,504A
; CURRENT FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 08/360,144
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/250,795
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide coding strand
US-09-012-504A-7

Query Match 63.8%; Score 16.6; DB 3; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 26
US-09-012-399A-7/c
; Sequence 7, Application US/09012399A
; Patent No. 6509152
; GENERAL INFORMATION:
; APPLICANT: Berlin, Vivian
; APPLICANT: Chiu, Maria Isabel
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,399A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/360,144
; FILING DATE: 20-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: APV-036.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-012-399A-7

Query Match 63.8%; Score 16.6; DB 4; Length 48;
Best Local Similarity 82.6%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTTCTGTACTCTCTCTGCTC 26
Db 42 TTCTACTTGTACTCTCCACCTC 20

RESULT 27
PCT-US95-06722-7/c
; Sequence 7, Application PC/TUS9506722
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Immunosuppressant Target Proteins
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)

```

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-993-008A-2
; Gaps 0;

Query Match 63.1%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTCTGTGACTCCTCTCTCTC 26
Db 28 CCTCTCTCTCCACCTCTCTCTCTC 3

RESULT 29
US-08-993-008A-3
; Sequence 3, Application US/08993008A
; Patent No. 6153596
; GENERAL INFORMATION:
; APPLICANT: Liotta, Dennis C.
; APPLICANT: Petros, John A.
; APPLICANT: Wey, Shioh-Jyi
; APPLICANT: Karr, Joan F.
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Polycationic Oligomers
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winmer and Sullivan
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,008A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,436
; FILING DATE: 18-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 33-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-993-008A-3
; Gaps 0;

Query Match 63.1%; Score 16.4; DB 3; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCTCTCTCTGTGACTCCTCTCTCTC 26
Db 1 CCTCTCTCTCCACCTCTCTCTCTC 26

RESULT 30
US-08-361-920-41/c

```

; Sequence 41, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-361-920-41

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 30 CCCTGCCTCTGGTGTCTCTGCTC 5

RESULT 31
US-08-361-920-52/c
; Sequence 52, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.

; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-361-920-52

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCTCTCTGCTC 26
Db 30 CCCTGCCTCTGGTGTCTCTGCTC 5

RESULT 32
US-08-479-939-41/c
; Sequence 41, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939


```
;
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE: 22-DEC-1994
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-479-939-41
;
; Query Match 63.1%; Score 16.4; DB 1; Length 40;
; Best Local Similarity 76.9%; Pred. No. 1.9e+03;
; Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 1 CCCTCCTTCTGTACTCTCTGCTC 26
;      ||||| ||||| ||||| |||||
; Db 30 CCCTGCCTCTGTGTCTCTGCTC 5
;
; RESULT 33
; US-08-479-939-52/c
; Sequence 52, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE: 22-DEC-1994
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
;
; Qy 1 CCCTCCTTCTGTACTCTCTGCTC 26
;      ||||| ||||| ||||| |||||
; Db 30 CCCTGCCTCTGTGTCTCTGCTC 5
;
; RESULT 34
; US-08-483-432-41/c
; Sequence 41, Application US/08483432
; Patent No. 5763254
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,432
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 41:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-432-41

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
|||||
Db 30 CCCTGCCTCTGTGTCTCTGCTC 5

RESULT 35

US-08-483-432-52/c
Sequence 52, Application US/08483432
Patent No. 5763254
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
STREET: 405 Lexington Avenue, 52nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-432-52

Query Match 63.1%; Score 16.4; DB 1; Length 40;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
|||||
Db 30 CCCTGCCTCTGTGTCTCTGCTC 5

RESULT 36

US-08-324-001-19
Sequence 19, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSFO
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-324-001-19

Query Match 63.1%; Score 16.4; DB 1; Length 43;
Best Local Similarity 76.9%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
|||||
Db 8 CCCTCCTCTCCACCTCCTCTCTC 33

RESULT 37

US-08-324-001-20/c
Sequence 20, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
APPLICANT: HUNT, C. ANTHONY
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
TITLE OF INVENTION: OLIGONUCLEOTIDES DERIVED THEREFROM
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD

RESULT 40
US-09-362-842-38/c
; Sequence 38, Application US/0936
; Patent No. 6511824

```

; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIX
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-362-842-38

Query Match      60.0%; Score 15.6; DB 4; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 TCCTTCTTGTAATCCTCTGCT 25
        |||||
Db      22 TCCTTCTTGGAATCGCCTACT 1

```

Search completed: November 18, 2005, 11:22:02
Job time : 51.5171 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 349.468 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-8

Perfect score: 26

Sequence: 1 CCTCTCTTCTGTACTCTCTCTGCTC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	US-08-469-172-8	Sequence 8, Appli
2	26	100.0	26	US-10-788-779-8	Sequence 8, Appli
3	17.8	68.5	25	US-10-843-527-11341	Sequence 11341, A
4	17.8	68.5	25	US-10-843-527-12315	Sequence 12315, A
5	17.8	68.5	25	US-10-843-527-224398	Sequence 224398

68.5	17.8	25	24	US-10-843-527-225372	Sequence 225372, A
67.7	17.6	25	26	US-11-036-317-60793	Sequence 60793, A
66.2	17.2	24	9	US-09-903-320-204	Sequence 204, App
66.2	17.2	24	9	US-09-903-088B-204	Sequence 204, App
66.2	17.2	24	9	US-09-905-231A-204	Sequence 204, App
66.2	17.2	24	9	US-09-902-853-204	Sequence 204, App
66.2	17.2	24	9	US-09-907-824-204	Sequence 204, App
66.2	17.2	24	9	US-09-841-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-011-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-640-204	Sequence 204, App
66.2	17.2	24	10	US-09-908-093-204	Sequence 204, App
66.2	17.2	24	10	US-09-906-742-204	Sequence 204, App
66.2	17.2	24	10	US-09-906-838-204	Sequence 204, App
66.2	17.2	24	10	US-09-907-613-204	Sequence 204, App
66.2	17.2	24	10	US-09-907-942-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-859-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-204-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-820-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-786-204	Sequence 204, App
66.2	17.2	24	10	US-09-906-646-204	Sequence 204, App
66.2	17.2	24	10	US-09-906-700-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-786-204	Sequence 204, App
66.2	17.2	24	10	US-09-902-903-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-749A-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-119-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-956-204	Sequence 204, App
66.2	17.2	24	10	US-09-902-736-204	Sequence 204, App
66.2	17.2	24	10	US-09-907-794-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-943-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-462-204	Sequence 204, App
66.2	17.2	24	10	US-09-907-925-204	Sequence 204, App
66.2	17.2	24	10	US-09-902-692-204	Sequence 204, App
66.2	17.2	24	10	US-09-903-520-204	Sequence 204, App
66.2	17.2	24	10	US-09-905-056-204	Sequence 204, App
66.2	17.2	24	10	US-09-909-064-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-553-204	Sequence 204, App
66.2	17.2	24	10	US-09-905-381-204	Sequence 204, App
66.2	17.2	24	10	US-09-904-485-204	Sequence 204, App
66.2	17.2	24	10	US-09-905-348-204	Sequence 204, App
66.2	17.2	24	10	US-09-905-088-204	Sequence 204, App

ALIGNMENTS

RESULT 1
US-08-469-172-8
; Sequence 8, Application US/08469172
; Publication No. US2003005433A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-469-172-8

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
Db 1 CCCTCCTTCTGTACTCCTCTGCTC 26

RESULT 2
US-10-788-779-8
; Sequence 8, Application US/10788779
; Publication No. US2004015212A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-10-788-779-8

Query Match 100.0%; Score 26; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 1 CCCTCCTTCTGTACTCCTCTGCTC 26
Db 1 CCCTCCTTCTGTACTCCTCTGCTC 26

RESULT 3
US-10-843-527-11341
; Sequence 11341, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 11341
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-11341

Query Match 68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
Db 2 CTCCTCTTGTACTCTCTCTG 22

RESULT 4
US-10-843-527-12315
; Sequence 12315, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12315
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-12315

Query Match 68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
Db 4 CTCCTCTTGTACTCTCTCTG 24
```

```

; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 60793
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-60793

Query Match      67.7%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCCTCTCTTCTGTACTCTCTCTGC 24
    |||||||
Db 25 CGTCCTTCTGTACTGTCTCTTC 2
    |||||||

RESULT 8
US-09-909-320-204/c
; Sequence 204, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

US-10-843-527-224398/c
; Sequence 224398, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-224398

Query Match      68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
    |||||||
Db 22 CTCCTCTTGTCTCTCTCTG 2
    |||||||

RESULT 6
US-10-843-527-225372/c
; Sequence 225372, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 225372
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-225372

Query Match      68.5%; Score 17.8; DB 24; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCCTCTTGTACTCTCTCTG 23
    |||||||
Db 24 CTCCTCTTGTACTCTCTCTG 4
    |||||||

RESULT 7
US-11-036-317-60793/c
; Sequence 60793, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

US-09-905-291A-204/c
: Sequence 204, Application US/09905291A
: Patent No. US20020160374A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.


```
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-291A-204

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTGCTC 26
Db 24 CCTACTACTCTCTCTGCTC 3

RESULT 11
US-09-902-853-204/c
; Sequence 204, Application US/0902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-853-204

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTGTACTCTCTGCTC 26
Db 24 CCTTCTGTACTCTCTGCTC 26
```

Db 24 CCTACTACTCTCTCTGCTC 3
|||||

RESULT 12

US-09-907-824-204/c
; Sequence 204, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-824-204

Query Match 66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTGTGACTCTCTCTGCTC 26
|||||
Db 24 CCTACTACTCTCTCTGCTC 3
|||||

RESULT 13

US-09-907-841-204/c
; Sequence 204, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05

```
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-841-204

Query Match          66.2%; Score 17.2; DB 9; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
    ||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 14
US-09-904-011-204/c
; Sequence 204, Application US/09904011
; Publication No. US2003003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-011-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTTGTAAGTCTCTCTGCTC 26
    ||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTCTGCTC 3

RESULT 15
US-09-903-640-204/c
; Sequence 204, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
```

```
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-640-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTAATCTCTCTGCTC 26
    ||| || ||||| ||||| |||
Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 16
US-09-908-093-204/c
; Sequence 204, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-908-093-204

Query Match          66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTAATCTCTCTGCTC 26
    ||| || ||||| ||||| |||
Db 24 CCTACTACTACTCTCTGCTC 3

RESULT 17
US-09-906-742-204/c
; Sequence 204, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
```

APPLICANT:	Genentech, Inc.
APPLICANT:	Ashkenazi, Avi
APPLICANT:	Botstein, David
APPLICANT:	Desnovers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, A.
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J.

RESULT 19
US-09-907-613-204/c
; Sequence 204, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 204
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
US-09-907-613-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTCTTGTTACTCCTCCTGCTC 26
Db 24 CCTACTACTACTCCTCCTGCTC 3

RESULT 20
US-09-907-942-204/c
Sequence 204, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16

```

, FILE REFERENCE: 10468-14
, CURRENT APPLICATION NUMBER: US/09/904,859
, CURRENT FILING DATE: 2001-07-12
, PRIOR APPLICATION NUMBER: 09/665,350
, PRIOR FILING DATE: 2000-09-18
, PRIOR APPLICATION NUMBER: PCT/US00/04414
, PRIOR FILING DATE: 2000-02-22
, PRIOR APPLICATION NUMBER: US 60/143,048
, PRIOR FILING DATE: 1999-07-07
, PRIOR APPLICATION NUMBER: US 60/145,698
, PRIOR FILING DATE: 1999-07-26
, PRIOR APPLICATION NUMBER: US 60/146,222
, PRIOR FILING DATE: 1999-07-28
, PRIOR APPLICATION NUMBER: PCT/US99/20594
, PRIOR FILING DATE: 1999-09-08
, PRIOR APPLICATION NUMBER: PCT/US99/20944

```

```
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-204-204
```

```
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 CCTTCTGTACTCTCTCTGCTC 26
||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCTCTCTGCTC 3
```

```
RESULT 23
US-09-904-820-204/c
; Sequence 204, Application US/09904820
; Publication No. US20030360941
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-820-204
```

```
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 CCTTCTGTACTCTCTCTGCTC 26
||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCTCTCTGCTC 3
```

RESULT 24


```

US-09-904-786-204/c
; Sequence 204, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Trans
; TITLE OF INVENTION: Acids Encoding
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/90
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligon
US-09-904-786-204

Query Match 66.2% Score
Best Local Similarity 86.4% Pred:
Matches 19; Conservative 0; Mismatches 5

QY 5 CCTCTTTGTACTCCTCTCTGCTC 26
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCCTCTCTGCTC 3

RESULT 25
US-09-906-646-204/c
; Sequence 204, Application US/09906646
; Publication No. US20030039971A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe

US-09-906-700-204
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CCTTCTGTACTCTCTCTGCTC 26
||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCTCTGCTC 3
RESULT 27
US-09-903-786-204/C
; Sequence 204, Application US/09903786
; Publication No. US20030044793A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,786
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565

RESULT 28
US-09-902-903-204/c
; Sequence 204, Application US/09902903
; Publication No. US20030044839A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Proteins
; TITLE OF INVENTION: Acids Encoding and Methods of Use
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902903
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/000000
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,143
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,145
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,146
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/200000
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/200000

RESULT 29
US-09-903-749A-204/c
; Sequence 204, Application US/09903749A
; Publication No. US20030045693A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashtkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Mathew, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Trans-


```
RESULT 31
US-09-904-956-204/c
; Sequence 204, Application US/09904956
; Publication No. US20030049622A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,956
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-904-956-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCTCTTGTACTCTCTCTGCTC 26
DB 24 CCTACTACTCTCTCTGCTC 3

RESULT 32
US-09-902-736-204/c
; Sequence 204, Application US/09902736
; Publication No. US20030049676A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
```

```
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-736-204
```

```
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 CCTCTTGTTACTCCTCTGCTC 26
||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCCTCTGCTC 3
```

RESULT 33

```
US-09-907-794-204/c
; Sequence 204, Application US/09907794
; Publication No. US20030049677A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
```

```
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-794-204
```

```
Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 CCTCTTGTTACTCCTCTGCTC 26
||| || ||||| ||||| |||||
Db 24 CCTACTACTACTCCTCTGCTC 3
```

RESULT 34

```
US-09-903-943-204/c
; Sequence 204, Application US/09903943
; Publication No. US20030054349A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
```



```
QY      5  CCTCTCTGTAAGCTCTCTCTGTC 26
      |||||
Db      24  CCTACTACTACTCTCTCTGTC 3

RESULT 36
; Sequence 204, Application US/09907925
; Publication No. US20030054352A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,925
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23069
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
```

```
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-925-204

Query Match      66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5  CCTCTCTGTAAGCTCTCTCTGTC 26
      |||||
Db      24  CCTACTACTACTCTCTCTGTC 3

RESULT 37
US-09-902-692-204/c
; Sequence 204, Application US/09902692
; Publication No. US20030054400A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,692
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
```


APPLICANT: Gurney, Austin L.

```
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,056
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 204
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-905-056-204

Query Match 66.2%; Score 17.2; DB 10; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTCTTGTACTCTCTCGTCTC 26
   ||| ||| ||| ||| ||| ||| |||
Db 24 CCTACTACTACTCTCTCGTCTC 3

RESULT 40
US-09-909-064-204/c
; Sequence 204, Application US/09909064
; Publication No. US2003005972A1
; GENERAL INFORMATION:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-064-204
```

Query Match 66.2%; Score 17.2; DB 10; Length 24;
 Best Local Similarity 86.4%; Pred. No. 2.4e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCTTCTGTACTCCTCTGCTC 26
 |||||
 Db 24 CCTACTACTACTCCTCTGCTC 3

Search completed: November 18, 2005, 15:41:09
 Job time : 351.468 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 18, 2005, 11:12:34 ; Search time 693.631 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-9
Perfect score: 25
Sequence: 1 CAACTCATCACCCTCTCTCCATC 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	100.0	25	6	I12902	I12902 Sequence 9
C 2	18.6	74.4	41	6	BD217302	BD217302 Mammalian
C 3	18.2	72.8	47	6	AR291854	AR291854 Sequence
C 4	17.6	70.4	41	6	BD217295	BD217295 Mammalian
5	16.2	64.8	46	6	AR023959	AR023959 Sequence
6	16.2	64.8	46	6	I15460	I15460 Sequence 38
7	16	64.0	42	6	AX080737	AX080737 Sequence
C 8	15.4	61.6	25	6	AR561920	AR561920 Sequence
C 9	15.2	60.8	20	6	AR002284	AR002284 Sequence
C 10	15.2	60.8	20	6	AR053135	AR053135 Sequence
11	15.2	60.8	42	6	AR078405	AR078405 Sequence
12	14.8	59.2	22	6	AX923032	AX923032 Sequence
C 13	14.8	59.2	24	6	CQ767675	CQ767675 Sequence
14	14.6	58.4	21	6	BD061255	BD061255 A method
15	14.6	58.4	31	6	E27249	E27249 Novel physi
C 16	14.6	58.4	50	3	GIAC270	L49327 STS of NotI
17	14.4	57.6	41	6	AX327047	AX327047 Sequence
18	14.4	57.6	41	6	AX327048	AX327048 Sequence
19	14.4	57.6	47	6	AR289466	AR289466 Sequence

C 20	14.2	56.8	20	6	AX496861	AX496861 Sequence
C 21	14.2	56.8	24	6	AR072405	AR072405 Sequence
C 22	14.2	56.8	24	6	I26516	I26516 Sequence 20
C 23	14.2	56.8	25	6	AX511858	AX511858 Sequence
24	14.2	56.8	41	6	AX521320	AX521320 Sequence
C 25	14	56.0	22	6	AR082996	AR082996 Sequence
C 26	14	56.0	22	6	BD005994	BD005994 An optima
C 27	14	56.0	22	6	BD070465	BD070465 Methods f
C 28	14	56.0	24	6	AX494081	AX494081 Sequence
C 29	14	56.0	25	6	AX610677	AX610677 Sequence
C 30	14	56.0	31	6	AX248216	AX248216 Sequence
C 31	14	56.0	31	6	AX249206	AX249206 Sequence
32	14	56.0	32	6	CQ786866	CQ786866 Sequence
C 33	13.8	55.2	20	6	E59389	E59389 Method for
C 34	13.8	55.2	20	6	AX118076	AX118076 Sequence
C 35	13.8	55.2	27	6	BD197187	BD197187 Method an
C 36	13.8	55.2	29	6	BD252384	BD252384 Regulatio
C 37	13.8	55.2	29	6	AX300835	AX300835 Sequence
38	13.8	55.2	29	6	AX300839	AX300839 Sequence
39	13.8	55.2	31	6	BD235713	BD235713 Targeted
40	13.8	55.2	33	6	BD235714	BD235714 Targeted
C 41	13.8	55.2	33	6	AR401446	AR401446 Sequence
C 42	13.8	55.2	33	6	AR401452	AR401452 Sequence
C 43	13.8	55.2	33	6	AR401454	AR401454 Sequence
C 44	13.8	55.2	33	6	AR453285	AR453285 Sequence
C 45	13.8	55.2	33	6	AR453291	AR453291 Sequence

ALIGNMENTS

RESULT 1
I12902
LOCUS I12902 25 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 9 from patent US 5429923.
ACCESSION I12902
VERSION I12902.1 GI:910879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Seidman,C., Seidman,J., Watkins,H. and Rosenzweig,A.
TITLE Method for detecting hypertrophic cardiomyopathy associated mutations
JOURNAL Patent: US 5429923-A 9 04-JUL-1995;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No.:5.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCCTCTCTCCATC 25
|||||
Db 1 CAACTCATCACCCTCTCTCCATC 25

RESULT 2
BD217302/c
LOCUS BD217302 41 bp DNA linear PAT 17-JUL-2003
DEFINITION Mammalian DED-caspase homolog usurin.
ACCESSION BD217302
VERSION BD217302.1 GI:33027072
KEYWORDS JP 2002520025-A/17.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 41)

AUTHORS Nicholson,D.W., Rasper,D.M., Xanthoudakis,S. and Roy,S.
TITLE Mammalian DED-caspase homolog usurpin
JOURNAL MERCK FROST CANADA AND CO
COMMENT OS Homo sapiens (human)
PN JP 2002520025-A/17
PD 09-JUL-2002
PF 07-JUL-1999 JP 2000559244
PR 08-JUL-1998 US 60/092005
PI DONALD W NICHOLSON,DITA M RASPER,STEVE XANTHOUDAKIS,SOPHIE ROY
PC D12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12Q1/02
PC G01N33/50//C12N9/64,C12N15/00,C12N5/00
CC Mammalian DED-caspase homolog usurpin
FH Key Location/Qualifiers
FT source 1..41
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..41
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES
source

ORIGIN

Query Match 74.4%; Score 18.6; DB 6; Length 41;
Best Local Similarity 84.0%; Pred. No. 3.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAACATCATCACCACTCTCTCCATC 25
Db 41 CAATCTCTCACCAATCTCTGCCATC 17

RESULT 3
AR291854/c AR291854 47 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 3589 from patent US 6537751.
DEFINITION AR291854
ACCESSION AR291854
VERSION AR291854.1 GI:31679138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 3589 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..47
/organism='unknown'
/mol_type='genomic DNA'

ORIGIN

Query Match 72.8%; Score 18.2; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAACATCATCACCACTCTCTCCATC 25
Db 32 CACCTCATYAGCACATCTCTCTCTC 8

RESULT 4
BD217295/c BD217295 41 bp DNA linear PAT 17-JUL-2003
LOCUS Mammalian DED-caspase homolog usurpin.
DEFINITION BD217295
ACCESSION BD217295
VERSION BD217295.1 GI:33027065
KEYWORDS JP 2002520025-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 41)
AUTHORS Nicholson,D.W., Rasper,D.M., Xanthoudakis,S. and Roy,S.
TITLE Mammalian DED-caspase homolog usurpin
JOURNAL MERCK FROST CANADA AND CO
COMMENT OS Homo sapiens (human)
PN JP 2002520025-A/10
PD 09-JUL-2002
PF 07-JUL-1999 JP 2000559244
PR 08-JUL-1998 US 60/092005
PI DONALD W NICHOLSON,DITA M RASPER,STEVE XANTHOUDAKIS,SOPHIE ROY
PC D12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12Q1/02
PC G01N33/50//C12N9/64,C12N15/00,C12N5/00
CC Mammalian DED-caspase homolog usurpin
FH Key Location/Qualifiers
FT source 1..41
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..41
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN

Query Match 70.4%; Score 17.6; DB 6; Length 41;
Best Local Similarity 83.3%; Pred. No. 8.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CAACATCATCACCACTCTCTCCAT 24
Db 40 CAATCTCTCACCAATCTCTGCCAT 17

RESULT 5

AR023959 AR023959 46 bp DNA linear PAT 05-DEC-1998
LOCUS Sequence 38 from patent US 5795762.
DEFINITION AR023959
ACCESSION AR023959
VERSION AR023959.1 GI:3977253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Abramson,R.D. and Gelfand,D.H.
TITLE 5' to 3' exonuclease mutations of thermostable DNA polymerases
JOURNAL Patent: US 5795762-A 38 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..46
/organism='unknown'
/mol_type='unassigned DNA'

ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 46;
Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CTCATCACCACCTCTCTTCCAT 24
Db 17 CTCATCACCACCTCTCTTCCAT 37

RESULT 6

II5460 II5460 46 bp DNA linear PAT 02-APR-1996
LOCUS Sequence 38 from patent US 5466591.
DEFINITION II5460
ACCESSION II5460
VERSION II5460.1 GI:1250368
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

```
Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Abramson,R.D. and Gelfand,D.H.
TITLE 5' to 3' exonuclease mutations of thermostable DNA polymerases
JOURNAL Patent: US 5466591-A 38 14-NOV-1995;
FEATURES
    source
        Location/Qualifiers
            1..46
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match 64.8%; Score 16.2; DB 6; Length 46;
Best Local Similarity 85.7%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 CTCATCACCACCTCTCTTCCAT 24
Db 17 CTCATCCCACTCTTTTCCAT 37
RESULT 7
AX080737 42 bp DNA linear PAT 27-FEB-2001
LOCUS AX080737
DEFINITION Sequence 14 from Patent WO0109189.
ACCESSION AX080737
VERSION AX080737.1 GI:13169725
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bodary,S.C. and Fisher,K.L.
TITLE Compositions and methods for the treatment of tumors
JOURNAL Patent: WO 0109189-A 14 08-FEB-2001;
Genentech, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..42
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer"
ORIGIN
Query Match 64.0%; Score 16; DB 6; Length 42;
Best Local Similarity 79.2%; Pred. No. 4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 AACTCATCACCACCTCTCTTCCATC 25
Db 6 AATGCATCAAGACTCTCTGCCATC 29
RESULT 8
AR561920/c 25 bp DNA linear PAT 08-OCT-2004
LOCUS AR561920
DEFINITION Sequence 147 from patent US 6759198.
ACCESSION AR561920
VERSION AR561920.1 GI:53975571
KEYWORDS
SOURCE
    ORGANISM
        Unknown.
        Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kris,R.M. and Felder,S.
TITLE High throughput assay system
JOURNAL Patent: US 6759198-A 147 06-JUL-2004;
FEATURES
    source
        Location/Qualifiers
            1..25
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match 61.6%; Score 15.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.7e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAATCATCACCACCTCTCTTCCATC 25
Db 25 CACCTCATAGACACTCTCAACCACC 1
RESULT 9
AR002284/c 20 bp DNA linear PAT 04-DEC-1998
LOCUS AR002284
DEFINITION Sequence 23 from patent US 5741645.
ACCESSION AR002284
VERSION AR002284.1 GI:3963838
KEYWORDS
SOURCE
    ORGANISM
        Unknown.
        Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
JOURNAL Patent: US 5741645-A 23 21-APR-1998;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match 60.8%; Score 15.2; DB 6; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAATCATCACCACCTCTCTT 20
Db 20 CAACTCATGACCCCTCTCCT 1
RESULT 10
AR053135/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR053135
DEFINITION Sequence 41 from patent US 5834183.
ACCESSION AR053135
VERSION AR053135.1 GI:5977997
KEYWORDS
SOURCE
    ORGANISM
        Unknown.
        Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis
JOURNAL Patent: US 5834183-A 41 10-NOV-1998;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match 60.8%; Score 15.2; DB 6; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAATCATCACCACCTCTCTT 20
Db 20 CAACTCATGACCCCTCTCCT 1
RESULT 11
AR078405 42 bp DNA linear PAT 31-AUG-2000
LOCUS AR078405
DEFINITION Sequence 24 from patent US 5962636.
ACCESSION AR078405
```

```

VERSION      AR078405.1  GI:10005151
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 42)
AUTHORS      Bachmaier,K., Hessel,A.,John., Neu,N. and Penninger,J.Martin.
TITLE        Peptides capable of modulating inflammatory heart disease
JOURNAL      Patent: US 5962636-A 24 05-OCT-1999;
FEATURES     Location/Qualifiers
             source
               1..42
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      60.8%; Score 15.2; DB 6; Length 42;
Best Local Similarity 85.0%; Pred. No. 8.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTC 21
    ||||| ||||| ||||| |||||
Db 8 AGCTCATGCCACTCTCTTC 27

RESULT 12
AX923032      AX923032      22 bp DNA linear PAT 18-DEC-2003
LOCUS         Sequence 1372 from Patent WO02068649.
ACCESSION     AX923032
VERSION       AX923032.1 GI:40216120
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS
JOURNAL
FEATURES      Location/Qualifiers
             source
               1..22
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Description of Artificial Sequence: Ag4532 Forward"

ORIGIN
Query Match      59.2%; Score 14.8; DB 6; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCATC 25
    ||||| ||||| ||||| |||||
Db 3 TCACCTCTCTCTTCATC 20

RESULT 13
CQ767675/c     CQ767675      24 bp DNA linear PAT 04-MAR-2004
LOCUS         Sequence 142 from Patent EP1386931.
DEFINITION     CQ767675
ACCESSION     CQ767675
VERSION       CQ767675.1 GI:45107802
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS      Wood,W.I., Goddard,A., Gurney,A., Yuan,J., Baker,K.P. and Chen,J.
TITLE        Human neurotrophin homologue
JOURNAL      Patent: EP 1386931-A 142 04-FEB-2004;
Genentech, Inc. (US)
FEATURES      Location/Qualifiers
             source
               1..24
               /organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Sequence"

ORIGIN
Query Match      59.2%; Score 14.8; DB 6; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
    ||||| ||||| ||||| |||||
Db 23 CACATCACCACCTCTTC 6

RESULT 14
BD061255      BD061255      21 bp DNA linear PAT 27-AUG-2002
LOCUS         A method to identify and breed corn with increased kernel oil
DEFINITION     concentration.
ACCESSION     BD061255
VERSION       BD061255.1 GI:22606861
KEYWORDS      JP 2001517951-A/72.
SOURCE        Medicago sativa
ORGANISM      Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Reiter,R.S.
TITLE        A method to identify and breed corn with increased kernel oil
JOURNAL
COMMENT       Patent: JP 2001517951-A 72 09-OCT-2001;
EI DU PONT DE NEMOURS & CO
PN JP 2001517951-A/72
PD 09-OCT-2001
PF 19-MAR-1998 JP 1998544487
PR 24-MAR-1997 US 60/041515
PI ROBERT STEFAN REITER
PC C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES      Location/Qualifiers
             source
               1..21
               /organism="Medicago sativa"
               /mol_type="genomic DNA"
               /db_xref="taxon:3879"

ORIGIN
Query Match      58.4%; Score 14.6; DB 6; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.7e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCATC 25
    ||||| ||||| ||||| |||||
Db 1 TCATCAGCTCTCTCTTCAAC 21

RESULT 15
E27249        E27249        31 bp DNA linear PAT 18-JUN-2001
LOCUS         Novel physiologically active substance, process for producing the
DEFINITION     same and utilization thereof.
ACCESSION     E27249
VERSION       E27249.1 GI:13025266
KEYWORDS      JP 1999009286-A/40.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Shuji,H. and Shoji,F.
TITLE        Novel physiologically active substance, process for producing the

```


same and utilization thereof
 Patent: JP 1999009286-A 40 19-JAN-1999;
 TAKEDA CHEM IND LTD
 OS Unidentified
 PN JP 1999009286-A/40
 PD 19-JAN-1999
 PF 27-APR-1998 JP 1998117189
 PR
 SHUJI HINUMA, SHOJI FUKUZUMI
 PI C12N15/09, A01K67/027, A61K38/00, A61K38/00, C07K14/47, C07K16/18,
 PC C12N1/21,
 PC C12N5/10, C12P21/02, G01N33/53, G01N33/577//C12P21/08, (C12N15/09,
 PC C12R1:91),
 PC (C12N1/21, C12R1:19), (C12N5/10, C12R1:91), (C12P21/02, C12R1:19),
 PC C12N15/00,
 PC A61K37/02, A61K37/02, C12N5/00, (C12N15/00, C12R1:91), (C12N5/00,
 PC C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT source 1. .31 Location/Qualifiers
 FT /organism='Unidentified'.
 FEATURES
 source
 1. .31
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'
 ORIGIN
 Query Match 58.4%; Score 14.6; DB 6; Length 31;
 Best Local Similarity 81.0%; Pred. No. 1.7e+05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 CAACTCATCACCACCTCTCTTC 21
 Db 3 CGACTCAGCAGCAGCTGTCTTC 23
 RESULT 16
 GIAC270/c 50 bp DNA linear INV 19-DEC-2001
 LOCUS STS of NotI segment E of chromosome 5 in Giardia duodenalis strain
 WB-1B.
 ACCESSION L49327
 VERSION L49327.1 GI:1100084
 KEYWORDS
 SOURCE Giardia intestinalis
 ORGANISM Giardia intestinalis
 Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Upcroft, J.A., Chen, N. and Upcroft, P.
 TITLE Mapping variation in chromosome homologues of different Giardia strains
 JOURNAL Mol. Biochem. Parasitol. 76 (1-2), 135-143 (1996)
 MEDLINE 97077435
 PUBMED 8920002
 COMMENT Original source text: Giardia lamblia DNA.
 FEATURES
 source
 1. .50
 Location/Qualifiers
 /organism='Giardia intestinalis'
 /mol_type='genomic DNA'
 /db_xref='taxon:5741'
 ORIGIN
 Query Match 58.4%; Score 14.6; DB 3; Length 50;
 Best Local Similarity 81.0%; Pred. No. 1.6e+05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 5 TCATCACCACCTCTCTTCATC 25
 Db 26 TCATCAACACTCTCATCGTTC 6

RESULT 17
 AX327047 41 bp DNA linear PAT 07-JAN-2002
 LOCUS Sequence 243 from Patent WO0178894.
 DEFINITION AX327047
 ACCESSION AX327047
 VERSION AX327047.1 GI:18097758
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Keith, T.
 TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
 JOURNAL Patent: WO 0178894-A 243 25-OCT-2001;
 GENOME Therapeutics Corp. (US)
 FEATURES
 source
 1. .41
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9606'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 41;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CAACTCATCACCACCTCTCTTCAT 24
 Db 4 CATCTCAGCTCCACACTCTTCTT 27
 RESULT 18
 AX327048 41 bp DNA linear PAT 07-JAN-2002
 LOCUS Sequence 244 from Patent WO0178894.
 DEFINITION AX327048
 ACCESSION AX327048
 VERSION AX327048.1 GI:18097759
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Keith, T.
 TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
 JOURNAL Patent: WO 0178894-A 244 25-OCT-2001;
 GENOME Therapeutics Corp. (US)
 FEATURES
 source
 1. .41
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9606'
 ORIGIN
 Query Match 57.6%; Score 14.4; DB 6; Length 41;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CAACTCATCACCACCTCTCTTCAT 24
 Db 5 CATCTCAGCTCCACACTCTTCTT 28
 RESULT 19
 AR289466 47 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 1201 from patent US 6537751.
 DEFINITION AR289466
 ACCESSION AR289466
 VERSION AR289466.1 GI:31676750
 KEYWORDS

```

SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 47)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 1201 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
              1..47
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN

Query Match      57.6%; Score 14.4; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
    ||||| ||||| ||||| |||||
Db 25 CTCCTCATCACTCTCTKC 42

RESULT 20
AX496861/c
LOCUS      AX496861                20 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 3 from Patent WO205749.
ACCESSION  AX496861
VERSION     AX496861.1 GI:23342381
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    Ho,S.P.
REFERENCE   1
AUTHORS     Crf 2? ligands in combination therapy
TITLE       Patent: WO 0205749-A 3 24-JAN-2002;
JOURNAL     Bristol-Myers Squibb Pharma Company (US)
FEATURES    Location/Qualifiers
            source
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Antisense Oligonucleotide"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCC 22
    ||||| ||||| ||||| |||||
Db 19 CTCATCACCACCTTCATCC 1

RESULT 21
AR072405/c
LOCUS      AR072405                24 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 208 from patent US 5948611.
ACCESSION  AR072405
VERSION     AR072405.1 GI:9999169
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unkown.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
            Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
TITLE       Primers and methods for detecting mutations in the procollagen II
            gene (COL2A1) that indicate a genetic predisposition for a
            COL2A1-associated disease
JOURNAL     Patent: US 5948611-A 208 07-SEP-1999;
FEATURES    Location/Qualifiers

SOURCE      1..24
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 24;
Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACCTCTCTTCCAT 24
    ||||| ||||| ||||| |||||
Db 24 CATCACCCTCTTTCCCAT 6

RESULT 22
I26516/c
LOCUS      I26516                24 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 208 from patent US 5558988.
ACCESSION  I26516
VERSION     I26516.1 GI:1606386
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unkown.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
TITLE       Primers and methods for detecting mutations in the procollagen II
            gene that indicate a genetic predisposition for osteoarthritis
JOURNAL     Patent: US 5558988-A 208 24-SEP-1996;
FEATURES    Location/Qualifiers
            source
              1..24
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 24;
Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACCTCTCTTCCAT 24
    ||||| ||||| ||||| |||||
Db 24 CATCACCCTCTTTCCCAT 6

RESULT 23
AX511858/c
LOCUS      AX511858                25 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 265 from Patent WO02055705.
ACCESSION  AX511858
VERSION     AX511858.1 GI:23392558
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    Mezes,P.S., Rastelli,L., Herrmann,J.L., Macdougall,J.R., Zhong,H.,
            Casman,S.J., Boldog,F., Shinkets,R.A., Gorman,L., Crasta,O.R.,
            Mysore,K.K., Folkerts,O., Martin,G.B., Eisen,A., Spaderna,S.K.,
            Vernet,C.A., Bergh,C., Spytek,K.A., Dipippo,V.A., Zerhusen,B.D.,
            Peyman,J.A., Ellerman,K., Stone,D.J., Grose,W.M., Alsobrook,J.P.,
            Lepley,D.M., Rieger,D.K., Burgess,C.E. and Edinger,S.
            Proteins and nucleic acids encoding same
            Patent: WO 02055705-A 265 18-JUL-2002;
            Curagen Corporation (US)
FEATURES    Location/Qualifiers
            source
              1..25
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="oligonucleotide primer"

ORIGIN

Query Match      56.8%; Score 14.2; DB 6; Length 25;

```

```

Best Local Similarity 84.2%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACTCATCACCACCTCTCT 19
Db 22 CAACTAATCACCATGCTCT 4

RESULT 24
AX521320
LOCUS AX521320 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 7518 from Patent WO02052044.
ACCESSION AX521320
VERSION AX521320.1 GI:23572190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
Detection of genetic polymorphisms
TITLE
JOURNAL Patent: WO 02052044-A 7518 04-JUL-2002;
Riken (JP)
FEATURES
source
1..41
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 56.8%; Score 14.2; DB 6; Length 41;
Best Local Similarity 84.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACTCATCACCACCTCTCTTC 21
Db 1 ACTCATATCAGTGTCTTC 19

RESULT 25
AR082996/c
LOCUS AR082996 22 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 22 from patent US 5976798.
ACCESSION AR082996
VERSION AR082996.1 GI:10009786
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 22)
Parker, W.D., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
JOURNAL Patent: US 5976798-A 22 02-NOV-1999;
Riken (JP)
FEATURES
source
1..22
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCATC 25
Db 22 CTCACACACCACTCTCTCGACC 1

RESULT 26
BD005994/c
LOCUS BD005994 22 bp DNA linear PAT 31-JAN-2002
DEFINITION An optimal procedure for isolation of mutant mitochondrial alleles.
ACCESSION BD005994
VERSION BD005994.1 GI:18634365
KEYWORDS
SOURCE JP 2001500020-A/2.
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 22)
Herrnstadt, C., Ghosh, S., Fahy, E.D. and Davis, R.E.
An optimal procedure for isolation of mutant mitochondrial alleles
TITLE
JOURNAL Patent: JP 2001500020-A 2 09-JAN-2001;
MITOKOR
COMMENT
OS Unidentified
PN JP 2001500020-A/2
PD 09-JAN-2001
PF 26-NOV-1997 JP 1998524745
PI CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D FAHY, ROBERT E DAVIS
PC C07H21/04, C12Q1/68, C12P19/34
CC Strandedness: Double;
CC Topology: Linear;
CC Location/Qualifiers
FH key
FT source
1..22
Location/Qualifiers
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCATC 25
Db 22 CTCACACCACTCTCTCGACC 1

RESULT 27
BD070465/c
LOCUS BD070465 22 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid.
ACCESSION BD070465
VERSION BD070465.1 GI:22616068
KEYWORDS
SOURCE JP 2001514500-A/22.
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 22)
Parker, W.D., Herrnstadt, C., Ghosh, S. and Fahy, E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
JOURNAL Patent: JP 2001514500-A 22 11-SEP-2001;
MITOKOR
COMMENT
OS Unidentified
PN JP 2001514500-A/22
PD 11-SEP-2001
PF 27-FEB-1998 JP 1998537738
PI WILLIAM DAVIS PARKER, CORINNA HERRNSTADT, SOUMITRA GHOSH, EOIN D
FAHY
PC C12Q1/68, C07H21/04
CC Strandedness: Double;
CC Topology: Linear;
CC Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's
CC disease and methods for determining heteroplasmy of CC

```

```

CC acid mitochondrial nucleic
FH key Location/Qualifiers
FT source 1..22
FT /organism='Unidentified'.
FEATURES
source 1..22
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||||| ||||| ||||| |||||
Db 22 CTCACACCACTTCTTCGACC 1

RESULT 28
AX494081/c
LOCUS AX494081 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1055 from Patent WO02059355.
ACCESSION AX494081
VERSION AX494081.1 GI:23339713
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Fieldhouse,D. and Kobler,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture
and use thereof
JOURNAL Patent: WO 02059355-A 1055 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
FEATURES
source 1..24
Location/Qualifiers
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Artificially Synthesized DNA Sequence'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCA 23
||||| ||||| ||||| |||||
Db 24 AACTCATAACACTTCTTACAA 3

RESULT 29
AX610677/c
LOCUS AX610677 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 1702 from Patent WO02072882.
ACCESSION AX610677
VERSION AX610677.1 GI:28406106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 1702 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1..25
Location/Qualifiers
/organism='Homo sapiens'

CC acid mitochondrial nucleic
FH key Location/Qualifiers
FT source 1..22
FT /organism='Unidentified'.
FEATURES
source 1..22
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 22;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||||| ||||| ||||| |||||
Db 22 CTCACACCACTTCTTCGACC 1

RESULT 28
AX494081/c
LOCUS AX494081 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1055 from Patent WO02059355.
ACCESSION AX494081
VERSION AX494081.1 GI:23339713
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Fieldhouse,D. and Kobler,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture
and use thereof
JOURNAL Patent: WO 02059355-A 1055 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
FEATURES
source 1..24
Location/Qualifiers
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Artificially Synthesized DNA Sequence'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 24;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCA 23
||||| ||||| ||||| |||||
Db 24 AACTCATAACACTTCTTACAA 3

RESULT 29
AX610677/c
LOCUS AX610677 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 1702 from Patent WO02072882.
ACCESSION AX610677
VERSION AX610677.1 GI:28406106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 1702 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1..25
Location/Qualifiers
/organism='Homo sapiens'

Query Match 56.0%; Score 14; DB 6; Length 25;
Best Local Similarity 77.3%; Pred. No. 3.1e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCAT 24
||||| ||||| ||||| |||||
Db 25 ACTCTCCCGAGTCACCTACAT 4

RESULT 30
AX248216/c
LOCUS AX248216 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 295 from Patent WO0166800.
ACCESSION AX248216
VERSION AX248216.1 GI:15862839
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 295 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source 1..31
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
||||| ||||| ||||| |||||
Db 30 CACCACCTCTTCCRT 15

RESULT 31
AX249206/c
LOCUS AX249206 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1285 from Patent WO0166800.
ACCESSION AX249206
VERSION AX249206.1 GI:15863829
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1285 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source 1..31
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

ORIGIN
Query Match 56.0%; Score 14; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
||||| ||||| ||||| |||||
Db 30 CACCACCTCTTCCRT 15

Query Match 56.0%; Score 14; DB 6; Length 31;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
||||| ||||| ||||| |||||

```

```

Db          30 CACCACACTCTTCCT 15
||||| ||||| ||||| ||||| |||||
Query Match          55.2%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.8e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 32
CQ786866
LOCUS          32 bp DNA linear PAT 24-MAR-2004
DEFINITION    Sequence 43 from Patent WO2004021010.
ACCESSION    CQ786866
VERSION      CQ786866.1 GI:45721858
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS      Nakamura,Y. and Furukawa,Y.
TITLE        Method of diagnosing colon and gastric cancers
JOURNAL      Patent: WO 2004021010-A 43 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
SOURCE
1..32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized primer sequence for
RT-PCR"

ORIGIN
Query Match          56.0%; Score 14; DB 6; Length 32;
Best Local Similarity 77.3%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY          2 AACTCATCACCACACTCTCTCCA 23
||||| ||||| ||||| ||||| |||||
Db          10 AAGTCATTGTCACACTCTCATCCA 31
||||| ||||| ||||| ||||| |||||

RESULT 33
E59389/c
LOCUS          20 bp DNA linear PAT 31-JAN-2002
DEFINITION    Method for differentiating varieties of pig by DNA sequence
polymorphism.
ACCESSION    E59389
VERSION      E59389.1 GI:18622524
KEYWORDS     JP 2000350586-A/13.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Mitsuhashi,T. and Okumura,N.
TITLE        Method for differentiating varieties of pig by DNA sequence
JOURNAL      Patent: JP 2000350586-A 13 19-DEC-2000;
LINESTOCK EXPERIMENT STATION MINISTRY OF AGRICULTURE FORESTRY AND
FISHERIES, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY
AND FISHERIES, TADAYOSHI MITSUHASHI
OS Artificial Sequence
PN JP 2000350586-A/13
PD 19-DEC-2000
PF 11-JUN-1999 JP 1999165269
PR TADAYOSHI MITSUHASHI,NAOHIKO OKUMURA
PI C12N15/09,C12Q1/68,G01N33/50,C12N15/00
PC
CC
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match          55.2%; Score 13.8; DB 6; Length 27;
Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          3 ACTCATCACCACACTCTCT 19
||||| ||||| ||||| ||||| |||||
Db          17 AGTCATCACCACACTCTCCT 1
||||| ||||| ||||| ||||| |||||

RESULT 35
BD197187/c
LOCUS          29 bp RNA linear PAT 17-JUL-2003
DEFINITION    Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION    BD197187
VERSION      BD197187.1 GI:33006957
KEYWORDS     JP 2002509721-A/213.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 29)
AUTHORS      Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Meswigen,J.A.
TITLE        Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
PATENT: JP 2002509721-A 213 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002509721-A/213
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00

```

```

CC      Synthesized Hammerhead Ribozyme
CC      The letter 'n' stands for any base or bases forming a loop or
CC      stem-loop
CC      that may contain multiple nucleic acid analogues or 2'- CC
        deoxynucleotides.
FH      Key
FT      Location/Qualifiers
FT      source
        1..29
        Location/Qualifiers
        /organism='Artificial Sequence'.
        /organism="synthetic construct"
        /mol_type="genomic RNA"
        /db_xref="taxon:32630"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CAACTCATCAGCACTCTC 18
Db      19 CGNCTCATCAGCACTCTC 2

RESULT 36
BD252384/c
LOCUS      29 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD252384
VERSION      BD252384.1 GI:33062154
KEYWORDS      JP 2002541795-A/177.
SOURCE      unidentified
            unclassified.
ORIGIN
REFERENCE      1 (bases 1 to 29)
AUTHORS      Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 177 10-DEC-2002;
COMMENT      RIBOZYME PHARMACEUTICALS INC
            OS      Eukaryote
            PN      JP 2002541795-A/177
            PD      10-DEC-2002
            PF      11-APR-2000 JP 2000611654
            PR      12-APR-1999 US 60/129390
            PI      LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
            C12R1:91),
            PC      (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC      A61K37/02,
            PC      (C12N5/00,C12R1:91)
            CC      N in position 17 represents stem II region of a HH ribozyme.
            FH      Key
            FT      Location/Qualifiers
            FT      source
                1..29
                Location/Qualifiers
                /organism='Eukaryote'.
                /organism="unidentified"
                /mol_type="genomic RNA"
                /db_xref="taxon:32644"

FEATURES
    source
        1..29
        /organism="unidentified"
        /mol_type="genomic RNA"
        /db_xref="taxon:32644"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 83.3%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CAACTCATCAGCACTCTC 18
Db      19 CGNCTCATCAGCACTCTC 2

```

```

RESULT 37
AX300835/c
LOCUS      29 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION      Sequence 4 from Patent WO0185955.
ACCESSION      AX300835
VERSION      AX300835.1 GI:17382113
KEYWORDS
SOURCE      Homo sapiens (human)
ORIGIN      Homo sapiens
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1
            Bahr,G., Cocude,C. and Capron,A.
            Rh16 polypeptides and its fragments and polynucleotides encoding
            said polypeptides and therapeutic uses
            Patent: WO 0185955-A 4 15-NOV-2001;
            Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
FEATURES
    source
        1..29
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
        ||||| ||||| |||||
Db      18 TCATCACCACCTCTCTC 2

RESULT 38
AX300839
LOCUS      29 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION      Sequence 8 from Patent WO0185955.
ACCESSION      AX300839
VERSION      AX300839.1 GI:17382117
KEYWORDS
SOURCE      Homo sapiens (human)
ORIGIN      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1
            Bahr,G., Cocude,C. and Capron,A.
            Rh16 polypeptides and its fragments and polynucleotides encoding
            said polypeptides and therapeutic uses
            Patent: WO 0185955-A 8 15-NOV-2001;
            Istac (FR) ; INSTITUT PASTEUR DE LILLE (FR)
FEATURES
    source
        1..29
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

ORIGIN
Query Match      55.2%; Score 13.8; DB 6; Length 29;
Best Local Similarity 88.2%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 TCATCACCACCTCTCTTC 21
        ||||| ||||| |||||
Db      12 TCATCACCACCTCTCTC 28

RESULT 39
BD235713
LOCUS      31 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Targeted alphavirus and alphaviral vectors.
ACCESSION      BD235713
VERSION      BD235713.1 GI:33045483
KEYWORDS      JP 2002523053-A/16.

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 172.148 Seconds
(without alignments)
859.686 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACTCATCACCACCTCTCTTCATC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq_16Dec04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	25	100.0	25	2	AaQ91129 Beta-card
2	25	100.0	25	9	ACA63119 Human bet
3	25	100.0	25	13	ADR05305 Human bet
C 4	18.6	74.4	41	3	AaZ57003 Forward a
C 5	18.6	74.4	47	3	AaZ56923 Human map
C 6	17.6	70.4	41	3	AaZ56996 Forward a
7	16.2	64.8	46	2	AaQ24360 Oligonule
8	16	64.0	42	4	AaF30389 Human ADA
C 9	15.6	62.4	33	6	ABQ83617 Human lys
C 10	15.6	62.4	41	6	ABQ83619 Human lys
C 11	15.4	61.6	25	8	ABZ72744 Attenuati
C 12	15.4	61.6	33	6	AaL50996 Human act
13	15.4	61.6	36	12	ADL23552 Worm tors
C 14	15.2	60.8	20	2	AaQ95137 Spinocere
15	15.2	60.8	42	2	AaZ28187 Human alp
16	15.2	60.8	42	3	AaZ99170 Human pap
C 17	15	60.0	41	6	ABQ83620 Human lys
18	15	60.0	50	6	ABZ06975 Human leu
C 19	15	60.0	50	6	ABZ06585 Human leu
20	14.8	59.2	22	6	ADL17836 Forward P

21	14.8	59.2	22	12	ADN42918	Adn42918 Human NOV
C 22	14.8	59.2	24	3	AAZ34011	Aaz34011 Human PRO
C 23	14.8	59.2	24	3	AAZ78692	Aaz78692 Human PRO
C 24	14.8	59.2	24	8	ACA63579	Acac63579 Novel hum
C 25	14.8	59.2	24	8	ACA71743	Acac71743 Human PRO
C 26	14.8	59.2	24	8	ABX92383	Abx92383 Human PRO
C 27	14.8	59.2	24	8	ACA66124	Acac66124 Human sec
C 28	14.8	59.2	24	9	ADA24681	Ada24681 Secreted
C 29	14.8	59.2	24	9	ACD29725	Adc29725 Novel hum
C 30	14.8	59.2	24	9	ADA12342	Ada12342 Human sec
C 31	14.8	59.2	24	9	ACD29140	Adc29140 Novel hum
C 32	14.8	59.2	24	10	ADB73648	Adb73648 Human PRO
C 33	14.8	59.2	24	10	ADB76364	Adb76364 Human PRO
C 34	14.8	59.2	24	10	ADC43790	Adc43790 Human PRO
C 35	14.8	59.2	24	10	ADC61550	Adc61550 Human PRO
C 36	14.8	59.2	24	10	ADC63514	Adc63514 Human PRO
C 37	14.8	59.2	24	10	ADC66614	Adc66614 Human PRO
C 38	14.8	59.2	24	10	ADC68738	Adc68738 Human PRO
C 39	14.8	59.2	24	10	ADC62798	Adc62798 Human PRO
C 40	14.8	59.2	24	10	ADC67863	Adc67863 Human PRO
C 41	14.8	59.2	24	10	ADC41183	Adc41183 Human PRO
C 42	14.8	59.2	24	10	ADC67238	Adc67238 Human PRO
C 43	14.8	59.2	24	10	ADC62174	Adc62174 Human PRO
C 44	14.8	59.2	24	10	ADC41807	Adc41807 Human PRO
C 45	14.8	59.2	24	10	ADE49176	Adc49176 Human PRO

ALIGNMENTS

RESULT 1

AAQ91129

ID AAQ91129 standard; cDNA; 25 BP.

XX AC AAQ91129;

XX DT 19-FEB-1996 (first entry)

XX DE Beta-cardiac myosin heavy chain PCR primer B9.1F.

XX KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

XX KW diagnosis; primer; mutation; detection; ss.

XX OS Synthetic.

XX PN US5429923-A.

XX PD 04-JUL-1995.

XX PF 11-DEC-1992; 92US-00989160.

XX PR 11-DEC-1992; 92US-00989160.

XX PA (HARD) HARVARD COLLEGE.

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX PI Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX DR WPI; 1995-245715/32.

XX PT Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX PT useful for testing asymptomatic individual(s).

XX PS Example 1; Col 10; 22pp; English.

XX CC AAQ91121-091130 are nested PCR primers used for the amplification and

XX CC identification of beta-cardiac myosin heavy-chain RNA. They are used in a

XX CC new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC),

XX CC the method involves detecting the presence or absence of specific HC- from

XX CC associated mutations in the beta-cardiac myosin heavy-chain obtained from

XX CC a blood sample. The method may be used to diagnose familial or sporadic

XX CC HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
 CC a broad applicability and may be used to detect mutations responsible for
 CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
 CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
 CC anaemia, Tay-Sachs disease and phenylketonuria
 CC
 SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACATCATCACCACTCTCTTCCATC 25

Db 1 CAACATCATCACCACTCTCTTCCATC 25

RESULT 2

ACA63119

ID ACA63119 standard; DNA; 25 BP.

XX AC

ACA63119;

XX 28-AUG-2003 (first entry)

XX Human beta cardiac myosin heavy chain PCR primer B9.1F.

DE Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;

XX familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;

KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;

KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;

KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

XX 20-MAR-2003.

XX 06-JUN-1995; 95US-00469172.

XX 11-DEC-1992; 92US-00989160.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with

XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or

PT hemophilia, by detecting a mutation in an amplified product of a beta

PT cardiac myosin heavy-chain DNA.

XX Example 1; Page 5; 22pp; English.

PS The invention relates to detecting the presence or absence of a mutation

XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC

CC and FHC) comprises detecting a mutation associated with hypertrophic

CC cardiomyopathy in an amplified product of a beta cardiac myosin heavy

CC chain DNA. The mutations associated with SHC/FHC are detected in the

CC myosin gene isolated from blood, by detecting mis-matched areas in RNA-

CC DNA hybrid double strands (RNA from the normal gene, DNA from the suspect

CC sample). FHC associated point mutation can be classified and used to

CC determine life expectancy in affected individuals e.g. using a Kaplan-

CC Meier curve for the classified type of FHC causing point mutation. Also

CC included are an RNA probe comprising ribonucleotides arranged in a

CC sequence which is complementary to at least a portion of beta-cardiac

CC myosin heavy-chain DNA and a set of DNA oligonucleotide primers for

CC amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
 CC DNA. The method is useful for detecting the presence or absence of a
 CC mutation associated with hypertrophic cardiomyopathy. This method is
 CC especially useful for diagnosing SHC and FHC, as well as for determining
 CC the estimated life expectancy of a person with familial hypertrophic
 CC cardiomyopathy. In particular, the method is useful for determining an
 CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
 CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
 CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
 CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
 CC chain gene containing an FHC-associated mutation

XX SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACATCATCACCACTCTCTTCCATC 25

Db 1 CAACATCATCACCACTCTCTTCCATC 25

RESULT 3

ADR05305

ID ADR05305 standard; DNA; 25 BP.

XX AC

ADR05305;

XX 21-OCT-2004 (first entry)

XX Human beta cardiac myosin heavy chain mutation detection primer B9.1F.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

KW familial hypertrophic cardiomyopathy;

KW sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

OS US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

PI WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to

XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

PT myosin heavy-chain DNA and detecting the mutation in the amplified

PT product.

XX Claim 18; SEQ ID NO 9; 22pp; English.

CC The invention relates to detecting the presence or absence of a mutation

CC associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,

CC SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,

CC comprising amplifying beta-cardiac myosin heavy-chain DNA forming an

CC amplified product, and detecting the presence or absence of a mutation

CC associated with hypertrophic cardiomyopathy in the amplified product,

CC thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also

CC included are a set of DNA oligonucleotide primers for amplifying beta-

CC cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX
SQ Sequence 25 BP; 6 A; 12 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATCATCACCACTCTCTCCATC 25
||| ||||| ||||| ||||| |||||
Db 1 CAATCATCACCACTCTCTCCATC 25

RESULT 4
AAZ57003/C
ID AAZ57003 standard; DNA; 41 BP.
XX AAZ57003;
XX
DT 12-MAY-2000 (first entry)
XX
DE Forward amplicon for generating usurpin constructs.
XX
KW Usurpin-alpha; death effector domain; DED; prodomain; usurpin-beta;
KW usurpin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
KW caspase; cytostatic; antiParkinsonian; antidiabetic; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200003023-A1.
XX
PD 20-JAN-2000.
XX
PF 07-JUL-1999; 99WO-CA000615.
XX
PR 08-JUL-1998; 98US-0092005P.
XX
PA (MERI) MERCK FROSST CANADA INC.
XX
PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;
XX WPI; 2000-160929/14.
XX
PT Novel recombinant DNA molecules and polypeptides for treating apoptosis
PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
XX disease.
XX
PS Example 7; Page 33; 69pp; English.
XX

CC The invention provides recombinant nucleic acid molecules encoding
CC usurpin-alpha (lacking the first death effector domain (DED) or its
CC prodomain), usurpin-beta or usurpin-gamma. Usurpin polypeptides are
CC useful in vitro and in vivo identification of usurpin-procaspase-8
CC interaction inhibitor. Usurpin is useful as modulator of the sensitivity
CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
CC is useful for treating diseases like autoimmune diabetes, cancer and
CC Parkinson's disease. Activators and inhibitors of usurpin-procaspase-8
CC interaction are also useful for treating various diseases mediated by
CC apoptosis. Usurpin provides an attractive model for modulating caspase
CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
CC regulated at several levels in the presence of usurpin, conferring
CC resistance to Fas-ligand cell death. The present sequence represents a
CC forward amplicon for generating usurpin-alpha, delDED-A usurpin
CC constructs for transfection into human cells

XX
SQ Sequence 41 BP; 9 A; 5 C; 16 G; 11 T; 0 U; 0 Other;

Query Match 74.4%; Score 18.6; DB 3; Length 41;
Best Local Similarity 84.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAATCATCACCACTCTCTCCATC 25
||| ||||| ||||| ||||| |||||
Db 41 CAATCTCTCACCAATCTCTGCATC 17

RESULT 5
AAZ69233/C
ID AAZ69233 standard; DNA; 47 BP.
XX AAZ69233;

XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:3589.

XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation; diagnosis;
KW single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX
FH Key Location/Qualifiers
FT variation replace(24,A)
FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.

XX Claim 3; Page 996; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 CC
 XX SQ Sequence 47 BP; 15 A; 9 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 74.4%; Score 18.6; DB 3; Length 47;
 Best Local Similarity 84.0%; Pred. No. 2.9e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACCTCATCACCACCTCTCTTCCATC 25
 |||||
 Db 32 CACCTCATCAGCACTGCTTCTCTTC 8

RESULT 6
 AAZ56996/C
 ID AAZ56996 standard; DNA; 41 BP.

XX AC AAZ56996;

XX DT 12-MAY-2000 (first entry)

XX DE Forward amplicon for generating delDED-A usurin construct.

XX USurin-alpha; death effector domain; DBD; prodomain; usurin-beta;
 KW usurin-gamma; procaspase-8; CD95; apoptosis; cancer; immunosuppressive;
 KW caspase; cytostatic; antiparkinsonian; antidiabetic; PCR primer; ss.

XX OS Homo sapiens.

XX FN WO200003023-A1.

XX PD 20-JAN-2000.

XX PF 07-JUL-1999; 99WO-CA000615.

XX PR 08-JUL-1998; 98US-0092005P.

XX PA (MERI) MERCK FROSST CANADA INC.

XX PI Nicholson DW, Rasper DM, Xanthoudakis S, Roy S;

XX DR WPI; 2000-160929/14.

XX Novel recombinant DNA molecules and polypeptides for treating apoptosis
 PT mediated diseases e.g. autoimmune diabetes, cancer and Parkinson's
 PT disease.

XX Example 7; Page 31; 69pp; English.

XX The invention provides recombinant nucleic acid molecules encoding
 CC usurin-alpha (lacking the first death effector domain (DED) or its
 CC prodomain), usurin-beta or usurin-gamma. Usurin polypeptides are
 CC useful for in vitro and in vivo identification of usurin-procaspase-8
 CC interaction inhibitor. Usurin is useful as modulator of the sensitivity
 CC of cells to CD95(Fas/Apo-1) mediated apoptosis. Modulation of apoptosis
 CC is useful for treating diseases like autoimmune diabetes, cancer and
 CC Parkinson's disease. Activators and inhibitors of usurin-procaspase-8
 CC interaction are also useful for treating various diseases mediated by
 CC apoptosis. Usurin provides an attractive model for modulating caspase
 CC activation. Sensitivity of cells bearing CD95(Fas/Apo-1) receptor can be
 CC regulated at several levels in the presence of usurin, conferring
 CC resistance to Fas-ligand cell death. The present sequence represents a
 CC forward amplicon for generating delDED-A usurin constructs

XX SQ Sequence 41 BP; 9 A; 7 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 70.4%; Score 17.6; DB 3; Length 41;
 Best Local Similarity 83.3%; Pred. No. 7.4e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACCTCATCACCACCTCTCTTCCAT 24
 |||||
 Db 40 CAAATCCTCACCACCTCTCTGCCAT 17

RESULT 7
 AAQ24360

ID AAQ24360 standard; DNA; 46 BP.

XX AC AAQ24360;

XX DT 26-OCT-1992 (first entry)

XX DE Oligonucleotide primer TAFR01.

XX Tag polymerase; mutant; thermostable; DNA polymerase; exonuclease; PCR;
 KW amplification; reverse primer; ss.

XX OS Synthetic.

XX FN WO9206200-A.

XX PD 16-APR-1992.

XX PF 30-SEP-1991; 91WO-US007035.

XX PR 28-SEP-1990; 90US-00590213.

XX PR 28-SEP-1990; 90US-00590466.

XX PR 28-SEP-1990; 90US-00590490.

XX PA (CETU) CETUS CORP.

XX Gelfand DH, Abramson RD;

XX WPI; 1992-150885/18.

XX Thermostable DNA polymerases with altered 5'-3' exo nuclease activity -
 PT having conserved regions mutated or deleted, for use in e.g. PCR,
 PT sequencing and detection assays.

XX Example 10; Page 102; 185pp; English.

XX The primer was used in conjunction with primer TAFI285 (see AAQ24359) to
 CC obtain a DNA fragment encoding a 5'-3' exonuclease deficient thermostable
 CC DNA polymerase from Thermosiphon africanus. A portion of the DNA
 CC polymerase gene comprising amino acids 285-892 was selectively amplified
 CC using the two PCR primers and the purified prod. isolated. The purified
 CC protein is deficient in 5'-3' exo- nuclease activity, is more
 CC thermoresistant than the corresp. native enzyme and is partic. useful in
 CC PCR of G+C rich templates. See also AAQ23993-Q24013, AAQ24320-36 and
 CC AAQ24343-59

XX SQ Sequence 46 BP; 12 A; 17 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 64.8%; Score 16.2; DB 2; Length 46;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCAT 24
 |||||
 Db 17 CTCATCACCACCTCTCTTCCAT 37

RESULT 8
 AAF30389

ID AAF30389 standard; DNA; 42 BP.

XX The present invention describes human lysyl oxidase 46.31 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) can be used in the treatment of several diseases, such as
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological disease and various inflammations. The present
CC sequence represents a probe for (I), which is used in an example from the
CC present invention
XX
SQ Sequence 41 BP; 15 A; 7 C; 13 G; 6 T; 0 U; 0 Other;

Query Match 62.4%; Score 15.6; DB 6; Length 41;
Best Local Similarity 81.8%; Pred. No. 5.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 23 CTCATTCCACTCTCTTCCATC 2

RESULT 11

ABZ72744/C

ID ABZ72744 standard; DNA; 25 BP.

XX AC ABZ72744;

XX 09-APR-2003 (first entry)

XX Attenuation factor oligonucleotide SEQ ID NO:147.

XX High throughput assay system; nucleic acid detection; anchor; target;
XX linker; ss.

XX Synthetic.

XX WO2003002750-A2.

XX 09-JAN-2003.

XX 26-JUN-2002; 2002WO-US020039.

XX 26-JUN-2001; 2001US-00888413.

XX (HIGH-) HIGH THROUGHPUT GENOMICS INC.

XX Kris RM, Felder S;

XX WPI; 2003-201508/19.

XX Detecting nucleic acid target in sample by using combination comprising
XX multiple regions each of which has two different loci of anchors in
XX association with a bifunctional linker that has portion specific for
XX anchor.

XX Example 30; Page 114; 129pp; English.

XX The present invention describes a method for detecting a nucleic acid
XX target (T) in a sample (S). The method involves: (a) contacting (S) which
XX may comprise the target(s) with a nuclease protection fragment(s) (I)
XX specific for and which binds to the target(s), exposing the (S) to a
XX nuclease effective to digest remaining single stranded nucleic acid, and
XX then contacting the resultant (S) with a combination (II) which
XX comprises, before addition of (S), a surface comprising multiple
XX spatially discrete regions, at least two of which are substantially
XX identical, each region comprising at least two different loci of anchors,
XX the anchors at each locus, each in association with a bifunctional linker
XX which has a first portion that is specific for the anchor, and a second
XX portion that comprises a probe which is specific for one of the (I),
XX under conditions effective for the (I) to bind to the combination, where
XX two or more of the anchors located at a first locus of a region are in
XX association with different bifunctional linkers, having different target
XX specificities; and (b) detecting the bound protection fragment(s), and
XX where the regions are tubes, and the loci of anchors are arranged in a

CC linear array in the tubes. Such an assay can be termed a multi array
CC plate screen (MAPS) method or assay. When the probes are
CC oligonucleotides, the MAPS can be used for diagnosing the presence of
CC genetic variations or defects e.g. polymorphisms or specific mutations
CC associated with disease such as cystic fibrosis or pathogenic organisms.
CC When the probes are antigen binding molecules, the assays can be used for
CC screening variant proteins or protein expression patterns. The assay can
CC also be used for mapping expressed sequences tags (ESTs). ABZ72599 to
CC ABZ72762, and ABP5611, represent sequences used in the exemplification
CC of the present invention
XX

SQ Sequence 25 BP; 4 A; 1 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 8; Length 25;
Best Local Similarity 76.0%; Pred. No. 5.9e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 25 CACCTCATAGCACTCTCAACCACC 1

RESULT 12

AAL50996/C

ID AAL50996 standard; DNA; 33 BP.

XX AC AAL50996;

XX 13-FEB-2003 (first entry)

XX Human actin 21-34 PCR primer #3.

XX Human; PCR; primer; ss; actin; 21.34; zinc finger; PHD structural domain;
XX malignant tumour; haemopathy; HIV; immunological disease; inflammation.

XX Homo sapiens.

XX CN1345794-A.

XX 24-APR-2002.

XX 22-SEP-2000; 2000CN-00125360.

XX 22-SEP-2000; 2000CN-00125360.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-548937/59.

XX Novel polypeptide-human actin 21.34 contained zinc finger and PHD finger
XX structural domain and its encoding polynucleotide useful for treating
XX e.g., HIV infection.

XX Example 4; Page 20; 33pp; Chinese.

XX The invention comprises the amino acid and coding sequence of the human
XX actin 21.34 protein (which contains a zinc finger and a PHD structural
XX domain). The 21.34 DNA and protein sequences are useful for treating:
XX malignant tumour; haemopathy; HIV; immunological disease; and
XX inflammations. The present DNA sequence represents a PCR primer for the
XX human actin 21.34 gene

SQ Sequence 33 BP; 8 A; 7 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 61.6%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACCTCTCTTCCATC 25
||| ||||| ||||| |||||
Db 33 CGACTCGTACCCGCTCTCTTCCATC 9

```
RESULT 13
ADL23552
ID ADL23552 standard; DNA; 36 BP.
XX
AC ADL23552;
XX
DT 20-MAY-2004 (first entry)
XX
DE Worm torsin-2 RT-PCR primer seqid 12.
XX
KW nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
XX protein aggregates formation suppressor; gene therapy; tor-1; tor-2;
XX torsin; protein-aggregation-associated disease; Alzheimer's disease;
XX Parkinson's disease; prion disease; taupathology; Huntington's disease;
XX polyglutamine disease; dystonia; familial amyotrophic lateral sclerosis;
XX worm; tor-2; reverse transcriptase PCR; primer; ss; torsin-2.
XX
OS Caenorhabditis elegans.
XX
PN US2003235823-A1.
XX
PD 25-DEC-2003.
XX
PF 24-JUN-2002; 2002US-00177104.
XX
PR 24-JUN-2002; 2002US-00177104.
XX
PA (UYAL-) UNIV ALABAMA.
XX
PI Caldwell GA, Caldwell KA;
XX
DR WPI; 2004-070571/07.
XX
PT Novel isolated tor-1, tor-2 polypeptides, useful for treating protein-
XX aggregation-associated diseases e.g. Alzheimer's disease, Parkinson's
XX disease, prion disease, taupathology and Huntington's disease.
XX
PS Example; SEQ ID NO 12; 48pp; English.
XX
CC The invention describes isolated tor-1, tor-2 polypeptides (I). A vector
XX comprising a polynucleotide (II) encoding (I) is useful for making a
XX torsin polypeptide which involves culturing the vector for a duration of
XX time under conditions suitable for expression of the torsin polypeptide.
XX A polynucleotide that is 70-90% or more identical to (II) is useful for
XX detecting a polynucleotide encoding a polypeptide having 70% or more
XX homology to (I) or a polypeptide having torsin activity. The
XX polynucleotides and polypeptides of the invention are useful for treating
XX symptoms or treating one or more protein-aggregation-associated disease
XX which involves administering the polynucleotides or polypeptides to a
XX human being or an animal in need. The one or more protein-aggregation-
XX associated disease is chosen from Alzheimer's disease, Parkinson's
XX disease, prion disease, taupathology, Huntington's disease, polyglutamine
XX disease, dystonia, and familial amyotrophic lateral sclerosis. (I) is
XX useful for controlling expression of one or more isolated polypeptides
XX having amino acid sequence identical to (I) in an organism. This sequence
XX represents a reverse transcriptase PCR primer used in the isolation of
XX cDNA encoding worm torsin-2 (tor-2).
XX
SQ Sequence 36 BP; 10 A; 11 C; 3 G; 12 T; 0 U; 0 Other;
Query Match 61.6%; Score 15.4; DB 12; Length 36;
Best Local Similarity 76.0%; Pred. No. 6.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCCTCTCTTCATC 25
Db 11 CAACTCATCATTAACACTCTTCTTC 35
RESULT 14
AAQ95137/c
ID AAQ95137 standard; DNA; 20 BP.
XX
AC AAQ95137;
XX
DT 25-MAR-2003 (revised)
XX 28-SEP-1995 (first entry)
XX
DE Spinocerebellar ataxia type 1 LR40A PCR primer.
XX
KW Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
XX LR40A PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9501437-A2.
XX
PD 12-JAN-1995.
XX
PF 29-JUN-1994; 94WO-US007336.
XX
PR 29-JUN-1993; 93US-00084365.
XX 28-JUN-1994; 94US-00267803.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Orr HT, Chung M, Zoghbi HY;
XX
DR WPI; 1995-061001/08.
XX
PT New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - used
XX to develop prods. for detection or presymptomatic diagnosis of a SCA1
XX disorder.
XX
PS Example I; Page 39; 111pp; English.
XX
CC AAQ95137 and AAQ95138 are a pair of primers for the PCR amplification of
XX AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1)
XX nucleic acid. The nucleic acid and its protein product (AAR7111) can be
XX used to develop products, for the presymptomatic detection of a SCA 1
XX disorder. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 60.8%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCCTCTCTT 20
Db 20 CAACTCATGACCCCTCTCCT 1
RESULT 15
AAZ28187
ID AAZ28187 standard; DNA; 42 BP.
XX
AC AAZ28187;
XX
DT 20-DEC-1999 (first entry)
XX
DE Human alpha myosin heavy chain-derived peptide M7A-alpha homologue DNA.
XX
KW Heart disease; inflammatory; autoimmune; cardiomyopathy; myosin;
XX Chlamydia; induction; vaccine; ds.
XX
OS Synthetic.
XX OS Homo sapiens.
XX PN US5962636-A.
XX
PD 05-OCT-1999.
XX
PF 12-AUG-1998; 98US-00133774.
```

XX PR 12-AUG-1998; 98US-00133774.
 XX PA (AMGE-) AMGEN CANADA INC.
 XX PI Bachmaier K, Hessel AJ, Penninger JM, Neu N;
 XX WPI; 1999-589735/50.
 DR P-PSDB; AAY42731.
 XX Peptides that induce or suppress inflammatory cardiomyopathy.
 XX Example 1; Col 20; 17pp; English.
 XX This sequence represents DNA encoding the human homologue of the murine
 CC alpha myosin heavy chain-derived peptide, M7A-alpha (AAY42723). Like M7A-
 CC alpha, the human homologue induces inflammatory cardiomyopathy (ICM) via
 CC an autoimmune response in mice immunised with it. It contains an amino
 CC acid sequence motif MxxxxS (AAY42722) which appears to be required for
 CC the induction of this disease. The motif was originally identified in M7A
 CC -alpha when it was compared with a peptide derived from a homologous
 CC region of the murine beta myosin heavy chain, M7A-beta (AAY42724) which
 CC did not cause the disease. Several peptide fragments containing the motif
 CC were identified from a database and were found to be fragments of
 CC cysteine rich outer membrane proteins from various species of Chlamydia.
 CC These peptides also induced ICM, indicating that infection with Chlamydia
 CC may be involved in the development of ICM. Inflammatory cardiomyopathy
 CC peptides are used to determine the risk of ICM by incubation with a
 CC subject's T cells and measuring the degree of proliferation (an increased
 CC degree being indicative of risk) or to raise specific antibodies which
 CC can be used therapeutically and for the detection of Chlamydia. Such
 CC peptides can also be used with an adjuvant and an excipient in a vaccine
 CC for decreasing ICM
 XX SQ Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.8%; Score 15.2; DB 2; Length 42;
 Best Local Similarity 85.0%; Pred. No. 7.6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AACTCATCCACCTCTCTTC 21
 DB 8 AGCTCATGGCCACTCTCTTC 27
 RESULT 16
 AAZ99170
 ID AAZ99170 standard; DNA; 42 BP.
 AC AAZ99170;
 XX 21-JUN-2000 (first entry)
 XX Human peptide M7A-alpha coding sequence.
 XX Cardiant; murine alpha myosin heavy chain; inflammatory myocarditis;
 KW autoimmune inflammatory cardiomyopathy; Chlamydia; antibody; vaccine;
 KW hybridization probe; ss.
 XX Homo sapiens.
 XX OS
 XX US6034230-A.
 XX 07-MAR-2000.
 XX 03-MAY-1999; 99US-00303862.
 XX 12-AUG-1998; 98US-00133774.
 XX (AMGE-) AMGEN CANADA INC.
 XX Neu N, Penninger JM, Bachmaier K, Hessel AJ;
 XX WPI; 1999-589735/50.

DR WPI; 2000-255712/22.
 DR P-PSDB; AAY83820.
 XX DNA molecules encoding novel myocardial peptides used for inhibiting and
 PT inducing inflammatory cardiomyopathy in vivo.
 XX Claim 1; Col 19; 17pp; English.
 PS This sequence represents the coding sequence of the human homologue of
 XX the murine M7A-alpha peptide (Y83811) derived from the murine alpha
 CC myosin heavy chain polypeptide. The peptide was used to evaluate its
 CC ability to induce autoimmune inflammatory cardiomyopathy. A similar
 CC experiment was carried out using the peptide M7A-beta (Y83821). The
 CC invention relates to the isolation of sequences coding for peptide
 CC sequences derived from bacteria and viruses which may cause inflammatory
 CC cardiomyopathy. The peptide sequences are searched based on the sequence
 CC of the M7A peptides derived from the murine alpha myosin heavy chain
 CC polypeptide. The consensus sequence of the murine M7A-alpha/beta peptides
 CC (Y83813) was used to search the PIR public database for similar bacterial
 CC and viral sequences able to cause inflammatory cardiomyopathy. The screen
 CC isolated the peptides Y83814-Y83819 and their corresponding coding
 CC sequences Z99164-Z99169. The peptides encoded by the DNAs are used, alone
 CC or in conjunction with other therapeutics, for inducing or inhibiting
 CC inflammatory cardiomyopathy in vivo, where the cardiomyopathy is
 CC autoimmune inflammatory cardiomyopathy, and inflammatory cardiomyopathy
 CC caused by Chlamydia or other bacterial or viral infections that cause
 CC inflammatory cardiomyopathy. The peptides may also be used for increasing
 CC inflammatory myocarditis in a mammal. Antibodies against the peptides and
 CC the peptides themselves are used for measuring the risk of inflammatory
 CC cardiomyopathy in a mammal. The peptides may also be used in vaccines.
 CC Nucleic acids encoding the peptides may be used as hybridization probes,
 CC e.g. in diagnostic assays to test for the presence of Chlamydia DNA
 XX SQ Sequence 42 BP; 7 A; 19 C; 4 G; 12 T; 0 U; 0 Other;
 Query Match 60.8%; Score 15.2; DB 3; Length 42;
 Best Local Similarity 85.0%; Pred. No. 7.6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AACTCATCCACCTCTCTTC 21
 DB 8 AGCTCATGGCCACTCTCTTC 27
 RESULT 17
 ABQ83620/c
 ID ABQ83620 standard; DNA; 41 BP.
 XX AC ABQ83620;
 XX 26-JAN-2003 (first entry)
 XX Human lysyl oxidase 46.31 probe 2 SEQ ID NO:9.
 XX Human; lysyl oxidase 46.31; enzyme; malignant tumour; haemopathy;
 KW human immunodeficiency virus infection; HIV infection; inflammation;
 KW immunological disease; probe; ss.
 XX Homo sapiens.
 XX OS
 XX CN1345944-A.
 XX 24-APR-2002.
 XX 26-SEP-2000; 2000CN-00125428.
 XX 26-SEP-2000; 2000CN-00125428.
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX Mao Y, Xie Y;
 XX WPI; 2002-539343/58.

XX New polypeptide-human lysyl oxidase 46.31 for treating malignant tumor,
PT hemopathy, human immunodeficiency virus infection, immunological disease
XX and various inflammations.

PS Example 6; Page 19 (Disclosure); 33pp; Chinese.

XX The present invention describes human lysyl oxidase 46.31 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) can be used in the treatment of several diseases, such as
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological disease and various inflammations. The present
CC sequence represents a probe for (I), which is used in an example from the
XX present invention

SQ Sequence 41 BP; 15 A; 8 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 CCACCTCTCTTCATC 25
DB 16 CCACCTCTCTTCATC 2

RESULT 18
ABZ06975
ID ABZ06975 standard; DNA; 50 BP.
XX
AC ABZ06975;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 6966.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PT 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
PF New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 53; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08132) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual.

CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 10 A; 23 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 9.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 AACTCATCACCACCTCTCTTCAT 24
DB 24 AACTCATCTCGAATCTCTCTCAT 46

RESULT 19
ABZ06585/c
ID ABZ06585 standard; DNA; 50 BP.
XX
AC ABZ06585;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 6576.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PT 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
PF New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 54; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08132) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

SQ Sequence 50 BP; 16 A; 1 C; 23 G; 10 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 9.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY      2  AACTCATCACCACCTCTCTTCCAT 24
      ||||| ||| ||| ||| |||
Db      27  AACTCATCTCGAATCTCTCTCAT 5
      ||||| ||| ||| ||| |||

RESULT 20
AD117836
ID  AD117836 standard; DNA; 22 BP.
XX
AC  AD117836;
XX
XX
DT  15-APR-2004 (first entry)
XX
XX  Forward PCR primer used to amplify human NOVX DNA SeqID1372.
XX
XX  PCR; ss; NOVX; metabolic disorder; diabetes; anorexia; cancer;
XX  cardiovascular; infectious; neurodegenerative; immune;
XX  haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
XX  antiinflammatory; neuroprotective; antilipemic; anabolic; cardiant;
XX  neurogenesis; wound healing; angiogenesis; chromosome mapping;
XX  tissue typing; preventive medicine; pharmacogenomic; primer; human.
XX
OS  Homo sapiens.
XX
XX  WO200268649-A2.
XX
XX  06-SEP-2002.
XX
XX  31-JAN-2002; 2002WO-US002785.
XX
XX  31-JAN-2001; 2001US-02653395P.
XX  31-JAN-2001; 2001US-02654422P.
XX  31-JAN-2001; 2001US-0265514P.
XX  31-JAN-2001; 2001US-0265517P.
XX  02-FEB-2001; 2001US-0266406P.
XX  05-FEB-2001; 2001US-0266767P.
XX  07-FEB-2001; 2001US-0266975P.
XX  07-FEB-2001; 2001US-0267057P.
XX  08-FEB-2001; 2001US-0267459P.
XX  09-FEB-2001; 2001US-0267823P.
XX  15-FEB-2001; 2001US-0268974P.
XX  26-FEB-2001; 2001US-0271664P.
XX  27-FEB-2001; 2001US-0271839P.
XX  27-FEB-2001; 2001US-0271855P.
XX  02-MAR-2001; 2001US-0272788P.
XX  02-MAR-2001; 2001US-0273046P.
XX  14-MAR-2001; 2001US-0275925P.
XX  14-MAR-2001; 2001US-0275947P.
XX  14-MAR-2001; 2001US-0275950P.
XX  14-MAR-2001; 2001US-0275989P.
XX  15-MAR-2001; 2001US-0276448P.
XX  16-MAR-2001; 2001US-0276450P.
XX  16-MAR-2001; 2001US-0276397P.
XX  16-MAR-2001; 2001US-0276768P.
XX  20-MAR-2001; 2001US-0278652P.
XX  26-MAR-2001; 2001US-0278775P.
XX  26-MAR-2001; 2001US-0278778P.
XX  29-MAR-2001; 2001US-0279882P.
XX  29-MAR-2001; 2001US-0279884P.
XX  30-MAR-2001; 2001US-0280147P.
XX  11-APR-2001; 2001US-0282922P.
XX  11-APR-2001; 2001US-0283083P.
XX  20-APR-2001; 2001US-0285133P.
XX  23-APR-2001; 2001US-0285749P.
XX  03-MAY-2001; 2001US-0288327P.
XX  03-MAY-2001; 2001US-0288504P.
XX  29-MAY-2001; 2001US-0284047P.
XX  30-MAY-2001; 2001US-0284473P.
XX  08-JUN-2001; 2001US-0296964P.
XX  18-JUN-2001; 2001US-0298959P.
XX  19-JUN-2001; 2001US-0299324P.
XX  13-AUG-2001; 2001US-0312020P.

```

```

PR  16-AUG-2001; 2001US-0312889P.
PR  16-AUG-2001; 2001US-0312908P.
PR  21-AUG-2001; 2001US-0313390P.
PR  28-AUG-2001; 2001US-0315470P.
PR  31-AUG-2001; 2001US-0316447P.
PR  07-SEP-2001; 2001US-0318115P.
PR  07-SEP-2001; 2001US-0318118P.
PR  12-SEP-2001; 2001US-0318740P.
PR  19-SEP-2001; 2001US-0323379P.
PR  18-OCT-2001; 2001US-0330245P.
PR  18-OCT-2001; 2001US-0330308P.
PR  14-NOV-2001; 2001US-0332701P.
XX
XX  (CURA-) CURAGEN CORP.
XX
XX  Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
XX  Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CB;
XX  Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX  Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX  WPI; 2002-706998/76.
XX
XX  New NOVX polypeptides and nucleic acids, useful for preventing or
XX  treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX  atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX  pharmacogenomics.
XX
XX  Example 2; SEQ ID NO 1372; 1498pp; English.
XX
XX  This invention relates to a novel nucleic acids, and encoded polypeptides
XX  thereof, which have properties related to the stimulation of biochemical
XX  or physiological responses in a cell, tissue, organ or organism.
XX  Specifically, it refers to the use of biologically active fragments for
XX  diagnostic and prognostic assays and furthermore in the treatment of
XX  diverse pathological conditions. The present invention describes novel
XX  human and murine NOVX proteins, as well as methods to modulate their
XX  expression using antisense oligos, ribozymes and peptide nucleic acids.
XX  The polypeptides, nucleic acid molecules and antibodies are useful in the
XX  manufacture of a medicament for treating metabolic disorders, diabetes,
XX  anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
XX  and haematopoietic diseases as well as various dyslipidaemias.
XX  Accordingly, these molecules have many activities including anorectic,
XX  virucide, nootropic, antiinflammatory, neuroprotective, antilipemic,
XX  anabolic and cardiant. Furthermore, they are useful in screening assays
XX  to identify small molecules that modulate or inhibit, for example,
XX  neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX  used as in chromosome mapping, tissue typing, preventive medicine and
XX  pharmacogenomics. This oligonucleotide is a PCR primer used to amplify
XX  human NOVX DNA of the invention.
XX
XX  Sequence 22 BP; 4 A; 11 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX  Query Match 59.2%; Score 14.8; DB 6; Length 22;
XX  Best Local Similarity 88.9%; Pred. No. 1e+04;
XX  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy  8 TCACCACCTCTCTTCCATC 25
   ||||| ||| ||| ||| |||
Db  3 TCACCTCTCTCTTCCATC 20

RESULT 21
ADN42918
ID  ADN42918 standard; DNA; 22 BP.
XX
XX  ADN42918;
XX
XX  17-JUN-2004 (first entry)
XX
XX  Human NOV96a/b/c RTQ-PCR forward primer #1.
XX  Human; ss; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; PCR;
XX  primer; RTQ PCR; real time quantitative PCR.

```

XX OS Homo sapiens.
 XX PN US2004033493-A1.
 XX PD 19-FEB-2004.
 XX PF
 XX PF 31-JAN-2002; 2002US-00072012.
 XX PR 31-JAN-2001; 2001US-0265395P.
 XX PR 31-JAN-2001; 2001US-0265412P.
 XX PR 31-JAN-2001; 2001US-0265514P.
 XX PR 31-JAN-2001; 2001US-0265517P.
 XX PR 02-FEB-2001; 2001US-0266406P.
 XX PR 05-FEB-2001; 2001US-0266767P.
 XX PR 07-FEB-2001; 2001US-0266975P.
 XX PR 07-FEB-2001; 2001US-0267057P.
 XX PR 08-FEB-2001; 2001US-0267459P.
 XX PR 09-FEB-2001; 2001US-0267823P.
 XX PR 15-FEB-2001; 2001US-0268974P.
 XX PR 26-FEB-2001; 2001US-0271664P.
 XX PR 27-FEB-2001; 2001US-0271839P.
 XX PR 27-FEB-2001; 2001US-0271855P.
 XX PR 02-MAR-2001; 2001US-0272788P.
 XX PR 02-MAR-2001; 2001US-0273046P.
 XX PR 14-MAR-2001; 2001US-0275925P.
 XX PR 14-MAR-2001; 2001US-0275947P.
 XX PR 14-MAR-2001; 2001US-0275950P.
 XX PR 14-MAR-2001; 2001US-0275989P.
 XX PR 15-MAR-2001; 2001US-0276448P.
 XX PR 15-MAR-2001; 2001US-0276450P.
 XX PR 16-MAR-2001; 2001US-0276397P.
 XX PR 16-MAR-2001; 2001US-0276768P.
 XX PR 20-MAR-2001; 2001US-0278652P.
 XX PR 26-MAR-2001; 2001US-0278775P.
 XX PR 26-MAR-2001; 2001US-0278778P.
 XX PR 29-MAR-2001; 2001US-0279882P.
 XX PR 29-MAR-2001; 2001US-0279884P.
 XX PR 30-MAR-2001; 2001US-0280147P.
 XX PR 11-APR-2001; 2001US-0282992P.
 XX PR 11-APR-2001; 2001US-0283083P.
 XX PR 20-APR-2001; 2001US-0285133P.
 XX PR 23-APR-2001; 2001US-0285749P.
 XX PR 03-MAY-2001; 2001US-0288327P.
 XX PR 03-MAY-2001; 2001US-0289504P.
 XX PR 29-MAY-2001; 2001US-0294047P.
 XX PR 30-MAY-2001; 2001US-0294473P.
 XX PR 08-JUN-2001; 2001US-0296964P.
 XX PR 18-JUN-2001; 2001US-0298959P.
 XX PR 19-JUN-2001; 2001US-0299324P.
 XX PR 13-AUG-2001; 2001US-0312020P.
 XX PR 16-AUG-2001; 2001US-0312889P.
 XX PR 16-AUG-2001; 2001US-0312908P.
 XX PR 21-AUG-2001; 2001US-0313930P.
 XX PR 28-AUG-2001; 2001US-0315470P.
 XX PR 31-AUG-2001; 2001US-0316447P.
 XX PR 07-SEP-2001; 2001US-0318115P.
 XX PR 07-SEP-2001; 2001US-0318118P.
 XX PR 12-SEP-2001; 2001US-0318740P.
 XX PR 19-SEP-2001; 2001US-0323379P.
 XX PR 18-OCT-2001; 2001US-0330245P.
 XX PR 18-OCT-2001; 2001US-0330308P.
 XX PR 14-NOV-2001; 2001US-0332701P.
 XX PR (TCHEV/) TCHERNEV V T.
 XX PA (SPYT/) SPYTEK K A.
 XX PA (ZERRH/) ZERHUSEN B D.
 XX PA (PATT/) PATTURAJAN M.
 XX PA (SHIM/) SHIMKETS R A.
 XX PA (LILL/) LI L.
 XX PA (GANG/) GANGOLLI E A.
 XX PA (PADI/) PADIGARU M.
 XX PA (ANDE/) ANDERSON D W.

PA (RAST/) RASTELLI L.
 PA (MILL/) MILLER C E.
 PA (GERL/) GERLACH V.
 PA (TAUP/) TAUPIER R J.
 PA (GUSE/) GUSEV V Y.
 PA (COLM/) COLMAN S D.
 PA (WOLE/) WOLENC A R.
 PA (PENNA/) PENNA C E A.
 PA (FURT/) FURTAK K.
 PA (GROS/) GROSSE W M.
 PA (ALSO/) ALSOBROOK J P.
 PA (LEPL/) LEPLEY D M.
 PA (RIEG/) RIEGER D K.
 PA (BURG/) BURGESS C E.
 XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
 PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
 PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Penna CE;
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2004-180039/17.
 DR Isolated NOVX polypeptides and polynucleotides, useful for preventing
 XX diagnosing and/or treating cancer, diabetes, cardiomyopathy and
 PT atherosclerosis.
 PT Example 2; SEQ ID NO 1372; 1309pp; English.
 PS The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
 CC including splice variants) and the nucleic acids (NA) that encode them.
 CC Also included are the mature NOVX proteins (and their encoding
 CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
 CC vector, an antibody that binds immunospecifically to NOVX, determining
 CC the presence or amount of NOVX in a sample, determining the presence or
 CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
 CC modulating the activity of NOVX, treating or preventing a disease
 CC disorder, determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX and treating a pathological state
 CC in a mammal comprising administering a polypeptide which is at least 95%
 CC identical to NOVX (or fragment). NOVX and NA may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
 CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
 CC antagonists may also be used to down regulate expression and activity of
 CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
 CC detecting the presence of NOVX in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA)). The agents and methods may be used in this
 CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
 CC and/or atherosclerosis. The present sequence is a real time quantitative
 CC PCR (RTQ PCR) primer for tissue specific expression studies for a NOVX
 CC gene.
 XX Sequence 22 BP; 4 A; 11 C; 0 G; 7 T; 0 U; 0 Other;
 SQ Query Match 59.2%; Score 14.8; DB 12; Length 22;
 Best Local Similarity 88.9%; Pred. No. 1e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 TCACCACTCTCTTCATC 25
 ||||| ||||| |||||
 Db 3 TCACCTCTCTCTTCATC 20
 RESULT 22
 AAZ34011/c
 ID AAZ34011 standard; DNA; 24 BP.
 XX AC AAZ34011;
 XX DT 07-DEC-1999 (first entry)
 XX DE Human PRO352 PCR reverse primer 2.
 XX

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein; ss.

OS Synthetic.
XX Homo sapiens.

PN WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077633P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-0040420.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079789P.

PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080165P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080328P.

PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 08-APR-1998; 98US-0081071P.

PR 09-APR-1998; 98US-0081195P.

PR 09-APR-1998; 98US-0081203P.

PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.

PR 15-APR-1998; 98US-0081838P.

PR 15-APR-1998; 98US-0081952P.

PR 15-APR-1998; 98US-0081955P.

PR 21-APR-1998; 98US-0082568P.

PR 21-APR-1998; 98US-0082569P.

PR 21-APR-1998; 98US-0082700P.

PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082804P.

PR 23-APR-1998; 98US-0082767P.

PR 23-APR-1998; 98US-0082796P.

PR 27-APR-1998; 98US-0083336P.

PR 28-APR-1998; 98US-0083332P.

PR 29-APR-1998; 98US-0083392P.

PR 29-APR-1998; 98US-0083495P.

PR 29-APR-1998; 98US-0083496P.

PR 29-APR-1998; 98US-0083500P.

PR 29-APR-1998; 98US-0083545P.

PR 29-APR-1998; 98US-0083558P.

PR 29-APR-1998; 98US-0083559P.

PR 30-APR-1998; 98US-0083742P.

PR 05-MAY-1998; 98US-0084366P.

PR 06-MAY-1998; 98US-0084414P.

PR 06-MAY-1998; 98US-0084441P.

PR 07-MAY-1998; 98US-0084598P.

PR 07-MAY-1998; 98US-0084600P.

PR 07-MAY-1998; 98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 07-MAY-1998; 98US-0084643P.

PR 13-MAY-1998; 98US-0085333P.

PR 13-MAY-1998; 98US-0085338P.

PR 13-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085582P.

PR 15-MAY-1998; 98US-0085689P.

PR 15-MAY-1998; 98US-0085697P.

PR 15-MAY-1998; 98US-0085700P.

PR 15-MAY-1998; 98US-0085704P.

PR 18-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 22-MAY-1998; 98US-0086414P.

PR 22-MAY-1998; 98US-0086430P.

PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.

PR 28-MAY-1998; 98US-0087106P.

PR 28-MAY-1998; 98US-0087208P.

PR 30-JUL-1998; 98US-0094651P.

PR 11-SEP-1998; 98US-0100038P.

XX (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

XX New secreted and transmembrane polypeptides and their polynucleotides,

XX useful for treating blood coagulation disorders, cancers and cellular

XX adhesion disorders.

XX Example 23; Page 200; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides

XX and their polynucleotides. The nucleotide sequences are useful as sources

XX of probes, primers, for chromosome mapping, and for generation of

XX antisense sequences. They can also be used to create transgenic animals.

XX The proteins can be used to treat a variety of diseases and disorders,

XX depending on their function. Diseases that may be treated include blood

XX coagulation disorders, cancers and cellular adhesion disorders. They may

XX also be used to raise antibodies. AAZ33891 to AAZ4338, and AAY41685 to

XX AA41774 represent polynucleotide and polypeptide sequence given in the

XX exemplification of the present invention

XX SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.8; DB 2; Length 24;

Best Local Similarity 88.9%; Pred. No. 1e+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACTCTCTTC 21

Db 23 CACATCACCACTCTCTTC 6

RESULT 23

AAC78692/c

ID AAC78692 standard; DNA; 24 BP.

XX AAC78692;

XX 08-FEB-2001 (first entry)

DT Human PRO352 reverse PCR primer SEQ ID NO.142.

DE

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
KW expressed sequence tag; detection; cancer; PCR primer; probe; ss.
OS Homo sapiens.
XX WO200053756-A2.
PN 14-SEP-2000.
PD 18-FEB-2000; 2000WO-US004341.
PP 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US028565.
PR 30-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Rotstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fillvaroff E, Pong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Klijavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PW, Wood WI;
XX WPI; 2000-611443/58.
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX Example 23; Page 253; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytosstatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
XX Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
SQ Query Match 59.2%; Score 14.8; DB 3; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 CTCATCACACCTCTTC 21
Db 23 CACATCACACCTCTTC 6
RESULT 24
ACA63579/c
ID ACA63579 standard; DNA; 24 BP.
XX

AC ACA63579;
XX 16-JUN-2003 (first entry)
XX Novel human secreted and transmembrane protein related primer #71.
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing; PCR; primer; ss.
OS Homo sapiens.
XX US2002192706-A1.
PN 19-DEC-2002.
PD 24-OCT-2001; 2001US-00999832.
PP 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 15-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 21-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 15-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 21-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.

PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031273.
PR 30-DEC-1999; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US003376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PA (GETH) GENENTECH INC.
XX
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-328499/31.
XX
XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
XX Disclosure; SEQ ID NO 142; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including

CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preclampsia; carcinogenesis. The present sequence represents a PRO
CC polypeptide associated oligonucleotide of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 8; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CTCATCACCACTCTCTTC 21
Db 23 CACATCACCACTCTCTTC 6
RESULT 26
ABX92383/c
ID ABX92383 standard; DNA; 24 BP.
XX
XX AC ABX92383;
XX
XX DT 08-MAY-2003 (first entry)
XX Human PRO DNA PCR primer SEQ ID NO 142.
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyperinsulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
XX cardiant; PCR; primer; ss.
OS Homo sapiens.
XX
XX US2002169284-A1.
XX
XX PD 14-NOV-2002.
XX
XX PF 16-OCT-2001; 2001US-00978697.
XX
XX PR 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0084249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0065364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.

PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078882P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-00204855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-0005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99US-000505190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00310733.
PR 02-JUN-1999; 99US-0012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028551.
PR 02-DEC-1999; 99US-0028565.
PR 16-DEC-1999; 99US-0030095.
PR 30-DEC-1999; 99US-0031274.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 06-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005001.
PR 01-MAR-2000; 2000US-0005604.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
PR 21-MAR-2000; 2000US-0007532.
PR 30-MAR-2000; 2000US-0008439.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000US-0030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.

PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 29-JUN-2001; 2001US-00886342.
PR 09-JUL-2001; 2001US-00886342.
PR 30-JUL-2001; 2001US-00886342.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Shelton DL;
XX Kijavini IU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-341189/32.
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.
XX Example 23; Page 135; 460pp; English.
XX The invention relates to a new isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, neurosis, atherosclerosis, infertility, premature aging, psoriasis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence is a PCR primer used in the isolation of a cDNA encoding a PRO polypeptide
SQ Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;
Query Match 59.2%; Score 14.8; DB 8; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 CTCATCACCACCTCTCTTC 21

```
Db      23 CACATCACCACCCCTTC 6
RESULT 28
ADA24681/c
ID ADA24681 standard; DNA; 24 BP.
XX
AC ADA24681;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE Secreted and transmembrane PRO protein associated primer #73.
XX
KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
XX
PF 16-OCT-2001; 2001US-00378564.
XX
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081839P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081953P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 10-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0139557P.
PR 16-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
```

```
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Klijavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
XX
XX New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
XX Example 23; Page 143; 461pp; English.
XX
XX The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739
CC polypeptide, and PRO735, PRO700 and PRO739 polypeptides are useful for
Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 CTCATCACCACTCTCTTC 21
Db 23 CACATCACCACTCTCTTC 6
RESULT 29
ACD29725/c
ID ACD29725 standard; DNA; 24 BP.
```

```
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083493P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087108P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005038.
PR 10-MAR-1999; 98WO-US005190.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126773P.
PR 21-APR-1999; 98US-0130232P.
PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 29-OCT-1999; 98US-0162506P.
PR 30-NOV-1999; 98WO-US028313.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001WO-US0918585.
XX
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
XX WPI; 2003-503575/47.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Example 23; Page 137; 459pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinaemia,
CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's
XX
XX Query Match 59.2%; Score 14.8; DB 9; Length 24;
XX Best Local Similarity 88.9%; Pred. No. 1e+04;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 4 CTCATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTCTTC 6
RESULT 30
ADAI2342/C
ID ADAI2342 standard; DNA; 24 BP.
XX
XX ADAI2342;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO352 primer #5.
XX
```

primer; ss; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication; tissue typing; human; PCR.

KW	primer; ss; inflammatory disease; organ failure; atherosclerosis;	PR 10-APR-1998;	98US-0083742P
KW	cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;	PR 05-MAY-1998;	98US-0084366P
KW	diabetic complication; tissue typing; human; PCR.	PR 06-MAY-1998;	98US-0084414P
XX		PR 06-MAY-1998;	98US-0084441P
OS		PR 07-MAY-1998;	98US-0084598P
XX		PR 07-MAY-1998;	98US-0084600P
XX		PR 07-MAY-1998;	98US-0084627P
XX		PR 07-MAY-1998;	98US-0084637P
XX		PR 07-MAY-1998;	98US-0084640P
XX		PR 07-MAY-1998;	98US-0084643P
XX		PR 13-MAY-1998;	98US-0085323P
XX		PR 13-MAY-1998;	98US-0085338P
XX		PR 13-MAY-1998;	98US-0085339P
XX		PR 15-MAY-1998;	98US-0085573P
XX		PR 15-MAY-1998;	98US-0085579P
XX		PR 15-MAY-1998;	98US-0085580P
XX		PR 15-MAY-1998;	98US-0085582P
XX		PR 15-MAY-1998;	98US-0085689P
XX		PR 15-MAY-1998;	98US-0085697P
XX		PR 15-MAY-1998;	98US-0085700P
XX		PR 15-MAY-1998;	98US-0085704P
XX		PR 18-MAY-1998;	98US-0086023P
XX		PR 22-MAY-1998;	98US-0086392P
XX		PR 22-MAY-1998;	98US-0086414P
XX		PR 22-MAY-1998;	98US-0086430P
XX		PR 22-MAY-1998;	98US-0086486P
XX		PR 28-MAY-1998;	98US-0087098P
XX		PR 28-MAY-1998;	98US-0087106P
XX		PR 28-MAY-1998;	98US-0087208P
XX		PR 26-JUN-1998;	98US-00105413
XX		PR 26-JUN-1998;	98US-0090863P
XX		PR 26-JUN-1998;	98US-0091010P
XX		PR 01-JUL-1998;	98US-0091359P
XX		PR 30-JUL-1998;	98US-0094651P
XX		PR 11-SEP-1998;	98US-0100038P
XX		PR 07-OCT-1998;	98US-00168978
XX		PR 07-OCT-1998;	98US-00211141
XX		PR 02-NOV-1998;	98US-00184216
XX		PR 06-NOV-1998;	98US-00187368
XX		PR 20-NOV-1998;	98US-0103030P
XX		PR 20-NOV-1998;	98US-00204855
XX		PR 07-DEC-1998;	98US-00202054
XX		PR 22-DEC-1998;	98US-00218517
XX		PR 22-DEC-1998;	98US-0113296P
XX		PR 23-DEC-1998;	98US-0113621P
XX		PR 05-JAN-1999;	99US-00000106
XX		PR 05-MAR-1999;	99US-00254465
XX		PR 08-MAR-1999;	99US-00505028
XX		PR 10-MAR-1999;	99US-00265686
XX		PR 10-MAR-1999;	99US-00505190
XX		PR 12-MAR-1999;	99US-00267213
XX		PR 12-MAR-1999;	99US-0123957P
XX		PR 29-MAR-1999;	99US-0126777P
XX		PR 12-APR-1999;	99US-00284291
XX		PR 21-APR-1999;	99US-0130232P
XX		PR 26-APR-1999;	99US-0131022P
XX		PR 28-APR-1999;	99US-0131445P
XX		PR 14-MAY-1999;	99US-00311832
XX		PR 14-MAY-1999;	99US-0134287P
XX		PR 14-MAY-1999;	99US-00107733
XX		PR 02-JUN-1999;	99US-0012252
XX		PR 16-JUN-1999;	99US-0139557P
XX		PR 23-JUN-1999;	99US-0141037P
XX		PR 07-JUL-1999;	99US-0145680P
XX		PR 26-JUL-1999;	99US-0145689P
XX		PR 28-JUL-1999;	99US-0146222P
XX		PR 25-AUG-1999;	99US-00380137
XX		PR 25-AUG-1999;	99US-00380138
XX		PR 25-AUG-1999;	99US-00380142
XX		PR 29-OCT-1999;	99US-0162506P
XX		PR 30-NOV-1999;	99US-00288313
XX		PR 02-DEC-1999;	99US-00288551

PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000227.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 21-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PA (GETH) GENENTECH INC.

XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred.No.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTTTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 23 CACATCACCACCTCTTTC 6

RESULT 31
ACD29140/c
ID ACD29140 standard; DNA; 24 BP.

XX
XX ACD29140;

XX
DT 27-AUG-2003 (first entry)

XX
DE Novel human secreted and transmembrane protein related primer #71.

XX Human; secreted and transmembrane protein; PRO: viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW reinitis pigmentosum; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;

KW cardiac- insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
XX 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978585.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066384P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 25-MAR-1998; 98US-0079234P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 21-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.

PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084411P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 13-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-0016897P.
PR 07-OCT-1998; 98US-0021141.
PR 02-NOV-1998; 98US-0018421P.
PR 06-NOV-1998; 98US-0018736P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-0204855.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0021851P.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98US-0000106.
PR 05-JAN-1999; 98US-00254465.
PR 08-MAR-1999; 98US-0005028.
PR 10-MAR-1999; 98US-0028568P.
PR 10-MAR-1999; 98US-000505190.
PR 12-MAR-1999; 98US-00267213.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126773P.
PR 12-APR-1999; 98US-00284291.
PR 21-APR-1999; 98US-0130232P.
PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-00311832.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98US-0010733.
PR 02-JUN-1999; 98US-0012252.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0148222P.
PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380138.
PR 25-AUG-1999; 98US-00380142.

PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US0816744.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.

Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. le+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 CTCATCACCACTCTCTTC 21
| | | | | | | | | | | | | | | | | | | |
Db 23 CACATCACCACTCTCTTC 6

RESULT 32
ADB73648/c
ID ADB73648 standard; DNA; 24 BP.

XX ADB73648;

XX 04-DEC-2003 (first entry)

DE Human PRO DNA PCR primer #71.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW Chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.

OS Homo sapiens.

XX US2003045462-A1.

XX 06-MAR-2003.

XX 16-OCT-2001; 2001US-00978608.

XX

PR 17-OCT-1997;	97US-0062250P.	PR 13-MAY-1998;	98US-0085338P.
PR 03-NOV-1997;	97US-0064249P.	PR 13-MAY-1998;	98US-0085339P.
PR 13-NOV-1997;	97US-0065311P.	PR 15-MAY-1998;	98US-0085573P.
PR 21-NOV-1997;	97US-0066364P.	PR 15-MAY-1998;	98US-0085579P.
PR 10-MAR-1998;	98US-0077450P.	PR 15-MAY-1998;	98US-0085580P.
PR 11-MAR-1998;	98US-0077632P.	PR 15-MAY-1998;	98US-0085582P.
PR 11-MAR-1998;	98US-0077641P.	PR 15-MAY-1998;	98US-0085689P.
PR 12-MAR-1998;	98US-0077649P.	PR 15-MAY-1998;	98US-0085697P.
PR 12-MAR-1998;	98US-0077791P.	PR 15-MAY-1998;	98US-0085700P.
PR 13-MAR-1998;	98US-0078004P.	PR 15-MAY-1998;	98US-0085704P.
PR 17-MAR-1998;	98US-0004020.	PR 18-MAY-1998;	98US-0086023P.
PR 20-MAR-1998;	98US-0078886P.	PR 22-MAY-1998;	98US-0086392P.
PR 20-MAR-1998;	98US-0078910P.	PR 22-MAY-1998;	98US-0086414P.
PR 20-MAR-1998;	98US-0078936P.	PR 22-MAY-1998;	98US-0086430P.
PR 20-MAR-1998;	98US-0078939P.	PR 22-MAY-1998;	98US-0086486P.
PR 25-MAR-1998;	98US-0079294P.	PR 28-MAY-1998;	98US-0087098P.
PR 26-MAR-1998;	98US-0079656P.	PR 28-MAY-1998;	98US-0087106P.
PR 27-MAR-1998;	98US-0079663P.	PR 28-MAY-1998;	98US-0087208P.
PR 27-MAR-1998;	98US-0079664P.	PR 26-JUN-1998;	98US-00105413.
PR 27-MAR-1998;	98US-0079689P.	PR 26-JUN-1998;	98US-0090863P.
PR 27-MAR-1998;	98US-0079728P.	PR 26-JUN-1998;	98US-0091010P.
PR 27-MAR-1998;	98US-0079786P.	PR 01-JUL-1998;	98US-0091359P.
PR 30-MAR-1998;	98US-0079920P.	PR 30-JUL-1998;	98US-0094651P.
PR 31-MAR-1998;	98US-0079923P.	PR 11-SEP-1998;	98US-0100038P.
PR 31-MAR-1998;	98US-0080105P.	PR 07-OCT-1998;	98US-00168978.
PR 31-MAR-1998;	98US-0080107P.	PR 07-OCT-1998;	98WO-US021141.
PR 31-MAR-1998;	98US-0080165P.	PR 02-NOV-1998;	98US-00184216.
PR 31-MAR-1998;	98US-0080194P.	PR 06-NOV-1998;	98US-00187368.
PR 01-APR-1998;	98US-0080327P.	PR 20-NOV-1998;	98US-0109304P.
PR 01-APR-1998;	98US-0080328P.	PR 20-NOV-1998;	98WO-US024855.
PR 01-APR-1998;	98US-0080333P.	PR 07-DEC-1998;	98US-00202054.
PR 01-APR-1998;	98US-0080334P.	PR 22-DEC-1998;	98US-00218517.
PR 08-APR-1998;	98US-0081049P.	PR 22-DEC-1998;	98US-0113296P.
PR 08-APR-1998;	98US-0081071P.	PR 05-JAN-1999;	99WO-US000106.
PR 09-APR-1998;	98US-0081195P.	PR 05-MAR-1999;	99US-00254465.
PR 09-APR-1998;	98US-0081203P.	PR 08-MAR-1999;	99WO-US005028.
PR 09-APR-1998;	98US-0081229P.	PR 10-MAR-1999;	99US-00265686.
PR 15-APR-1998;	98US-0081817P.	PR 10-MAR-1999;	99WO-US005190.
PR 15-APR-1998;	98US-0081819P.	PR 12-MAR-1999;	99US-00267213.
PR 15-APR-1998;	98US-0081838P.	PR 12-MAR-1999;	99US-0123957P.
PR 15-APR-1998;	98US-0081952P.	PR 29-MAR-1999;	99US-0126773P.
PR 15-APR-1998;	98US-0081955P.	PR 12-APR-1999;	99US-00284291.
PR 21-APR-1998;	98US-0082568P.	PR 21-APR-1999;	99US-0130232P.
PR 21-APR-1998;	98US-0082569P.	PR 26-APR-1999;	99US-0131022P.
PR 22-APR-1998;	98US-0082700P.	PR 28-APR-1999;	99US-00311445P.
PR 22-APR-1998;	98US-0082704P.	PR 14-MAY-1999;	99US-00311832.
PR 22-APR-1998;	98US-0082797P.	PR 14-MAY-1999;	99US-0134287P.
PR 23-APR-1998;	98US-0082804P.	PR 14-MAY-1999;	99WO-US010733.
PR 27-APR-1998;	98US-0082796P.	PR 02-JUN-1999;	99WO-US012252.
PR 27-APR-1998;	98US-0083336P.	PR 16-JUN-1999;	99US-00380137.
PR 28-APR-1998;	98US-0083322P.	PR 23-JUN-1999;	99US-0139557P.
PR 29-APR-1998;	98US-0083392P.	PR 07-JUL-1999;	99US-0141037P.
PR 29-APR-1998;	98US-0083495P.	PR 26-JUL-1999;	99US-0142680P.
PR 29-APR-1998;	98US-0083496P.	PR 28-JUL-1999;	99US-0145698P.
PR 29-APR-1998;	98US-0083499P.	PR 25-AUG-1999;	99US-0146222P.
PR 29-APR-1998;	98US-0083500P.	PR 25-AUG-1999;	99US-00380137.
PR 29-APR-1998;	98US-0083545P.	PR 25-AUG-1999;	99US-00380138.
PR 29-APR-1998;	98US-0083554P.	PR 25-AUG-1999;	99US-00380142.
PR 29-APR-1998;	98US-0083558P.	PR 30-NOV-1999;	99US-0162506P.
PR 30-APR-1998;	98US-0083559P.	PR 02-DEC-1999;	99WO-US028313.
PR 05-MAY-1998;	98US-0083742P.	PR 02-DEC-1999;	99WO-US028551.
PR 06-MAY-1998;	98US-0084414P.	PR 16-DEC-1999;	99WO-US028565.
PR 06-MAY-1998;	98US-008441P.	PR 30-DEC-1999;	99WO-US031243.
PR 07-MAY-1998;	98US-0084598P.	PR 05-JAN-2000;	99WO-US031274.
PR 07-MAY-1998;	98US-0084600P.	PR 06-JAN-2000;	2000WO-US000219.
PR 07-MAY-1998;	98US-0084627P.	PR 06-JAN-2000;	2000WO-US000277.
PR 07-MAY-1998;	98US-0084637P.	PR 11-FEB-2000;	2000WO-US000376.
PR 07-MAY-1998;	98US-0084639P.	PR 18-FEB-2000;	2000WO-US003565.
PR 07-MAY-1998;	98US-0084640P.	PR 24-FEB-2000;	2000WO-US004341.
PR 07-MAY-1998;	98US-0084643P.	PR 02-MAR-2000;	2000WO-US005004.
PR 13-MAY-1998;	98US-0085323P.	PR 10-MAR-2000;	2000WO-US005841.
			2000WO-US006319.

PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001WO-US00863428.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH) GENENTECH INC.
PA

Query Match 59.2%; Score 14.8; DB 10; Length 24;

Best Local Similarity 88.9%; Pred. No. 1e+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTTC 6

RESULT 33

ADB76364/c

ID ADB76364 standard; DNA; 24 BP.

XX ADB76364;

XX 04-DEC-2003 (first entry)

XX Human PRO DNA PCR primer #71.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.

OS Homo sapiens.

XX US2003083248-A1.

XX 01-MAY-2003.

PF 16-OCT-2001; 2001US-00978757.

XX 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0065364P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.

```
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0136773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 18-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 28-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 30-OCT-1999; 99US-0162506P.
PR 20-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028531.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015284.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2000WO-US034956.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021056.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
( GETH ) GENENTECH INC.
PA
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
```

```
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI; 2003-755118/71.
XX
XX New PRO polypeptides useful for treating peripheral neuropathy,
PT neuropathies associated with systemic disease such as post-polio syndrome
PT or AIDS-associated syndrome.
XX
XX Example 23; Page 137; 425pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides
CC are useful for treating neuropathy and neuropathy related diseases such
CC as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
Query Match 59.2%; Score 14.6; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CTGATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTTC 6
| | | | | | | | | | | | | |
RESULT 34
ID ADC43790 standard; DNA; 24 BP.
AC ADC43790;
XX
XX 18-DEC-2003 (first entry)
DT Human PRO 352 PCR primer #5.
DE
XX
XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytostatic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
XX
XX Homo sapiens.
XX
XX US2003054986-A1.
XX
XX 20-MAR-2003.
XX
XX 16-OCT-2001; 2001US-00981915.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064249P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
```

PR	22-MAY-1998;	98US-008648466
PR	28-MAY-1998;	98US-00870988P
PR	28-MAY-1998;	98US-00871066P
PR	28-MAY-1998;	98US-00872088P
PR	26-JUN-1998;	98US-00105413P
PR	26-JUN-1998;	98US-00908639P
PR	26-JUN-1998;	98US-00910106P
PR	01-JUL-1998;	98US-00911359P
PR	11-JUL-1998;	98US-00946513P
PR	11-SEP-1998;	98US-01000388P
PR	07-OCT-1998;	98US-00168978
PR	07-OCT-1998;	98WO-US021141P
PR	02-NOV-1998;	98US-00184216P
PR	06-NOV-1998;	98US-00187368
PR	20-NOV-1998;	98US-01093046P
PR	20-NOV-1998;	98WO-US024855
PR	07-DEC-1998;	98US-00202054
PR	22-DEC-1998;	98US-00218511P
PR	23-DEC-1998;	98US-01132966P
PR	23-DEC-1998;	98US-01136219P
PR	05-JAN-1999;	99WO-US000106P
PR	05-JAN-1999;	99US-00254465
PR	08-MAR-1999;	99WO-US005028
PR	10-MAR-1999;	99US-00265686P
PR	10-MAR-1999;	99WO-US0005190
PR	12-MAR-1999;	99US-00267213P
PR	12-MAR-1999;	99US-01239579P
PR	29-MAR-1999;	99US-01267739P
PR	12-APR-1999;	99US-00284291P
PR	21-APR-1999;	99US-01302322P
PR	26-APR-1999;	99US-01310422P
PR	28-APR-1999;	99US-01314459P
PR	14-MAY-1999;	99US-00311832P
PR	14-MAY-1999;	99US-01342872P
PR	14-MAY-1999;	99WO-US0010733
PR	02-JUN-1999;	99WO-US0012252
PR	16-JUN-1999;	99US-01395579P
PR	23-JUN-1999;	99US-01410379P
PR	07-JUL-1999;	99US-01426809P
PR	26-JUL-1999;	99US-01455989P
PR	25-AUG-1999;	99US-00380137P
PR	25-AUG-1999;	99US-00380138P
PR	25-AUG-1999;	99US-00380142P
PR	29-OCT-1999;	99US-01625069P
PR	30-NOV-1999;	99WO-US028313P
PR	02-DEC-1999;	99WO-US028551P
PR	16-DEC-1999;	99WO-US028565P
PR	30-DEC-1999;	99WO-US031243P
PR	05-JAN-2000;	200WO-US000219P
PR	06-JAN-2000;	200WO-US000277P
PR	06-JAN-2000;	200WO-US000376P
PR	11-FEB-2000;	200WO-US003565P
PR	18-FEB-2000;	200WO-US004341P
PR	24-FEB-2000;	200WO-US005004P
PR	02-MAR-2000;	200WO-US0058641P
PR	10-MAR-2000;	200WO-US0066319P
PR	21-MAR-2000;	200WO-US007532P
PR	30-MAR-2000;	200WO-US008439P
PR	17-MAY-2000;	200WO-US013705P
PR	22-MAY-2000;	200WO-US014042P
PR	30-MAY-2000;	200WO-US014941P
PR	02-JUN-2000;	200WO-US015264P
PR	28-JUL-2000;	200WO-US020710P
PR	24-AUG-2000;	200WO-US02328P
PR	08-NOV-2000;	200US-00709238P
PR	27-NOV-2000;	200US-00723749P
PR	01-DEC-2000;	200WO-US032678P
PR	20-DEC-2000;	200US-00747259P
PR	28-DEC-2000;	200WO-US034956P
PR	28-FEB-2001;	200WO-US006520P


```
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 23-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 12-APR-1999; 99US-00284291.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US003565.
PR 24-FEB-2000; 2000WO-US004341.
PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001WO-US0016920.
PR 22-MAR-2001; 2001US-009552.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918595.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCATCACCACTCTCTTC 21
Db 23 CACATCACCACTCTCTTC 6

RESULT 36
ADC63514/c
ID ADC63514 standard; DNA; 24 BP.
XX
AC ADC63514;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 352 PCR primer #5.
XX
Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosstatic;
ophtalmological; antiarthritic; osteopathic; antirheumatic; vulnerary;
auditory; tumour growth; retinal disorder; sports-related joint problem;
articular cartilage defects; osteoarthritis; rheumatoid arthritis;
wound healing; hearing loss; primer.
XX
OS Homo sapiens.
XX
PN US2003054405-A1.
XX
PD 20-MAR-2003.
XX
PF 24-OCT-2001; 2001US-00999833.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
```

PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 08-APR-1998; 98US-0081155P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083332P.
PR 29-APR-1998; 98US-0083435P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 15-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-00211141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-0109304P.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98US-0113621P.
PR 05-JAN-1999; 98US-0113621P.
PR 08-MAR-1999; 98US-00254465.
PR 08-MAR-1999; 98US-00254465.
PR 10-MAR-1999; 98US-00265686.
PR 10-MAR-1999; 98US-00265686.
PR 12-MAR-1999; 98US-00267213.
PR 12-MAR-1999; 98US-00267213.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126773P.
PR 12-APR-1999; 98US-00284291.
PR 21-APR-1999; 98US-0130232P.
PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-00311832.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98US-0134287P.
PR 02-JUN-1999; 98US-0139557P.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 23-JUN-1999; 98US-0141037P.
PR 26-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0142680P.
PR 28-JUL-1999; 98US-0142680P.
PR 28-JUL-1999; 98US-0142680P.
PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380138.
PR 25-AUG-1999; 98US-00380138.
PR 29-OCT-1999; 98US-0162506P.
PR 30-NOV-1999; 98US-00283151.
PR 02-DEC-1999; 98US-00283151.
PR 02-DEC-1999; 98US-00283151.
PR 16-DEC-1999; 98US-00285565.
PR 16-DEC-1999; 98US-00285565.
PR 30-DEC-1999; 98US-0031243.
PR 30-DEC-1999; 98US-0031243.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005004.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
PR 21-MAR-2000; 2000US-0007532.
PR 30-MAR-2000; 2000US-0008439.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014042.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-0017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.

```
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH ) GENENTECH INC.
XX

Query Match      59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCATCACACCTCTCTTC 21
Db 23 CACATCACACCTCTCTTC 6

RESULT 37
ADC66614/c
ID ADC66614 standard; DNA; 24 BP.
XX
AC ADC66614;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 352 PCR primer #5.
XX
KW vulnery; virucide; neuroprotective; cytostatic; gene therapy;
KW tumour cell proliferation inhibitor;
KW secreted and transmembrane protein; PRO; viral infection; wound healing;
KW tissue growth; muscle generation; muscle regeneration;
KW amyotrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;
KW diabetic peripheral neuropathy; chromosome identification; antagonist;
KW tissue typing; immunohistochemical staining; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003060406-A1.
XX
PD 27-MAR-2003.
XX
PF 30-JUL-2001; 2001US-00918585.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98WO-US0202054.
PR 22-DEC-1998; 98US-00218517.

05-JAN-1999; 99WO-US000106.
05-MAR-1999; 99US-00254465.
08-MAR-1999; 99WO-US005028.
10-MAR-1999; 99US-00265886.
12-MAR-1999; 99WO-US005190.
12-MAR-1999; 99US-00267213.
14-APR-1999; 99US-00284291.
14-MAY-1999; 99US-00311832.
14-MAY-1999; 99WO-US010733.
02-JUN-1999; 99WO-US012252.
25-AUG-1999; 99US-00380137.
25-AUG-1999; 99US-00380138.
25-AUG-1999; 99US-00380142.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028565.
16-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US031243.
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
28-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000US-00709238.
27-NOV-2000; 2000US-00723749.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816744.
22-MAR-2001; 2001US-00816920.
22-MAR-2001; 2001WO-US009552.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00872035.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Kl javin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Stewart TA, Tumas D, Williams PM, Wood WI;
WPI; 2003-596568/56.

Novel secreted and transmembrane polypeptides and polynucleotides
encoding them, useful for treating wound healing, tissue growth and
muscle generation and regeneration, amyotrophic lateral sclerosis or
neuropathy.

Example 23; SEQ ID NO 142; 472pp; English.
```

CC The invention describes an isolated secreted and transmembrane PRO
 CC polypeptide (I). PRO polypeptide such as PRO213, PRO700, PRO320 or PRO615
 CC is useful in biotechnological and medical research, as well as in various
 CC industrial applications. PRO polypeptide such as PRO300, PRO866, PRO703,
 CC PRO708, PRO320, PRO351, PRO352, PRO381, PRO615, PRO618, PRO772, PRO853,
 CC PRO860 or PRO846 is useful for therapeutic purposes. PRO363 is useful
 CC therapeutically in vivo for lessening the effects of viral infection.
 CC PRO200 is useful for the treatment of wound healing, tissue growth and
 CC muscle generation and regeneration. PRO337 is useful for treating
 CC amyotrophic lateral sclerosis, neuropathy, AIDS-associated neuropathy or
 CC diabetic peripheral neuropathy. A polynucleotide (II) encoding (I) is
 CC useful for generating transgenic animals or knockout animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents, as probes for generating a pool of sequences for identifying
 CC related PRO coding sequences, and to construct hybridisation probes for
 CC mapping the gene which encodes the PRO and for the genetic analysis of
 CC individuals with genetic disorders, for recombinantly expressing (I) and
 CC for chromosome identification. (I) is useful as molecular marker for
 CC protein electrophoresis purposes, and as therapeutic agents. (I) is also
 CC useful for screening compounds to identify those that mimic the PRO
 CC polypeptide (agonists) or prevent the effect of the PRO polypeptide
 CC (antagonists). (I) and (II) are useful for tissue typing. PRO antibodies
 CC are useful for immunohistochemical staining and/or assay of sample
 CC fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. This sequence represents a human secreted and transmembrane PRO
 CC protein associated primer.

XX Sequence 24 BP; 6 A; 0 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.8; DB 10; Length 24;

Best Local Similarity 88.9%; Pred. No. le+04;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qv 4 CTATCACCACCTCTCTTC 21

|||||||

23 CACATCACCACCTCTTC 6

RESULT 38

ADC68738/c

ID ADC68738 standard; DNA; 24 BP.

XX ADC68738;

AC ADC68738;

XX 18-DEC-2003 (first entry)

XX Human PRO 352 PCR primer #5.

XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytostatic;
 KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss; primer.

XX Homo sapiens.

XX US2003064407-A1.

XX 03-APR-2003.

XX 24-OCT-2001; 2001US-00999834.

XX 17-OCT-1997; 97US-0062250P.

XX 03-NOV-1997; 97US-0064249P.

XX 13-NOV-1997; 97US-0065311P.

XX 21-NOV-1997; 97US-0066364P.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077641P.

XX 11-MAR-1998; 98US-0077649P.

XX 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079234P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 21-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083558P.
 PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 06-MAY-1998; 98US-0084441P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 07-MAY-1998; 98US-0084627P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 13-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.


```
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0093010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-01168978.
PR 07-OCT-1998; 98US-01168978.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-00202054.
PR 07-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99US-00000106.
PR 05-JAN-1999; 99US-00254465.
PR 08-MAR-1999; 99US-00005028.
PR 10-MAR-1999; 99US-00285686.
PR 10-MAR-1999; 99US-00005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 12-APR-1999; 99US-00284291.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99US-00107233.
PR 16-JUN-1999; 99US-0012252.
PR 23-JUN-1999; 99US-0139557P.
PR 07-JUL-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028551.
PR 16-DEC-1999; 99US-00300095.
PR 30-DEC-1999; 99US-00311243.
PR 30-DEC-1999; 99US-00311274.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 11-FEB-2000; 2000US-0003376.
PR 18-FEB-2000; 2000US-0003565.
PR 24-FEB-2000; 2000US-0004341.
PR 02-MAR-2000; 2000US-0005004.
PR 10-MAR-2000; 2000US-0005841.
PR 21-MAR-2000; 2000US-0006319.
PR 30-MAR-2000; 2000US-0007532.
PR 17-MAY-2000; 2000US-0008439.
PR 22-MAY-2000; 2000US-0013705.
PR 30-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0014941.
PR 28-JUL-2000; 2000US-0015264.
PR 24-AUG-2000; 2000US-0020710.
PR 08-NOV-2000; 2000US-0023328.
PR 27-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-0034956.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918595.
XX
XX (GETH ) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CTCATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTTC 6
RESULT 39
ADC62798/c
ID ADC62798 standard; DNA; 24 BP.
XX
AC ADC62798;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 352 PCR primer #5.
XX
KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosolic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnary;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
XX
OS Homo sapiens.
XX
XX US2003068648-A1.
XX
PD 10-APR-2003.
XX
XX
XX 25-OCT-2001; 2001US-00013921.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 12-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079565P.
```

PR	27-MAR-1998;	98US-0079663P.	PR	26-JUN-1998;	98US-0090863P.
PR	27-MAR-1998;	98US-0079664P.	PR	26-JUN-1998;	98US-0091010P.
PR	27-MAR-1998;	98US-0079668P.	PR	01-JUL-1998;	98US-0091359P.
PR	27-MAR-1998;	98US-0079728P.	PR	30-JUL-1998;	98US-0094651P.
PR	27-MAR-1998;	98US-0079786P.	PR	11-SEP-1998;	98US-0100038P.
PR	30-MAR-1998;	98US-0079920P.	PR	07-OCT-1998;	98WO-US021141.
PR	30-MAR-1998;	98US-0079923P.	PR	20-NOV-1998;	98US-0109304P.
PR	31-MAR-1998;	98US-0080105P.	PR	20-NOV-1998;	98WO-US024855.
PR	31-MAR-1998;	98US-0080107P.	PR	22-DEC-1998;	98US-0113296P.
PR	31-MAR-1998;	98US-0080165P.	PR	22-DEC-1998;	98US-0113296P.
PR	31-MAR-1998;	98US-0080194P.	PR	23-DEC-1998;	98US-0113621P.
PR	01-APR-1998;	98US-0080327P.	PR	05-JAN-1999;	99WO-US000106.
PR	01-APR-1998;	98US-0080328P.	PR	08-MAR-1999;	99WO-US005028.
PR	01-APR-1998;	98US-0080333P.	PR	10-MAR-1999;	99WO-US005190.
PR	01-APR-1998;	98US-0080333P.	PR	12-MAR-1999;	99US-0123957P.
PR	07-APR-1998;	98US-0080334P.	PR	29-MAR-1999;	99US-0126773P.
PR	08-APR-1998;	98US-0081049P.	PR	21-APR-1999;	99US-0130232P.
PR	08-APR-1998;	98US-0081070P.	PR	26-APR-1999;	99US-0131022P.
PR	08-APR-1998;	98US-0081071P.	PR	28-APR-1999;	99US-0131445P.
PR	09-APR-1998;	98US-0081195P.	PR	14-MAY-1999;	99US-0134287P.
PR	09-APR-1998;	98US-0081203P.	PR	14-MAY-1999;	99WO-US010733.
PR	09-APR-1998;	98US-0081229P.	PR	02-JUN-1999;	99WO-US012252.
PR	15-APR-1998;	98US-0081817P.	PR	16-JUN-1999;	99US-0139557P.
PR	15-APR-1998;	98US-0081838P.	PR	30-NOV-1999;	99WO-US028313.
PR	15-APR-1998;	98US-0081952P.	PR	02-DEC-1999;	99WO-US028551.
PR	15-APR-1998;	98US-0081955P.	PR	02-DEC-1999;	99WO-US028565.
PR	21-APR-1998;	98US-0082568P.	PR	16-DEC-1999;	99WO-US030095.
PR	21-APR-1998;	98US-0082569P.	PR	30-DEC-1999;	99WO-US031243.
PR	22-APR-1998;	98US-0082700P.	PR	30-DEC-1999;	99WO-US031274.
PR	22-APR-1998;	98US-0082704P.	PR	06-JAN-2000;	2000WO-US000219.
PR	22-APR-1998;	98US-0082797P.	PR	06-JAN-2000;	2000WO-US000277.
PR	22-APR-1998;	98US-0082804P.	PR	06-JAN-2000;	2000WO-US000376.
PR	23-APR-1998;	98US-0082796P.	PR	11-FEB-2000;	2000WO-US003565.
PR	27-APR-1998;	98US-0083336P.	PR	18-FEB-2000;	2000WO-US004341.
PR	28-APR-1998;	98US-0083332P.	PR	24-FEB-2000;	2000WO-US005004.
PR	29-APR-1998;	98US-0083392P.	PR	02-MAR-2000;	2000WO-US005841.
PR	29-APR-1998;	98US-0083495P.	PR	10-MAR-2000;	2000WO-US006319.
PR	29-APR-1998;	98US-0083496P.	PR	21-MAR-2000;	2000WO-US007532.
PR	29-APR-1998;	98US-0083499P.	PR	30-MAR-2000;	2000WO-US008439.
PR	29-APR-1998;	98US-0083500P.	PR	17-MAY-2000;	2000WO-US013705.
PR	29-APR-1998;	98US-0083545P.	PR	22-MAY-2000;	2000WO-US014042.
PR	29-APR-1998;	98US-0083554P.	PR	30-MAY-2000;	2000WO-US014941.
PR	29-APR-1998;	98US-0083558P.	PR	02-JUN-2000;	2000WO-US015264.
PR	30-APR-1998;	98US-0083559P.	PR	28-JUL-2000;	2000WO-US020710.
PR	05-MAY-1998;	98US-0084366P.	PR	24-AUG-2000;	2000WO-US023328.
PR	06-MAY-1998;	98US-0084414P.	PR	01-DEC-2000;	2000WO-US032678.
PR	06-MAY-1998;	98US-0084414P.	PR	20-DEC-2000;	2000WO-US034956.
PR	07-MAY-1998;	98US-0084598P.	PR	28-FEB-2001;	2001WO-US006520.
PR	07-MAY-1998;	98US-0084600P.	PR	22-MAR-2001;	2001WO-US009552.
PR	07-MAY-1998;	98US-0084602P.	PR	25-MAY-2001;	2001WO-US017092.
PR	07-MAY-1998;	98US-0084637P.	PR	01-JUN-2001;	2001WO-US017800.
PR	07-MAY-1998;	98US-0084637P.	PR	20-JUN-2001;	2001WO-US019692.
PR	07-MAY-1998;	98US-0084640P.	PR	29-JUN-2001;	2001WO-US021066.
PR	07-MAY-1998;	98US-0084643P.	PR	09-JUL-2001;	2001WO-US021735.
PR	13-MAY-1998;	98US-0085323P.	PR	30-JUL-2001;	2001US-00918585.
PR	13-MAY-1998;	98US-0085339P.	XX		
PR	15-MAY-1998;	98US-0085573P.	XX		
PR	15-MAY-1998;	98US-0085579P.	XX		
PR	15-MAY-1998;	98US-0085580P.	XX		
PR	15-MAY-1998;	98US-0085582P.	XX		
PR	15-MAY-1998;	98US-0085689P.	XX		
PR	15-MAY-1998;	98US-0085697P.	XX		
PR	15-MAY-1998;	98US-0085700P.	XX		
PR	18-MAY-1998;	98US-0085704P.	XX		
PR	22-MAY-1998;	98US-0086023P.	XX		
PR	22-MAY-1998;	98US-0086392P.	XX		
PR	22-MAY-1998;	98US-0086414P.	XX		
PR	22-MAY-1998;	98US-0086430P.	XX		
PR	22-MAY-1998;	98US-0086486P.	XX		
PR	28-MAY-1998;	98US-0087098P.	XX		
PR	28-MAY-1998;	98US-0087106P.	XX		
PR	28-MAY-1998;	98US-0087208P.	XX		
					(GETH) GENENTECH INC.
					Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
					Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
					Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
					Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
					Stewart TA, Tumas D, Williams PM, Wood WI;
					WPI; 2003-695924/66.
					New isolated secreted and transmembrane PRO polypeptides, useful in the
					Preparation of a medicament for treating a condition responsive to the
					polypeptide, and as therapeutic agents e.g. vaccines.
					Example 23; SEQ ID NO 142; 467pp; English.
					The invention relates to an isolated PRO polypeptide (secreted or
					transmembrane protein) having at least 80% amino acid sequence identity

CC to an amino acid sequence chosen from 94 fully defined sequences as given
 CC in the specification (including PRO lacking its associated signal
 CC peptide, a PRO extracellular domain with or without its associated signal
 CC peptide). Also included are nucleic acids encoding the PRO proteins
 CC mentioned above, a vector comprising a PRO nucleic acid), a host cell
 CC comprising the vector and producing PRO, a chimeric molecule comprising
 CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
 CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
 CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
 CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
 CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
 CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
 CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
 CC molecule is the toxin, cellolabel, or an antibody. The bioactive molecule
 CC causes death of the cell. PRO337 polypeptide is useful for linking a

Query Match 59.2%; Score 14.8; DB 10; Length 24;

Best Local Similarity 88.9%; Pred. No. 1e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACTCTCTTC 21

Db 23 CACATCACCACTCTCTTC 6

RESULT 40

IDC67863/c

ID ADC67863 standard; DNA; 24 BP.

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

XX AC ADC67863;

PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.
 PR 15-APR-1998; 98US-0081955P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082700P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 22-APR-1998; 98US-0082804P.
 PR 23-APR-1998; 98US-0082796P.
 PR 27-APR-1998; 98US-0083336P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083392P.
 PR 29-APR-1998; 98US-0083455P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083500P.
 PR 29-APR-1998; 98US-0083545P.
 PR 29-APR-1998; 98US-0083554P.
 PR 29-APR-1998; 98US-0083558P.
 PR 29-APR-1998; 98US-0083559P.
 PR 30-APR-1998; 98US-0083742P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 06-MAY-1998; 98US-0084441P.
 PR 07-MAY-1998; 98US-0084598P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 07-MAY-1998; 98US-0084627P.
 PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 26-JUN-1998; 98US-0091010P.
 PR 01-JUL-1998; 98US-0091359P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 PR 07-OCT-1998; 98WO-US021141.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.

PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US0000106.
PR 08-MAR-1999; 99WO-US0005028.
PR 10-MAR-1999; 99WO-US0005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US0107133.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918595.
PA (GETH) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2003-657582/62.
XX
XX Novel secreted and transmembrane polypeptides, designated PRO
PT polypeptides, and polynucleotides encoding them useful for treating
PT kidney diseases, bone, cartilage and retinal disorders.
XX
XX Example 23; SEQ ID NO 142; 468pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 94 fully defined sequences as given
CC in the specification (including PRO lacking its associated signal
CC peptide, a PRO extracellular domain with or without its associated signal

CC peptide). Also included are nucleic acids encoding the PRO proteins
CC mentioned above, a vector comprising a PRO nucleic acid), a host cell
CC comprising the vector and producing PRO, a chimeric molecule comprising
CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting

Query Match 59.2%; Score 14.8; DB 10; Length 24;
Best Local Similarity 88.9%; Pred.No. 1e+04; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
Qy 4 CTCATCACCACCTCTCTTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 23 CACATCACCACCTCTCTTC 6

Search completed: November 18, 2005, 11:52:35
Job time : 174.148 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1195.82 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACCTCATCACCACTCTCTTCCATC 25

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	62.4	48	BH627451	BH627451 1007071B0
2	15	60.0	32	AZ641286	AZ641286 1M0503C14
3	14.6	58.4	48	AA576280	AA576280 nm60g01.s
4	14.2	56.8	29	TA133D12P	AL465919 T. brucei
5	14	56.0	34	W69493	W69493 zd47g08.e1
6	14	56.0	44	AZ983982	AZ983982 2M0265013
7	13.8	55.2	44	AZ340483	AZ340483 1M0072N19
8	13.6	54.4	33	AG188152	AG188152 Pan trogl
9	13.6	54.4	46	BZ377820	BZ377820 SALK_1062
10	13.6	54.4	48	BH866288	BH866288 SALK_1011
11	13.6	54.4	49	AI201105	AI201105 qf69g04.x
12	13.4	53.6	42	AZ590062	AZ590062 1M0399M23
13	13.2	52.8	35	AZ635993	AZ635993 1M0493B20
14	13.2	52.8	39	AZ576137	AZ576137 AST-T33E0
15	13.2	52.8	43	AI192173	AI192173 qc96b07.x
16	13.2	52.8	43	AA488318	AA488318 ae30d03.r
17	13.2	52.8	47	BH903423	BH903423 SALK_1025
18	13.2	52.8	47	BZ766487	BZ766487 SALK_1374
19	13	52.0	33	AZ308699	AZ308699 1M0011N24
20	13	52.0	33	BX534557	BX534557 Arabidops
21	13	52.0	36	AZ938244	AZ938244 2M0196E13
22	13	52.0	43	CD531219	CD531219 09P20 Ara
23	13	52.0	44	AJ546976	AJ546976 Drosophil
24	13	52.0	46	AA179783	AA179783 zp50f06.r

c	25	13	52.0	46	1	AV833578	AV833578
	26	13	52.0	48	9	CL528695	CL528695
	27	13	52.0	50	1	AU103975	AU103975
	28	12.8	51.2	31	1	AT441968	AT441968
c	29	12.8	51.2	32	9	TA221E12Q	TA221E12Q
	30	12.8	51.2	36	8	BH909685	BH909685
	31	12.8	51.2	37	1	AI188273	AI188273
c	32	12.8	51.2	39	8	BH903343	BH903343
	33	12.8	51.2	39	9	TA110A12Q	TA110A12Q
c	34	12.8	51.2	40	9	AJ595714	AJ595714
	35	12.8	51.2	41	8	BZ381485	BZ381485
	36	12.8	51.2	42	7	CF920754	CF920754
c	37	12.8	51.2	42	8	AZ828302	AZ828302
	38	12.8	51.2	43	8	BH903344	BH903344
c	39	12.8	51.2	44	8	BH861884	BH861884
	40	12.8	51.2	45	8	BH901162	BH901162
	41	12.8	51.2	46	1	AA717367	AA717367
	42	12.8	51.2	48	8	BH813018	BH813018
c	43	12.8	51.2	50	1	AU103251	AU103251
	44	12.8	51.2	50	9	CG695865	CG695865
c	45	12.6	50.4	23	8	AZ790388	AZ790388

ALIGNMENTS

RESULT 1
LOCUS BH627451
DEFINITION 1007071B08.1EL_x1 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence.
ACCESSION BH627451
VERSION BH627451.1 GI:18440702
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 48)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007071 column: 20
Class: transposon-tagged.
Location/Qualifiers
1. .48
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using

BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

```

Query Match      62.4%; Score 15.6; DB 8; Length 48;
Best Local Similarity 81.8; Pred.No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 CTCATCACCACTCTCTCCATC 25
Db 2 CTCCTCTCCCTCTCTCCACC 23

```

RESULT 2					
AZ641286					
LOCUS	AZ641286	32 bp	DNA	linear	GSS 14-DEC-2000
DEFINITION	LM0503C14R Mouse 10kb plasmid UGNCIM library Mus musculus genomic clone UGCINM0503C14 R, genomic survey sequence.				

Accession	Version	Keywords	Source	Organism
AZ641286	AZ641286.1	GSS	Mus musculus (house mouse)	Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa: Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus
1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isslam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0503 row: C column: 14
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.

```

FEATURES
    source
        1. 32
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0503C14"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (Gll4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
```

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```

Query Match      60.0%; Score 15; DB 8; Length 32;
Best Local Similarity 78.3%; Pred. NO. 5.4e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACTCTCTTCCATC 25
Db 7 ACTCATCACCCCACTCTCTACCC 29

```

RESULT 3	AA576280/c	AA576280	48 bp	linear	EST 09-SEP-1997
LOCUS		nm60g01.s1	NCI CGAP Br3	Homo sapiens	CDNA clone IMAGE:1072656 3'
DEFINITION			similar to gb:X63563	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (HUMAN) i,	mRNA sequence.

ACCESSION	AA576280	
VERSION	AA576280.1	GI:2350795
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48)

REFERENCE
AUTHORS NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbr/image/image.html

Trace considered overall poor quality
Insert Length: 1214 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1

```

FEATURES
source
Location/Qualifiers
1. .48
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1072656"
/sex="female"
/tissue type="breast tumor"
/lab host="SOLR (kanamycin resistant)"
/clone_lib="NCI CGAP Br3"
/note="Organ: breast; Vector: Bluescript SK-; Site 1: EcoR; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Ductal breast tumor. 5' adaptor sequence: 5' GAATTCGGCAGCAG 3' 3' adaptor sequence: 5' CTCGAGTCTTTTTTTTTTTT 3' Average insert size: 0.9 kb."

```

ORIGIN

Query Match	58.4%	Score 14.6;	DB 1;	Length 48;
Best Local Similarity	81.0%;	Pred. No. 8.6e+04;		
Matches 17;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

RESULT 4
TA133D12P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 133d12, forward sequence,
genomic survey sequence.
ACCESSION
AL465919
VERSION
AL465919.1
KEYWORDS
GI:11835041
SOURCE
GSS.
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
FEATURES
source
1..29
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="133d12"
ORIGIN
Query Match 56.8%; Score 14.2; DB 9; Length 29;
Best Local Similarity 84.2%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 6 CATCACCACTCTCTCCAT 24
Db 28 CTTACCCCTCCCTCCAT 10
RESULT 5
W69493/c
LOCUS
DEFINITION
W69493 34 bp mRNA linear EST 16-OCT-1996
IMAGE:343838 3', similar to PIR:S24168 S24168 hypothetical protein -
human ;, mRNA sequence.
ACCESSION
W69493
VERSION
W69493.1
KEYWORDS
GI:1378774
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 983 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
FEATURES
source
1..34
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1269213"
/db_xref="taxon:9606"
/clone="IMAGE:343838"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGACATCTTTTCTTTTCTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
ORIGIN
Query Match 56.0%; Score 14; DB 7; Length 34;
Best Local Similarity 77.3%; Pred. No. 1.5e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 CTCATCACCACTCTCTCCATC 25
Db 25 CTCACACCACTCTCCACATC 4
RESULT 6
AZ983982/c
LOCUS
DEFINITION
AZ983982 44 bp DNA linear GSS 27-APR-2001
Clone UUC2M0265013 F, genomic survey sequence.
ACCESSION
AZ983982
VERSION
AZ983982.1
KEYWORDS
GI:13855209
SOURCE
GSS.
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 44)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0265 row: 0 column: 13
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES

Location/Qualifiers
 1. .44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0265013"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 56.0%; Score 14; DB 8; Length 44;
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 4 CTCATCACCCTCTTCCATC 25
 |||||
 Db 42 CTCCTTTACCTCTTCCATC 21

RESULT 7

AZ340483
 LOCUS AZ340483 44 bp DNA linear GSS 29-SEP-2000
 DEFINITION lM0072N19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0072N19 F, genomic survey sequence.
 ACCESSION AZ340483
 VERSION AZ340483.1 GI:10415782
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 44)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0072 row: N column: 19
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 44.

FEATURES

Location/Qualifiers
 1. .44
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0072N19"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.2%; Score 13.8; DB 8; Length 44;
 Best Local Similarity 88.2%; Pred. No. 1.9e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 CAACATCATCACCCTCT 17
 |||||
 Db 23 CAACAGATCACCCTCT 39

RESULT 8

AG188152/c
 LOCUS AG188152 33 bp DNA linear GSS 06-MAR-2004
 DEFINITION Pan troglodytes DNA, clone: RP43-061L05.T7, genomic survey sequence.
 ACCESSION AG188152
 VERSION AG188152.1 GI:45220321
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of Library RP-43
 Unpublished
 2 (bases 1 to 33)
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..33

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-061L05.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 54.4%; Score 13.6; DB 9; Length 33;
Best Local Similarity 80.0%; Pred. No. 2.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTCATCACCACCTCTCTC 21

Db 28 ACCTCATCACCACCTCTCTC 9

RESULT 9

BZ377820

LOCUS

DEFINITION SALK_106264.42.05.x Arabidopsis thaliana DNA linear GSS 26-NOV-2002
Arabidopsis thaliana genomic clone SALK_106264.42.05.x, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

THE Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_106264.42.05.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAATCATCACCACCTCTCTT 20

Db 16 CTACTAATCTCACTAATCTT 35

RESULT 10

BH866288

LOCUS

DEFINITION SALK_101113 Arabidopsis thaliana DNA linear GSS 05-AUG-2002
thaliana genomic clone SALK_101113, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

The Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 5' end of

ATlg59520.

Class: TDNA tagged.

Location/Qualifiers

1..48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_101113"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 54.4%; Score 13.6; DB 8; Length 48;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CATCACCACCTCTCTTCATC 25

Db 11 CATCTGGCTCTCTTCTATC 30

RESULT 11

AI201105

LOCUS

DEFINITION AT201105 49 bp mRNA linear EST 14-OCT-1998
qf69g04.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755318
3' similar to gb:X68285 GLYCEROL KINASE (HUMAN);, mRNA sequence.

ACCESSION AI201105
 VERSION AI201105.1 GI:3753711
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 49)
 REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1755318"
 /sex="male"
 /lab_host="DH10B"
 /clone_lib="Soares testis NHT"
 /note="Vector: p77T3p-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech
 Laboratories, Inc., and primed with a Not I - oligo(dT)
 primer [5].
 TGTACCAATCTGAAGTGGGAGCGCGCCCAATTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p77T3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 54.4%; Score 13.6; DB 1; Length 49;
 Best Local Similarity 80.0%; Pred. No. 2.3e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACACATCTCTTCCAT 24
 ||||| ||||| ||||| |||||
 Db 16 TCATTACTGCTTCTTCCAT 35

RESULT 12
 AZ590062/c
 LOCUS 42 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0399M23F Mouse 10kb plasmid UGCLM library Mus musculus genomic
 clone UUGCLM0399M23 F, genomic survey sequence.

ACCESSION AZ590062
 VERSION AZ590062.1 GI:11712252
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 1 (bases 1 to 42)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0399 row: M column: 23
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 42.

FEATURES

Location/Qualifiers
 1..42
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0399M23"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 53.6%; Score 13.4; DB 8; Length 42;
 Best Local Similarity 73.3%; Pred. No. 2.8e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ACTCATCACCATCTCTTCCATC 25
 ||||| ||||| ||||| |||||
 Db 40 AATCATTAATACACTCTTCTTC 18

RESULT 13
 AZ635993/c

LOCUS 25 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0493E20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0493E20 R, genomic survey sequence.

ACCESSION AZ635993
 VERSION AZ635993.1 GI:11758183
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.


```

/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NBHPU"
/notes="Organ: uterus; Vector: pT7T3-Pac; Site:1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
AACGGAAGAATCGCGCCGCTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

```

ORIGIN

```

Query Match      52.8%; Score 13.2; DB 1; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 8 TCACCACTCTCTTCCATC 25
    |||||
Db 12 TCCTCACACTCTTCCATC 29

```

RESULT 16

```

AA488318/c
LOCUS
DEFINITION
ae30d03.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897317
5' similar to TR:G1216387 G1216387 SPKAP115. ;, mRNA sequence.
ACCESSION
AA488318
VERSION
AA488318.1 GI:2215749
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 779 Std Error: 0.00
High quality sequence stop: 1.

```

FEATURES

```

source
1..43
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/c1one="IMAGE:897317"
/sex="pooled (6)"
/lab_host="DH10B"
/clone_lib="Gessler Wilms tumor"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dT selection. cDNA library preparation was with
the BRL/Life Tech. Superscript Plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
gcggcgccctt at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcggaccacgcgtcg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."

```

ORIGIN

```

Query Match      52.8%; Score 13.2; DB 1; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 8 TCACCACTCTCTTCCATC 25
    |||||
Db 27 TGACGACTCTCTACCATC 10

```

RESULT 17

```

BH903423/c
LOCUS
DEFINITION
SALK_102585.22.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_102585.22.30.x, genomic
survey sequence.
ACCESSION
BH903423
VERSION
BH903423.1 GI:22714608
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 47)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At3g23970.
Class: TDNA tagged.

```

FEATURES

```

source
1..47
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_102585.22.30.x"
/notes="SALK_102585.22.30.x"
/notes="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

```

ORIGIN

```

Query Match      52.8%; Score 13.2; DB 8; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 CAACTCATCACCACCTCTC 18
    |||||
Db 19 CAACTCTTCATCATGCTC 2

```

RESULT 18

```

BZ766487
LOCUS
DEFINITION
SALK_137474.23.60.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_137474.23.60.x, genomic
survey sequence.

```

```

BZ766487
LOCUS
DEFINITION
SALK_137474.23.60.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_137474.23.60.x, genomic
survey sequence.

```

```

ACCESSION BZ766487
VERSION BZ766487.1 GI:28939040
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 47)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g20200 and 300 bases of the 5' end of At1g20210.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_137474.23.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notice="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACTCTCTTCC 22
||||| ||||| |||||
Db 22 TCATCATCACTTTCTCCC 39

RESULT 19
ACZ308699
LOCUS Arabidopsis thaliana 33 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0011N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0011N24 R, genomic survey sequence.
ACCESSION ACZ308699
VERSION ACZ308699.1 GI:10348959
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

ACCESSION BZ766487
VERSION BZ766487.1 GI:28939040
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 47)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1g20200 and 300 bases of the 5' end of At1g20210.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_137474.23.60.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notice="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 52.8%; Score 13.2; DB 8; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACTCTCTTCC 22
||||| ||||| |||||
Db 22 TCATCATCACTTTCTCCC 39

RESULT 19
ACZ308699
LOCUS Arabidopsis thaliana 33 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0011N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0011N24 R, genomic survey sequence.
ACCESSION ACZ308699
VERSION ACZ308699.1 GI:10348959
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: N column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011N24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notice="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 52.0%; Score 13; DB 8; Length 33;
Best Local Similarity 76.2%; Pred. No. 3.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAACTCATCACTCTCTTTC 21
||||| ||||| |||||
Db 4 CATCTCTCATCACCTCATC 24

RESULT 20
BX534557
LOCUS Arabidopsis thaliana 33 bp DNA linear GSS 04-APR-2004
DEFINITION BX534557
Arabidopsis thaliana T-DNA flanking sequence GK-510D07-019532,
genomic survey sequence.
ACCESSION BX534557
VERSION BX534557.1 GI:31411687
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
COMMENT MEDLINE 22755829
PUBMED 12874060
REFERENCE 2

```



```

1. 1.11
/note="p element insertion in the 3' to 5' orientation"

```

Query Match 52.0%; Score 13; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 13; Conservative 0; Mismatches 0; Indels

RESULT 24

AA1179783 46 bp mRNA linear EST 10-MAR-1998
 zps0f06.r1 StrataGene HeLa cell s3 937216 Homo sapiens cDNA clone
 IMAGE:612899 5' similar to SW:R27A_HUMAN P14798 40S RIBOSOMAL
 PROTEIN S27A. [1] ; mRNA sequence.

VERSION AA179783.1 GI:1761049

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

REFERENCES

EVOLUTION

FILE
JOINT

Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES

source

ORIGIN

.....

Query Match

Best Local

Matches

 Qy

Query Match 52.0%; Score 13; DB 1; Length 50;
 Best Local Similarity 76.2%; Pred. No. 4.2e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTTTCAT 24
 |||||
 Db 3 CTGACCACCCCTCTTTTCAT 23

RESULT 28
 AI441968 31 bp mRNA linear EST 23-JUL-2004
 LOCUS sa83dl1.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-cl004-5902 5' similar to TR:024099 024099 MTN12 ;, mRNA
 sequence.

ACCESSION AI441968.1 GI:4292882
 VERSION AI441968.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

1 (bases 1 to 31)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, J., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R., and Wilson, R.
 Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
 Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. Trace
 considered overall poor quality possible reversed clone: similarity
 on wrong strand This clone is available through: Biogenetic
 Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
 4163; email: info@biogeneticservices.com)

Insert Length: 969 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

Location/Qualifiers
 1..31

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-5902"

/tissue_type="root"

/lab_host="XL10-Gold"

/clone_lib="Gm-cl004"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
 XhoI; Root cDNA. The mRNA was isolated from entire roots
 of 8 day old 'Williams' seedlings which were propagated on
 paper towels with distilled water. Stragene's cDNA
 Synthesis Kit (catalog #200401) was used to synthesize the
 cDNA. First- strand synthesis was performed with 5-methyl
 dCTP, hence the ligated cDNA is hemimethylated.
 Stragene's first-strand synthesis primer was used
 [GAGAGAGAGAGAGAGAGTAGTCGAG(T)-18]. After
 second-strand synthesis, the cDNA ends were 'polished'
 with clone Pfu DNA polymerase, ligated to EcoRI adaptors,
 and phosphorylated. The XhoI site within the first-strand
 synthesis primer was restricted by digestion with XhoI;

all XhoI sites in the cDNA would be protected by their
 hemimethylated status. The cDNA constructs were
 size-fractionated with a 500bp cutoff, using GibcoBRL Life
 Technologies' cDNA Size Fractionation column. The column
 eluent was then ligated into Stragene's pBluescript II
 XR predigested vector (pBluescript II SK(+)) that had been
 digested with EcoRI and XhoI, and phosphorylated. Both
 the white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts. Blue colonies 9n=15) have been
 sequenced, and possess putative cDNA inserts. This library
 was constructed by Dr. Paul Keim & Virginia H. Coryell,
 Department of Biology, Box5640, Northern Arizona
 University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
 Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
 520-523-7500, email: paul.keim@nau.edu,
 virginia.coryell@nau.edu"

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 31;

Best Local Similarity 87.5%; Pred. No. 4.7e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 ACCACTCTCTTCCATC 25

|||||

Db 12 ACCACTCTCTCCACC 27

RESULT 29

LOCUS

DEFINITION

TA221E12Q 32 bp DNA linear GSS 13-DEC-2000
 T. brucei sheared genomic DNA clone 221e12, reverse sequence,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

```

Qy 1 CAACTCATCACCACCTCTCTCCAT 24
   ||| ||||| ||| ||| ||| |||
Db 25 CAATACATCATCATCCGCTTCAT 2

RESULT 30
BH909685          36 bp   DNA      linear      GSS 04-SEP-2002
LOCUS             SALK_055402.24.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_055402.24.05.x, genomic
                  survey sequence.
ACCESSION         BH909685
VERSION           BH909685.1 GI:22722618
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of
                  TDNA.
FEATURES
  source
    Location/Qualifiers
      1..36
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /ecotype="Col-0"
      /db_xref="taxon:3702"
      /clone="SALK_055402.24.05.x"
      /clone_lib="Arabidopsis thaliana TDNA insertion lines"
      /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          51.2%; Score 12.8; DB 8; Length 36;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CACCACCTCTCTTCCAT 24
   ||| ||||| ||| ||| ||| |||
Db 18 CTCAACTCTCTTCCAT 33

RESULT 31
AL188273          37 bp   mRNA      linear      EST 28-OCT-1998
LOCUS             qd1g10.x1 Soares_placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
DEFINITION        clone IMAGE:1723458 3' similar to TR:O42204 O42204 PUTATIVE
                  TRANSMEMBRANE PROTEIN E3-16. ;, mRNA sequence.
ACCESSION         AL188273
VERSION           AL188273.1 GI:3739482
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 37)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1920 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
  source
    Location/Qualifiers
      1..37
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:1723458"
      /dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares_placenta 8to9weeks 2NbHP8to9W"
      /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
ORIGIN
Query Match          51.2%; Score 12.8; DB 1; Length 37;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CATCACACCTCTCTTC 21
   ||| ||||| ||| ||| ||| |||
Db 15 CAACACCACTCTCTTC 30

RESULT 32
BH903343/c        39 bp   DNA      linear      GSS 04-SEP-2002
LOCUS             SALK_102465.31.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_102465.31.50.x, genomic
                  survey sequence.
ACCESSION         BH903343
VERSION           BH903343.1 GI:22714519
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Arabidopsis thaliana
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of

```

```

TDNA.
Class: TDNA tagged.
FEATURES
    source
        1..39
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_102465.31.50.x"
            /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
            /note="each of which contains one or more TDNA insertion"
            /note="elements. The resultant fragment for each line was"
            /note="directly sequenced to determine the genomic sequence at"
            /note="the site of insertion. Details of the protocols used can"
            /note="be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
    Query Match      51.2%; Score 12.8; DB 8; Length 39;
    Best Local Similarity 70.8%; Pred. No. 4.9e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy  2  AACTCATCACCACCTCTCTCCATC 25
      ||||| ||||| ||||| |||||
Db  39  AATTCTACACTACTTAACCCATC 16

RESULT 33
LOCUS      TAl10A12Q/c
DEFINITION T. brucei sheared genomic DNA clone 110a12, reverse sequence,
            genomic survey sequence.
ACCESSION  AL461172
VERSION    AL461172.1 GI:11832134
KEYWORDS  GSS.
SOURCE    Trypanosoma brucei
ORGANISM  Trypanosoma brucei
REFERENCE 1 (bases 1 to 39)
AUTHORS  Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE    Direct Submission
JOURNAL  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: Barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT  Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1..39
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="110a12"
ORIGIN
    Query Match      51.2%; Score 12.8; DB 9; Length 39;
    Best Local Similarity 70.8%; Pred. No. 4.9e+05;
    Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy  1  CAACTCATCACCACCTCTCTCCAT 24
      ||||| ||||| ||||| |||||
Db  36  CACGTCAGCATCACTCTCTCGCAT 13

RESULT 34
LOCUS      AJ595714/c
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            422E10, genomic survey sequence.
ACCESSION  AJ595714
VERSION    AJ595714.1 GI:37945342
KEYWORDS  GSS; left border; T-DNA flanking sequence.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS  Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE    T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL  EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE  22363535
PUBMED  12446565
REFERENCE 2 (bases 1 to 40)
AUTHORS  Balzerque,S.
TITLE    Direct Submission
JOURNAL  Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT  PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..40
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassiljewskij"
            /db_xref="taxon:3702"
            /clone="422E10"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /note="T-DNA flanking sequence"
            /note="left border"
            misc_feature
                1..40
                    /note="T-DNA flanking sequence"
ORIGIN
    Query Match      51.2%; Score 12.8; DB 9; Length 40;
    Best Local Similarity 87.5%; Pred. No. 5e+05;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3  ACTCATCACCACCTCTC 18
      ||||| ||||| |||||
Db  32  ACTCGTCACCACCTCAC 17

RESULT 35
LOCUS      BZ381485/c
DEFINITION SALK_116783.20.40.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_116783.20.40.x, genomic
            survey sequence.
ACCESSION  BZ381485
VERSION    BZ381485.1 GI:25475482

```

```

KEYWORDS
SOURCE
ORGANISM
Arabisopsis thaliana (thale cress)
Arabisopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 41)
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabisopsis Genome
Unpublished (2001)
JOURNAL
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At5g30852.
Class: TDNA tagged.
FEATURES
source
1..41
Location/Qualifiers
1..41
/organism="Arabisopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="Arabisopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
Query Match 51.2%; Score 12.8; DB 8; Length 41;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 AACTCATCACCACTCTCTTCATC 25
Db 41 AATTCACACTACTCTAACCCATC 18
RESULT 36
CF920754
LOCUS
DEFINITION
CF920754-01_C02_1_012 Soybean root hair subtracted cDNA library
gmhrw3 Glycine max cDNA, mRNA sequence.
ACCESSION
CF920754
VERSION
CF920754.1 GI:38191548
KEYWORDS
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 42)
AUTHORS
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
Expressed sequence tags from soybean root hair subtractive cDNA
library
Unpublished (2003)
JOURNAL
COMMENT
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: F7.
Location/Qualifiers
1..42
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmhrw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."
ORIGIN
Query Match 51.2%; Score 12.8; DB 7; Length 42;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCACTCTCTTCAT 24
Db 1 CAAGACCTCGTCATCTCTTCAAT 24
RESULT 37
AZ828302/c
LOCUS
DEFINITION
AZ828302 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105011 F, genomic survey sequence.
ACCESSION
AZ828302
VERSION
AZ828302.1 GI:12998210
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 42)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: 0 column: 11
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 42;
Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 39 ACCACCTCATCACTCACTCCAGC 16

RESULT 38

BH903344/c

LOCUS BH903344 43 bp DNA linear GSS 04-SEP-2002
DEFINITION SALK_102466.48.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_102466.48.25.x, genomic survey sequence.

ACCESSION BH903344

VERSION BH903344.1 GI:22714520

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 43)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

source

1. .43

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clones="SALK_102466.48.25.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match

51.2%; Score 12.8; DB 8; Length 43;

Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 43 AATTCTACTACTACTTAACCCATC 20

RESULT 39

BH861884

LOCUS BH861884

DEFINITION SALK_088239 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_088239, genomic survey sequence.

ACCESSION BH861884

VERSION BH861884.1 GI:22097210

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 44)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3g62020.

Class: TDNA tagged.

FEATURES

source

1. .44

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clones="SALK_088239"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.2%; Score 12.8; DB 8; Length 44;

Best Local Similarity 70.8%; Pred. No. 5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCATC 25

Db 12 ACCACATCACTCTTCTCCAC 35

RESULT 40

BH901162

LOCUS BH901162

DEFINITION SALK_073346.39.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_073346.39.40.x, genomic survey sequence.

ACCESSION BH901162

VERSION BH901162.1 GI:22712043

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J., and Ecker, J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 At1g76170.
 Class: TDNA tagged.
 FEATURES Location/Qualifiers
 source 1..45
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_073346.39.40.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 51.2%; Score 12.8; DB 8; Length 45;
 Best Local Similarity 70.8%; Pred. No. 5.1e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CAAGTCATCACCACCTCTCTTCAT 24
 Db 19 CAGCTAATCAACAAACATTCAT 42

Search completed: November 18, 2005, 21:12:57
 Job time : 1198.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACTCATCACCACCTCTCTTCATC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	1	US-07-989-160-9
2	18.2	72.8	47	4	US-09-422-978-3589
3	16.2	64.8	46	1	US-07-977-434-38
4	16.2	64.8	46	1	US-08-458-819-38
5	16.2	64.8	46	5	PCT-US91-07035-38
6	15.4	61.6	25	4	US-09-888-413-147
7	15.4	61.6	47	3	US-09-641-638-1288
8	15.4	61.6	47	4	US-10-170-097-1288
9	15.2	60.8	20	1	US-08-469-802B-23
10	15.2	60.8	20	2	US-08-267-803B-41
11	15.2	60.8	42	2	US-09-133-774-24
12	15.2	60.8	42	3	US-09-303-862-24
13	15	60.0	25	4	US-09-396-196G-7617
14	14.8	59.2	25	3	US-08-943-731-312
15	14.6	58.4	25	4	US-09-396-196G-75841
16	14.6	58.4	25	4	US-09-396-196G-75842
17	14.6	58.4	25	4	US-09-396-196G-100658
18	14.4	57.6	47	4	US-09-422-978-1201
19	14.2	56.8	24	1	US-07-977-284A-208
20	14.2	56.8	24	2	US-08-256-426B-208
21	14.2	56.8	25	4	US-09-396-196G-75840
22	14	56.0	22	2	US-08-810-599-22
23	14	56.0	22	3	US-08-757-438-2
24	14	56.0	25	4	US-09-396-196G-22970
25	14	56.0	25	4	US-09-396-196G-52198
26	14	56.0	25	4	US-09-396-196G-52200
27	14	56.0	25	4	US-09-396-196G-83551

c	28	14	56.0	40	3	US-08-646-538-20	Sequence 20, Appl
c	29	14	56.0	40	3	US-09-503-222-20	Sequence 20, Appl
c	30	13.8	55.2	26	5	PCT-US91-03680-144	Sequence 144, App
c	31	13.8	55.2	26	5	PCT-US91-03680-145	Sequence 145, App
c	32	13.8	55.2	33	4	US-09-009-893A-13	Sequence 13, Appl
c	33	13.8	55.2	33	4	US-09-009-893A-19	Sequence 19, Appl
c	34	13.8	55.2	33	4	US-09-009-893A-21	Sequence 21, Appl
c	35	13.8	55.2	33	4	US-09-489-155-13	Sequence 13, Appl
c	36	13.8	55.2	33	4	US-09-489-155-19	Sequence 19, Appl
c	37	13.8	55.2	33	4	US-09-489-155-21	Sequence 21, Appl
c	38	13.8	55.2	39	1	US-07-744-282C-64	Sequence 64, Appl
c	39	13.8	55.2	39	5	PCT-US92-06821A-107	Sequence 107, App
c	40	13.8	55.2	47	3	US-09-641-638-1287	Sequence 1287, Ap
c	41	13.8	55.2	47	4	US-10-170-097-1287	Sequence 1287, Ap
c	42	13.6	54.4	25	4	US-09-396-196G-22971	Sequence 22971, A
c	43	13.6	54.4	25	4	US-09-396-196G-41212	Sequence 41212, A
c	44	13.6	54.4	25	4	US-09-396-196G-80104	Sequence 80104, A
c	45	13.6	54.4	28	3	US-09-121-539-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-989-160-9
; Sequence 9, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-07-989-160-9

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCACCTCTCTTCATC 25
|||||

```
Db      1 CAACTCATCACCACCTCTCTTCCATC 25
US-09-422-978-3589/c
; Sequence 3589, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3589
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6834-307 : polymorphic base G or A
US-09-422-978-3589

Query Match      72.8%; Score 18.2; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCCATC 25
      |||||:|||||:|||||:|||||:
Db      32 CACCTCATYAGCACTGTCTTCCTTC 8

RESULT 3
US-07-977-434-38
; Sequence 38, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION NUMBER: US/07/977,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cseri
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-977-434-38

Query Match      64.8%; Score 16.2; DB 1; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 CTCATCACCACCTCTCTTCCAT 24
      |||||:|||||:|||||:
Db      17 CTCATCCCACTCTTTTCCAT 37

RESULT 4
US-08-458-819-38
; Sequence 38, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
```



```

; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: WordPerfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/458,819
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,434
; FILING DATE: 23-FEB-1993
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA primer TAFR01
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-458-819-38
;
; Query Match 64.8%; Score 16.2; DB 1; Length 46;
; Best Local Similarity 85.7%; Pred. No. 5.2e+02;
; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; OY 4 CTCATCACCACCTCTTTCAT 24
;
; DB 17 CTCATCACCACCTCTTTCAT 37
;
; RESULT 5
; PCT-US91-07035-38
; Sequence 38, Application PC/TUS9107035
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street
; CITY: Emeryville
; STATE: California
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07035
; FILING DATE: 19910930
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: Case No. 2580
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-420-3300

```

```

; INFORMATION FOR SEQ ID NO: 38:
;-----
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 46 nucleotides
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;-----
; MOLECULE TYPE: DNA primer TA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;-----
PCT-US91-07035-38

```

```
Query Match          64.8%; Score 16.2; DB 5; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 4 CTCATCACCACTCTCTTCCAT 24
Db 17 CTCATTCCCACTCTTTTCCAT 37

```

RESULT 6
US-09-888-413-147/c
; Sequence 147, Application US/09888413
; Patent No. 6759198
; GENERAL INFORMATION:
; APPLICANT: KRIS, RICHARD M.
; APPLICANT: FELDER, STEPHEN
; TITLE OF INVENTION: HIGH THROUGHPUT
; FILE REFERENCE: NEOGEN-1 P4
; CURRENT APPLICATION NUMBER: US/09/888
; CURRENT FILING DATE: 2001-06-26

```

Query Match 61.6%; Score 15.4; DB 4; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAACTCATCACCACACTCTCTTCCATC 25
|||
Db 25 CACCTCATAGCACTCTCAACC 1

```

RESULT 7
US-09-641-638-1288
; Sequence 1288, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKER
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641
; CURRENT FILING DATE: 2000-08-16

```

```

, PRIOR APPLICATION NUMBER: US 09/502,330
, PRIOR FILING DATE: 2000-02-11
, PRIOR APPLICATION NUMBER: US 60/133,200
, PRIOR FILING DATE: 1999-05-07
, PRIOR APPLICATION NUMBER: US 09/275,267
, PRIOR FILING DATE: 1999-03-23
, PRIOR APPLICATION NUMBER: US 60/119,917
, PRIOR FILING DATE: 1999-02-12
, NUMBER OF SEQ ID NOS: 1304
, SOFTWARE: Patent.pm
, SEQ ID NO 1288
, LENGTH: 47

```

Query Match	61.6%	Score 15.4;	DB 3;	Length 47;
Best Local Similarity	84.2%	Pred. No. 1.2e+03;		
Matches 16;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 4 CTATCACCACCTCTCTTCC 22
||||| : |||||
Db 11 CTATCACGCCTCTCTTCC 29

```

RESULT 8
US-10-170-097-1288
; Sequence 1288, Application US/10170097
; Patent No. 6794143
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1288
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-507-364 : polymorphic base C or T
US-10-170-097-1288

```

Query Match	61.6%	Score 15.4;	DB 4;	Length 47;
Best Local Similarity	84.2%;	Pred. No. 1.2e+03;		
Matches 16;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

QY 4 CTCATCACCACCTCTCTTCC 22
|||||
Db 11 CTCATCAGCCTCYCTTCC 29
|||||

RESULT 9
US-08-469-802B-23/c
; Sequence 23, Application US/08469802B
; Patent No. 5741645
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5741645
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: 119 No. 5741645th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,802B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueiting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00030101
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1225
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-469-802B-23
Query Match 60.8%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCCTCTCTT 20
Db 20 CAACTCATGACCCCTCTCT 1
RESULT 10
US-08-267-803B-41/c
; Sequence 41, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN

COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-267-803B-41
Query Match 60.8%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CAACTCATCACCCTCTCTT 20
Db 20 CAACTCATGACCCCTCTCT 1
RESULT 11
US-09-133-774-24
; Sequence 24, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
US-09-133-774-24
Query Match 60.8%; Score 15.2; DB 2; Length 42;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AACTCATCACCCTCTCTT 21
Db 8 AGCTCATGGCCTCTCTT 27
RESULT 12
US-09-303-862-24
; Sequence 24, Application US/09303862
; Patent No. 6034230
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt

```
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 6034230e1 Peptides Capable of Modulating Inflammatory Heart
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/303,862
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: 09/133,774
; EARLIER FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Human
US-09-303-862-24

Query Match          60.8%; Score 15.2; DB 3; Length 42;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AACATCATCACCACTCTCTTC 21
    ||||| ||||| |||||
Db  8 AGCTCATGGCCACTCTCTTC 27

RESULT 13
US-09-396-196G-7617
; Sequence 7617, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-7617

Query Match          60.0%; Score 15; DB 4; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 AACATCATCACCACTCTCTTCAT 24
    ||||| ||||| ||||| |||||
Db  3 AACATCATCTGACTCTCACCCAT 25

RESULT 14
US-08-943-731-312/c
; Sequence 312, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA W.
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
```

```
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-312

Query Match          59.2%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  8 TCACCACTCTCTTCCATC 25
    ||||| ||||| ||||| |||||
Db  25 TCCCCACTCTCTTCCCTC 8

RESULT 15
US-09-396-196G-75841
; Sequence 75841, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75841
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: mus musculus
US-09-396-196G-75841

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCA 23
Db 4 ACTCATGGCTACTCTCTTCAA 24

RESULT 16
US-09-396-196G-75842
; Sequence 75842, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75842

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCA 23
Db 1 ACTCATGGCTACTCTCTTCAA 21

RESULT 17
US-09-396-196G-100658
; Sequence 100658, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100658
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-100658

Query Match      58.4%; Score 14.6; DB 4; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCAATC 25
Db 5 TCATCACCACCTCTCTTCAATC 25

; ORGANISM: mus musculus
US-09-422-978-1201
; Sequence 1201, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1201
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-21370-87 : polymorphic base C or T
US-09-422-978-1201

Query Match      57.6%; Score 14.4; DB 4; Length 47;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTTC 21
Db 25 CTCCTCATCCTCTCTTTC 42

RESULT 19
US-07-977-284A-208/c
; Sequence 208, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
; FILE REFERENCE: 261
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,284A
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-07-977-284A-208

Query Match 56.8%; Score 14.2; DB 1; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTCCAT 24
Db 24 CATCACCCCTCTTCCCAT 6

RESULT 20
US-08-256-426B-208/c
; Sequence 208, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
```

```
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-08-256-426B-208

Query Match 56.8%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTCCAT 24
Db 24 CATCACCCCTCTTCCCAT 6

RESULT 21
US-09-396-196G-75840
; Sequence 75840, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75840

Query Match 56.8%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACTCTCTTC 21
Db 7 ACTCATGGCTACTCTCTTC 25

RESULT 22
US-08-810-599-22/c
; Sequence 22, Application US/08810599
; Patent No. 5976798
; GENERAL INFORMATION:
; APPLICANT: PARKER, W. Davis
; APPLICANT: HERNSTADT, Corinna
; APPLICANT: GHOSH, Soumitra S.
; APPLICANT: FAHY, Bojin
; TITLE OF INVENTION: Methods for Detecting Mitochondrial Mutations
; TITLE OF INVENTION: Diagnostic for Alzheimer's Disease and Methods for Determining
; TITLE OF INVENTION: of Mitochondrial Nucleic Acid
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1 for Windows
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/810,599
FILING DATE: Concurrent Herewith
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,438
FILING DATE: 27 NO. 5976798 1996
APPLICATION NUMBER: US 08/614,072
FILING DATE: 12 Mar 1996
APPLICATION NUMBER: US 08/536,036
FILING DATE: 29 Sep 1995
APPLICATION NUMBER: US 08/414,969
FILING DATE: 31 Mar 1995
APPLICATION NUMBER: US 08/413,740
FILING DATE: 30 Mar 1995
APPLICATION NUMBER: US 08/410,658
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: US 08/397,808
FILING DATE: 3 Mar 1995
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2105/17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: No
ANTI-SENSE: No
US-08-810-599-22

Query Match 56.0%; Score 14; DB 2; Length 22;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 22 CTCACACCACTTCTTCGACC 1

RESULT 23
US-08-757-438-2/c
Sequence 2, Application US/08757438
Patent No. 6027883
GENERAL INFORMATION:
APPLICANT: Hernstadt, Corinna
APPLICANT: Ghosh, Soumitra
APPLICANT: Fahy, Eoin D.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: OPTIMAL PROCEDURE FOR ISOLATION OF
TITLE OF INVENTION: MUTANT MITOCHONDRIAL ALLELES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,438

FILING DATE: 27-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.407C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-438-2

Query Match 56.0%; Score 14; DB 3; Length 22;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 22 CTCACACCACTTCTTCGACC 1

RESULT 24
US-09-396-196G-22970
Sequence 22970, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22970
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-22970

Query Match 56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTTCCATC 25
|||||
DB 2 CCCATCAGCATCTTGTCCATC 23

RESULT 25
US-09-396-196G-52198/c
Sequence 52198, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678

```
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52198
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52198

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 24 ACTCATCACCACCTC 11

RESULT 26
US-09-396-196G-52200/c
; Sequence 52200, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52200
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52200

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 22 ACTCATCACCACCTC 9

RESULT 27
US-09-396-196G-83551
; Sequence 83551, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-83551

Query Match      56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTC 16
    |||||
Db 22 ACTCATCACCACCTC 9

RESULT 28
US-08-646-538-20/c
; Sequence 20, Application US/08646538
; Patent No. 6027881
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,538
; FILING DATE: No. 6027881 yet assigned
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..40
; OTHER INFORMATION: /note="oligonucleotide #bio25"
US-08-646-538-20

Query Match      56.0%; Score 14; DB 3; Length 40;
Best Local Similarity 77.3%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTCATCACCACCTCTCTTCCAT 24
    ||| |||||
Db 33 ACTAGTCACCTACTCTCTCTCAT 12

RESULT 29
US-09-503-222-20/c
; Sequence 20, Application US/09503222
; Patent No. 6265548
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Gaitanaris, George A.
```



```
;
; APPLICANT: Stauber, Roland H.
; APPLICANT: Vournakis, John N.
; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
; TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503.222
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646.538
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 015280-249000
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..40
; OTHER INFORMATION: /note= "oligonucleotide #bic25"
;
; US-09-503-222-20
;
; Query Match 56.0%; Score 14; DB 3; Length 40;
; Best Local Similarity 77.3%; Pred. No. 4.7e+03;
; Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 3 ACTCATCACCACCTCTCTTCCAT 24
; ||| ||||| ||||| |||||
; Db 33 ACTAGTCACTACTCTCTCTCAT 12
;
; RESULT 30
; PCT-US91-03680-144
; Sequence 144. Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 144:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1..4
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 6
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 7
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 9
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 11
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 12
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 21
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 23
```

```
; OTHER INFORMATION: /mod_base= OTHER
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 7
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 9
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 11
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 12
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 14
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 16
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 21
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 23
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 24
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "5-methylcytosine"
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 26
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N4,N4-ethanocytosine"
; PCT-US91-03680-145
;
; Query Match 55.2%; Score 13.8; DB 5; Length 26;
; Best Local Similarity 57.1%; Pred. No. 5.3e+03;
; Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
;
; Qy 1 CAACTCATCACCACTCTCTTC 21
; Db 1 MMMTMTCTMTCTCTCTTC 21
;
; RESULT 31
; PCT-US91-03680-145
; Sequence 145, Application PC/TUS9103680
; GENERAL INFORMATION:
; APPLICANT: Matteucci, Mark D.
; APPLICANT: Krawczyk, Steven
; TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
; TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
; TITLE OF INVENTION: DUPLEX DNA
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03680
; FILING DATE: 19910524
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4610-0011.40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1..4
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 6
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
```

; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Receptor
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-009-893A-13

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 33
US-09-009-893A-19/c
; Sequence 19, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Receptor
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-009-893A-19

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 34
US-09-009-893A-21/c
; Sequence 21, Application US/09009893A
; Patent No. 6623938
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.

; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6623938el Inhibitor of Tumor Necrosis Factor Receptor
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/009,893A
; CURRENT FILING DATE: 1998-02-21
; PRIOR APPLICATION NUMBER: US 60/054,800
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-009-893A-21

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 35
US-09-489-155-13/c
; Sequence 13, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Receptor
; FILE REFERENCE: 1488.0970002
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-13

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 36
US-09-489-155-19/c
; Sequence 19, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.

```
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-19

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
      ||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 37
US-09-489-155-21/c
; Sequence 21, Application US/09489155
; Patent No. 6680171
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Dixit, Vishva M.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kenny, Joseph J.
; TITLE OF INVENTION: I-FLICE, A No. 6680171el Inhibitor of Tumor Necrosis Factor Recep
; FILE REFERENCE: CD-95 Induced Apoptosis
; CURRENT APPLICATION NUMBER: US/09/489,155
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/009,893
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: US 60/034,205
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 33
; TYPE: DNA
; ORGANISM: primer
US-09-489-155-21

Query Match 55.2%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 5.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACTCTCTTCCAT 24
      ||||| ||||| |||||
Db 32 TCACCAATCTCTGCCAT 16

RESULT 38
US-07-744-282C-64
; Sequence 64, Application US/07744282C
; Patent No. 5521300
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
```

```
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,282C
; FILING DATE: August 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin M. Farrell
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: GTR90-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-744-282C-64

Query Match 55.2%; Score 13.8; DB 1; Length 39;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CATCACCACTCTCTTCC 22
      ||||| ||||| |||||
Db 2 CATCACCACTCTCTTCC 18

RESULT 39
PCT-US92-06821A-107
; Sequence 107, Application PC/TUS9206821A
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; APPLICANT: Liu, Jing
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
; NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 200 East Randolph Drive, P.O. Box 87703
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06821A
; PRIOR APPLICATION DATA: US 07/744,282
; FILING DATE: 13-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B.
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: CN 5851
```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-856-7180
 TELEFAX: 312-856-4972
 INFORMATION FOR SEQ ID NO: 107:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 PCT-US92-06821A-107

Query Match 55.2%; Score 13.8; DB 5; Length 39;
 Best Local Similarity 88.2%; Pred. No. 5.7e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CATCACCACCTCTCTTCC 22
 |||||
 DB 2 CATCACCACCTCTCTCC 18

RESULT 40
 US-09-641-638-1287
 ; Sequence 1287, Application US/09641638
 ; Patent No. 6432648
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Cohen, Annick
 ; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
 ; FILE REFERENCE: GENSET 051CPI
 ; CURRENT APPLICATION NUMBER: US/09/641,638
 ; CURRENT FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: US 09/502,330
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: US 60/133,200
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: US 09/275,267
 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: US 60/119,917
 ; PRIOR FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 1304
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 1287
 ; LENGTH: 47
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 24
 ; OTHER INFORMATION: 10-507-353 : polymorphic base C or T
 US-09-641-638-1287

Query Match 55.2%; Score 13.8; DB 3; Length 47;
 Best Local Similarity 78.9%; Pred. No. 5.8e+03;
 Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTCATCACCACCTCTCTTCC 22
 |||||
 DB 22 CTATCAGCGCTCCCTTCC 40

Search completed: November 18, 2005, 11:22:03
 Job time : 49.5741 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-9

Perfect score: 25

Sequence: 1 CAACCTCATCACCACCTCTCTCCATC 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/PCT PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10_NEW PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10_NEW PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	US-08-469-172-9
2	25	100.0	47	20	US-10-788-779-9
3	18.2	72.8	47	18	US-10-349-143-3589
4	17.6	70.4	25	26	US-11-036-317-879180
5	17.6	70.4	25	26	US-11-036-317-961186

c 6	17.2	68.8	25	26	US-11-036-317-979596	Sequence 979596,
c 7	16.2	64.8	25	22	US-10-719-900-264364	Sequence 264364,
c 8	16.2	64.8	25	22	US-10-719-900-381320	Sequence 381320,
c 9	16.2	64.8	25	22	US-10-719-900-381320	Sequence 754829,
c 10	16	64.0	25	26	US-11-036-317-879179	Sequence 879179,
c 11	16	64.0	25	26	US-11-036-317-961185	Sequence 961185,
c 12	16	64.0	42	16	US-10-326-844-14	Sequence 14, Appl
c 13	15.8	63.2	25	22	US-10-719-900-224994	Sequence 224994,
c 14	15.6	62.4	25	24	US-10-681-773-718222	Sequence 718222, A
c 15	15.6	62.4	25	24	US-10-681-773-105909	Sequence 105909,
c 16	15.6	62.4	25	26	US-11-036-317-853737	Sequence 853737,
c 17	15.6	62.4	25	26	US-11-036-317-979595	Sequence 979595,
c 18	15.4	61.6	25	10	US-09-888-413-147	Sequence 147, App
c 19	15.4	61.6	25	22	US-10-865-853-147	Sequence 147, App
c 20	15.4	61.6	47	18	US-10-170-097-1288	Sequence 1288, Ap
c 21	15.4	61.6	47	22	US-10-326-884-1288	Sequence 1288, Ap
c 22	15.2	60.8	25	24	US-10-719-956-5098	Sequence 5098, Ap
c 23	15.2	60.8	25	24	US-10-719-956-666093	Sequence 666093,
c 24	15.2	60.8	25	24	US-10-719-956-691491	Sequence 691491,
c 25	15.2	60.8	25	26	US-11-036-317-768601	Sequence 768601,
c 26	15.2	60.8	25	26	US-11-060-756-294238	Sequence 294238,
c 27	15.2	60.8	33	24	US-10-891-260-7937	Sequence 7937, Ap
c 28	15	60.0	25	22	US-10-809-189-7617	Sequence 7617, Ap
c 29	15	60.0	25	22	US-10-956-157-53600	Sequence 53600, A
c 30	15	60.0	25	22	US-10-956-157-53604	Sequence 53604, A
c 31	15	60.0	25	22	US-10-956-157-53605	Sequence 53605, A
c 32	15	60.0	25	24	US-10-719-956-602018	Sequence 602018,
c 33	15	60.0	50	18	US-10-131-827-6576	Sequence 6576, Ap
c 34	15	60.0	50	18	US-10-131-827-6966	Sequence 6966, Ap
c 35	14.8	59.2	21	22	US-10-861-304-1	Sequence 1, Appli
c 36	14.8	59.2	22	19	US-10-072-012-1372	Sequence 1372, Ap
c 37	14.8	59.2	24	9	US-09-978-295A-142	Sequence 142, App
c 38	14.8	59.2	24	9	US-09-978-697-142	Sequence 142, App
c 39	14.8	59.2	24	9	US-09-978-192A-142	Sequence 142, App
c 40	14.8	59.2	24	10	US-09-999-832A-142	Sequence 142, App
c 41	14.8	59.2	24	10	US-09-978-189-142	Sequence 142, App
c 42	14.8	59.2	24	10	US-09-978-608A-142	Sequence 142, App
c 43	14.8	59.2	24	10	US-09-978-585A-142	Sequence 142, App
c 44	14.8	59.2	24	10	US-09-978-191A-142	Sequence 142, App
c 45	14.8	59.2	24	10	US-09-978-403A-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-469-172-9
; Sequence 9, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-469-172-9

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCATCACACTCTCTTCCATC 25
Db 1 CAACTCATCACACTCTCTTCCATC 25

RESULT 2
US-10-788-779-9
; Sequence 9, Application US/10788779
; Publication No. US20040152121A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: cDNA
US-10-788-779-9

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCATCACACTCTCTTCCATC 25
Db 1 CAACTCATCACACTCTCTTCCATC 25

RESULT 3
US-10-349-143-3589/c
; Sequence 3589, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3589
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6834-307 : polymorphic base G or A
US-10-349-143-3589

Query Match 72.8%; Score 18.2; DB 18; Length 47;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAACTCATCACACTCTCTTCCATC 25
Db 32 CACCTCATYAGCACTGTCTTCCCTTC 8

RESULT 4
US-11-036-317-879180/c
; Sequence 879180, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 879180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
```


US-11-036-317-879180

Query Match 70.4%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCATC 25
|||||
Db 25 AACTCATCACCACCTGATTTCAC 2

RESULT 5

US-11-036-317-961186/c
; Sequence 961186, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 961186
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-961186

Query Match 70.4%; Score 17.6; DB 26; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCATC 25
|||||
Db 24 AACTCATCACCACCTGATTTCAC 1

RESULT 6

US-11-036-317-979596/c
; Sequence 979596, Application US/11036317
; Publication No. US20050214823A1

; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979596
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-11-036-317-979596

Query Match 68.8%; Score 17.2; DB 26; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCCA 23
|||||
Db 22 AACTCATCACCACCTGATTCCA 1

RESULT 7

US-10-719-900-264364/c

; Sequence 264364, Application US/10719900
; Publication No. US20050026164A1

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 264364
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-719-900-264364

Query Match 64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTTCCAT 24
|||||
Db 21 CTCATCACCACGTCTTGCCAT 1

RESULT 8

US-10-719-900-381320/c
; Sequence 381320, Application US/10719900
; Publication No. US20050026164A1

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 381320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-719-900-381320

Query Match 64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTTCC 22
|||||
Db 25 AACTGATGACCACTGTCTCC 5

RESULT 9

US-10-719-900-754829
; Sequence 754829, Application US/10719900
; Publication No. US20050026164A1

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 754829
; LENGTH: 25
; TYPE: DNA

```
; ORGANISM: Mus musculus
US-10-719-900-754829

Query Match      64.8%; Score 16.2; DB 22; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCATC 25
   ||| ||||| ||||| |||||
Db 1 TAATAACCACTCTCTTCCCTC 21

RESULT 10
US-11-036-317-879179/c
; Sequence 879179, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 879179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-879179

Query Match      64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.8e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||||
Db 25 AACTCATCACCACTGATTTCCAAAC 2

RESULT 11
US-11-036-317-961185/c
; Sequence 961185, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 961185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-961185

Query Match      64.0%; Score 16; DB 26; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.8e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||||
Db 24 AACTCATCACCTGATTTCCAAAC 1

RESULT 12
```

```
US-10-226-844-14
; Sequence 14, Application US/10226844
; Publication No. US20030113764A1
; GENERAL INFORMATION:
; APPLICANT: Bodary, Sarah C.
; APPLICANT: Fisher, Karen L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: P1773R1
; CURRENT APPLICATION NUMBER: US/10/226,844
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US/09/627,202
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/146,217
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 14
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-226-844-14

Query Match      64.0%; Score 16; DB 16; Length 42;
Best Local Similarity 79.2%; Pred. No. 4.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACTCTCTTCCATC 25
   ||| ||||| ||||| |||||
Db 6 AATGCATCAAGACTCTCTGCCATC 29

RESULT 13
US-10-719-900-224994
; Sequence 224994, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224994
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-224994

Query Match      63.2%; Score 15.8; DB 22; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ATCACCACCTCTCTTCCATC 25
   ||| ||||| ||||| |||||
Db 1 ATAACCACTCTCTTCCCTC 19

RESULT 14
US-10-681-773-71822
; Sequence 71822, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
```

```
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71822
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-71822

Query Match      62.4%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CAATCATCACCACCTCTCTTCC 22
Db 3 CAAATCATTAGCTCTCTCTTCC 24

RESULT 15
US-10-681-773-105909
; Sequence 105909, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 105909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-105909

Query Match      62.4%; Score 15.6; DB 24; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 CAATCATCACCACCTCTCTTCC 22
Db 4 CAAATCATTAGCTCTCTCTTCC 25

RESULT 16
US-11-036-317-853737/c
; Sequence 853737, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 853737
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-853737

Query Match      62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCATC 25
Db 25 CTCATCACCACCTGATTTCCAAAC 4

RESULT 17
US-11-036-317-979595/c
; Sequence 979595, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979595
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-979595

Query Match      62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCA 23
Db 22 AACTCATCACCCTCTGATTTCCA 1

RESULT 18
US-09-888-413-147/c
; Sequence 147, Application US/09888413
; Publication No. US20030096232A1
; GENERAL INFORMATION:
; APPLICANT: KRIS, RICHARD M.
; APPLICANT: FEJDER, STEPHEN
; TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
; FILE REFERENCE: NEOGEN-1 P4
; CURRENT APPLICATION NUMBER: US/09/888,413
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/337,325
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/218,166
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/109,076
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/068,291
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: attenuation factor oligonucleotide
US-09-888-413-147
```


Publication No. US20040146910A1

GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 5098
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-5098

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCAT 24
Db 24 TCATCAGCACTCTCAGCCAT 5

RESULT 23

US-10-719-956-666093
Sequence 666093, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 666093
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-666093

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCAT 24
Db 2 TCATCATGACTCTCTTCTT 21

RESULT 24

US-10-719-956-691491
Sequence 691491, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 691491
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus

US-10-719-956-691491

Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTCCA 23
Db 4 CTCATGACTACTTCTTCCA 23

RESULT 25

US-11-036-317-768601
Sequence 768601, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:

APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 768601
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-768601

Query Match 60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCATCACCACCTCTCTTCCAT 24
Db 1 TCATCAACTCTCTTCTTCAAT 20

RESULT 26

US-11-060-756-294238
Sequence 294238, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:

APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 294238
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-294238

Query Match 60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTC 21
Db 5 AAGTAATCACCACCTTCTTTC 24

RESULT 27

US-10-891-260-7937
Sequence 7937, Application US/10891260

```
; Publication No. US20050227244A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
; FILE REFERENCE: 3522.3
; CURRENT APPLICATION NUMBER: US/10/891,260
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 10/681,773
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 10244
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7937
; LENGTH: 33
; TYPE: DNA
; ORGANISM: homo sapien
US-10-891-260-7937

Query Match      60.0%; Score 15.2; DB 24; Length 33;
Best Local Similarity 77.3%; Pred. No. 1.2e+04;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCC 22
      ||||| ||||| ||||| |||||
Db      11 CAAATCTTAGCTCTCTCTTCC 32

RESULT 28
US-10-809-189-7617
; Sequence 7617, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-7617

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AACTCATCACCACCTCTCTTCCAT 24
      ||||| ||||| ||||| |||||
Db      3 AACTCATCTGACTCTCACCCAT 25

RESULT 29
US-10-956-157-53600/c
; Sequence 53600, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53600
```

```
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53600

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCCA 23
      ||||| ||||| ||||| |||||
Db      23 CATCTCATTAAACACTCTGGTCCA 1

RESULT 30
US-10-956-157-53604/c
; Sequence 53604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53604
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53604

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCCA 23
      ||||| ||||| ||||| |||||
Db      24 CATCTCATTAAACACTCTGGTCCA 2

RESULT 31
US-10-956-157-53605/c
; Sequence 53605, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53605
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-53605

Query Match      60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CAACTCATCACCACCTCTCTTCCA 23
      ||||| ||||| ||||| |||||
```

Db 25 CATCTCATTAACACTCTGCTCCA 3

RESULT 32

US-10-719-956-602018
; Sequence 602018, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 602018
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-602018

Query Match 60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCAT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AAATCATCAGCATTTTCTCTCTT 25

RESULT 33

US-10-131-827-6576/c
; Sequence 6576, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6576
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6576

Query Match 60.0%; Score 15; DB 18; Length 50;
Best Local Similarity 78.3%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCAT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 27 AACTCATCTCGAATCTCTCTCAT 5

RESULT 34

US-10-131-827-6966
; Sequence 6966, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6966
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6966

Query Match 60.0%; Score 15; DB 18; Length 50;
Best Local Similarity 78.3%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTCATCACCACCTCTCTTCCAT 24
| | | | | | | | | | | | | | | | | | | | | |
Db 24 AACTCATCTCGAATCTCTCTCAT 46

RESULT 35

US-10-861-304-1/c
; Sequence 1, Application US/10861304
; Publication No. US20050014697A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Liu, Limin
; TITLE OF INVENTION: Compositions and Methods for Modulating S-Nitrosoglutathione
; FILE REFERENCE: 28195-516 UTIL
; CURRENT APPLICATION NUMBER: US/10/861,304
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/550,833
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/545,965
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/476,055
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-861-304-1

Query Match 59.2%; Score 14.8; DB 22; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TCACCACCTCTCTTCCATC 25
| | | | | | | | | | | | | | | | | | | | | |
Db 18 TCACCACCTCTTCCATC 1

RESULT 36

US-10-072-012-1372
; Sequence 1372, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly

```
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastell, Valerie
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1372
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ag4532 Forward
US-10-072-012-1372
Query Match 59.2%; Score 14.8; DB 19; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 TCACACTCTCTTCATC 25
Db 3 TCACCTCTCTCTCCATC 20
RESULT 37
US-09-978-295A-142/c
; Sequence 142, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
```


; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 23 CACATCACCACCTCTCTTC 6

RESULT 38
US-09-978-697-142/c
; Sequence 142, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30

```

, PRIOR APPLICATION NUMBER: 60/084366
, PRIOR FILING DATE: 1998-05-05
, PRIOR APPLICATION NUMBER: 60/084414
, PRIOR FILING DATE: 1998-05-06
, PRIOR APPLICATION NUMBER: 60/084441
, PRIOR FILING DATE: 1998-05-06
, PRIOR APPLICATION NUMBER: 60/084637
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084639
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084640
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084598
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084600
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084627
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/084643
, PRIOR FILING DATE: 1998-05-07
, PRIOR APPLICATION NUMBER: 60/085339
, PRIOR FILING DATE: 1998-05-13
, PRIOR APPLICATION NUMBER: 60/085338
, PRIOR FILING DATE: 1998-05-13
, PRIOR APPLICATION NUMBER: 60/085323
, PRIOR FILING DATE: 1998-05-13
, PRIOR APPLICATION NUMBER: 60/085582
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085700
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085689
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085579
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085580
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085573
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697

```

Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels

Qy 4 CTCATCACCACTCTCTTC 21
| | | | | | | | | |
Db 23 CACATCACCACTCTCTTC 6

RECIT.T 39

```

US-09-978-192A-142/c
; Sequence 142, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferraris, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Giang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gritsenen, Mary E.
; APPLICANT: Goddard, Audrey A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillman, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

```

; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637

; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 59.2%; Score 14.8; DB 9; Length 24;

Best Local Similarity 88.9%; Pred. No. 1.5e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 CTCATCACCACCTCTCTTC 21
Db 23 CACATCACCACCTCTTC 6

RESULT 40

US-09-999-832A-142/c
; Sequence 142, Application US/09999832A
; Publication No US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT FILING DATE: 2001-10-24
CURRENT FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07

```

; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

Query Match 59.2%; Score 14.8; DB 9; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCATCACCACCTCTCTTC 21
| | | | | | | | | |
Db 23 CACATCACCACCCCTCTTC 6

Search completed: November 18, 2005, 15:41:10
Job time : 337.027 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:12:34 ; Search time 693.631 Seconds
(without alignments)
1746.433 Million cell updates/sec

Title: US-10-788-779-10
Perfect score: 25
Sequence: 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	I12903 Sequence 10
C 2	14.6	58.4	25	6	CQ774405 Sequence
3	14.6	58.4	29	6	AR526910 Sequence
C 4	14.2	56.8	22	6	AX703317 Sequence
5	14.2	56.8	25	6	A83424 Sequence 10
6	14.2	56.8	39	6	AR481983 Sequence
7	14.2	56.8	41	6	A18467 light chain
8	14.2	56.8	41	6	A24273 Oligonucleo
9	14.2	56.8	41	6	AR028581 Sequence
10	14.2	56.8	41	6	AR085792 Sequence
11	14.2	56.8	41	6	AR474145 Sequence
12	14.2	56.8	48	6	I03017 Sequence 7
13	14.2	56.8	49	6	A08605 Oligonucleo
14	14.2	56.8	49	6	AR337938 Sequence
C 15	14.2	56.8	50	6	CQ009070 Sequence
C 16	14	56.0	50	6	CQ003048 Sequence
17	13.8	55.2	21	6	BD134567 Method fo
C 18	13.8	55.2	33	6	AX787200 Sequence
C 19	13.8	55.2	33	6	AX787202 Sequence

C 20	13.8	55.2	33	6	AX787209 Sequence
C 21	13.8	55.2	33	6	AX787211 Sequence
C 22	13.8	55.2	49	6	CQ848579 Sequence
23	13.8	55.2	50	6	CQ003302 Sequence
24	13.8	55.2	50	6	CQ848580 Sequence
C 25	13.6	54.4	20	6	AX294559 Sequence
C 26	13.6	54.4	21	6	AR148747 Sequence
C 27	13.6	54.4	24	6	AX289926 Sequence
C 28	13.6	54.4	25	6	CQ620789 Sequence
C 29	13.6	54.4	25	6	CQ620790 Sequence
C 30	13.6	54.4	25	6	CQ620791 Sequence
C 31	13.6	54.4	25	6	CQ620792 Sequence
C 32	13.6	54.4	25	6	CQ620793 Sequence
C 33	13.6	54.4	25	6	CQ620794 Sequence
C 34	13.6	54.4	25	6	AR461852 Sequence
C 35	13.6	54.4	25	6	AR461853 Sequence
C 36	13.6	54.4	25	6	AR461854 Sequence
C 37	13.6	54.4	25	6	AR461855 Sequence
C 38	13.6	54.4	25	6	AR461856 Sequence
C 39	13.6	54.4	25	6	AR461857 Sequence
40	13.6	54.4	43	6	AX427664 Sequence
41	13.6	54.4	47	6	AR291369 Sequence
42	13.4	53.6	33	6	AX280482 Sequence
43	13.4	53.6	45	6	AX467369 Sequence
C 44	13.4	53.6	49	6	AR123855 Sequence
C 45	13.4	53.6	49	6	BD133105 Novel hum

ALIGNMENTS

RESULT 1	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
VERSION	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
SOURCE	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
ORGANISM	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
REFERENCE	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
AUTHORS	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
TITLE	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
JOURNAL	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
FEATURES	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
source	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
ORIGIN	I12903.1	GI:910880	25 bp	DNA	linear	PAT 26-JUL-1995
Query Match	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Best Local Similarity	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Matches	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Conservative	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Mismatches	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Indels	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Gaps	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Qy	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
Db	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
RESULT 2	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
LOCUS	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
DEFINITION	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ACCESSION	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
VERSION	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
KEYWORDS	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
SOURCE	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
ORGANISM	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
REFERENCE	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995
AUTHORS	I12903	Sequence 10 from patent US 5429923.	25 bp	DNA	linear	PAT 26-JUL-1995

```

TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
           1. .25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide primer GVK30"

ORIGIN
Query Match      58.4%; Score 14.6; DB 6; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 23 GAGCATAGTCGATCCATGGCA 3

RESULT 3
LOCUS      AR526910
DEFINITION Sequence 24 from patent US 6723520.
ACCESSION  AR526910
VERSION     AR526910.1 GI:53913800
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 29)
AUTHORS   Wang, W., Gish, K.C., Schall, T.J., Vicari, A. and Zlotnik, A.
TITLE     Antibodies that bind chemokine teck
JOURNAL   Patent: US 6723520-A 24 20-APR-2004;
           Location/Qualifiers
FEATURES   source
           1. .29
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      58.4%; Score 14.6; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 8 AGCAGAGCAGAGTGTATGGCAC 28

RESULT 4
LOCUS      AX703317/c
DEFINITION Sequence 546 from Patent WO02059313.
ACCESSION  AX703317
VERSION     AX703317.1 GI:29538363
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Li, L., Ballinger, R.A., Padigaru, M., Kekuda, R., Colman, S.D.,
           Spytek, K.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
           Malyankar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
           Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
           Gangolli, E.A. and Millet, I.
TITLE     G-protein coupled receptors and nucleic acids encoding same
JOURNAL   Patent: WO 02059313-A 546 01-AUG-2002;
           Curagen Corporation (US)
           Location/Qualifiers
FEATURES   source
           1. .22
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
           1. .25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide primer GVK30"

ORIGIN
Query Match      58.4%; Score 14.6; DB 6; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 23 GAGCATAGTCGATCCATGGCA 3

RESULT 3
LOCUS      AR526910
DEFINITION Sequence 24 from patent US 6723520.
ACCESSION  AR526910
VERSION     AR526910.1 GI:53913800
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 29)
AUTHORS   Wang, W., Gish, K.C., Schall, T.J., Vicari, A. and Zlotnik, A.
TITLE     Antibodies that bind chemokine teck
JOURNAL   Patent: US 6723520-A 24 20-APR-2004;
           Location/Qualifiers
FEATURES   source
           1. .29
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      58.4%; Score 14.6; DB 6; Length 29;
Best Local Similarity 81.0%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 8 AGCAGAGCAGAGTGTATGGCAC 28

RESULT 4
LOCUS      AX703317/c
DEFINITION Sequence 546 from Patent WO02059313.
ACCESSION  AX703317
VERSION     AX703317.1 GI:29538363
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Li, L., Ballinger, R.A., Padigaru, M., Kekuda, R., Colman, S.D.,
           Spytek, K.A., Casman, S.J., Vernet, C.A., Shenoy, S.G., Gusev, V.,
           Malyankar, U.M., Edinger, S., Gerlach, V., Smithson, G., Stone, D.J.,
           Sciore, P., Macdougall, J.R., Gunther, E., Peyman, J.A., Ellerman, K.,
           Gangolli, E.A. and Millet, I.
TITLE     G-protein coupled receptors and nucleic acids encoding same
JOURNAL   Patent: WO 02059313-A 546 01-AUG-2002;
           Curagen Corporation (US)
           Location/Qualifiers
FEATURES   source
           1. .22
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

TITLE      Corn root preferential promoters and uses thereof
JOURNAL    Patent: WO 2004013169-A 10 12-FEB-2004;
           Bayer BioScience N.V. (BE)
FEATURES   source
           1. .25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide primer GVK30"

ORIGIN
Query Match      58.4%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 21 TGGTCTTACCAGATTCATG 3

RESULT 5
LOCUS      A83424
DEFINITION Sequence 10 from Patent WO9850067.
ACCESSION  A83424
VERSION     A83424.1 GI:6732762
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 25)
AUTHORS   Goebel, W. and Demuth, A.
TITLE     USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION
JOURNAL   Patent: WO 9850067-A 10 12-NOV-1998;
           GOEBEL WERNER (DE); SCHERING AG (DE)
           Location/Qualifiers
FEATURES   source
           1. .25
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCA 24
    ||||| ||||| ||||| |||||
Db 1 GCCTAGAGGATGCATGGCA 19

RESULT 6
LOCUS      AR481983
DEFINITION Sequence 50 from patent US 6699974.
ACCESSION  AR481983
VERSION     AR481983.1 GI:47243890
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 39)
AUTHORS   Ono, K., Ohtomo, T., Tsuchiya, M., Yoshimura, Y., Koishihara, Y. and
           Kosaka, M.
TITLE     Reshaped human anti-HM 1.24 antibody
JOURNAL   Patent: US 6699974-A 50 02-MAR-2004;
           Location/Qualifiers
FEATURES   source
           1. .39
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 39;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTC 19
    ||||| ||||| ||||| |||||
Db 19 GGTGTGCCAAGCAGATTC 37
```


REFERENCE	1 (bases 1 to 41)	Score	DB	Length	DB	Length	DB	Length
AUTHORS	Crowe, J. Scott, and Lewis, A. Peter.							
TITLE	Preparation of chimaeric antibodies using the recombinant PCR strategy							
JOURNAL	Patent: US 5858725-A 17 12-JAN-1999;							
FEATURES	Location/Qualifiers							
source	1..41							
ORIGIN	/organism="unknown"							
	/mol_type="unassigned DNA"							
Query Match	56.8%;	Score 14.2;	DB 6;	Length 41;				
Best Local Similarity	84.2%;	Pred. No. 3.1e+04;						
Matches	16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;			
QY	1 GCTGAGCCTAGCAGATTCA 19							
Db	22 GGTGTGCCAAGCAGATTCA 40							
RESULT 10								
AR085792								
LOCUS	AR085792	41 bp	DNA	linear	PAT 07-SEP-2000			
DEFINITION	Sequence 22 from patent US 5985279.							
ACCESSION	AR085792							
VERSION	AR085792.1	GI:10012558						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 41)							
AUTHORS	Waldmann, H., Sims, M. and Crowe, S.							
TITLE	Humanized antibody against CD18							
JOURNAL	Patent: US 5985279-A 22 16-NOV-1999;							
FEATURES	Location/Qualifiers							
source	1..41							
	/organism="unknown"							
	/mol_type="unassigned DNA"							
Query Match	56.8%;	Score 14.2;	DB 6;	Length 41;				
Best Local Similarity	84.2%;	Pred. No. 3.1e+04;						
Matches	16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;			
QY	1 GCTGAGCCTAGCAGATTCA 19							
Db	22 GGTGTGCCAAGCAGATTCA 40							
RESULT 11								
AR474145								
LOCUS	AR474145	41 bp	mRNA	linear	PAT 20-FEB-2004			
DEFINITION	Sequence 22 from patent US 6689869.							
ACCESSION	AR474145							
VERSION	AR474145.1	GI:42712951						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 41)							
AUTHORS	Waldmann, H., Sims, M. J. and Crowe, J. S.							
TITLE	Labeled humanized anti-CD18 antibodies and fragments and kits comprising same							
JOURNAL	Patent: US 6689869-A 22 10-FEB-2004;							
FEATURES	Location/Qualifiers							
source	1..41							
	/organism="unknown"							
	/mol_type="mRNA"							
Query Match	56.8%;	Score 14.2;	DB 6;	Length 41;				
Best Local Similarity	84.2%;	Pred. No. 3.1e+04;						
Matches	16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;			

```

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      22 GGTGTGCCAAGCAGATTCA 40

RESULT 12
LOCUS   I03017               48 bp ss-DNA          linear    PAT 21-MAY-1993
DEFINITION   Sequence 7 from Patent US 4618578.
ACCESSION   I03017
VERSION     I03017.1 GI:268476
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 48)
AUTHORS    Burke,R.L., Urdea,M.S. and Valenzuela,P.D.T.
TITLE      Expression of glycoprotein D of herpes simplex virus
JOURNAL    Patent: US 4618578-A 7 21-OCT-1986;
           Chiron Corporation; Emeryville, CA
FEATURES
   source   1..48
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 48;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      13 GCTGACCCAAACAGATTCA 31

RESULT 13
LOCUS   A08605               49 bp      DNA          linear    PAT 10-SEP-1993
DEFINITION   Oligonucleotide KK2.
ACCESSION   A08605
VERSION     A08605.1 GI:411672
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 49)
AUTHORS
JOURNAL    Patent: WO 8907452-A 7 24-AUG-1989;
           Location/Qualifiers
           1..49
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 49;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      12 GGTGTGCCAAGCAGATTCA 30

RESULT 14
LOCUS   AR337938             49 bp      DNA          linear    PAT 17-AUG-2003
DEFINITION   Sequence 41 from patent US 6569430.
ACCESSION   AR337938
VERSION     AR337938.1 GI:33724583
KEYWORDS
SOURCE      Unknown.

```

```

ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 49)
AUTHORS    Waldmann,H., Clark,M.R., Winter,G.P. and Riechmann,L.
TITLE      Antibodies to the antigen Campath-1
JOURNAL    Patent: US 6569430-A 41 27-MAY-2003;
           Location/Qualifiers
           1..49
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 49;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      12 GGTGTGCCAAGCAGATTCA 30

RESULT 15
LOCUS   CQ009070/c           50 bp      DNA          linear    PAT 16-JAN-2004
DEFINITION   Sequence 7710 from Patent WO0147944.
ACCESSION   CQ009070
VERSION     CQ009070.1 GI:41015796
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL    Patent: WO 0147944-A 7710 05-JUL-2001;
           Curagen Corporation (US)
           Location/Qualifiers
           1..50
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           misc_feature 25..26
           /note="Nucleotide deleted between bases 25 and 26"
           Accession number cg43950029"

ORIGIN
Query Match      56.8%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
Db      25 GCAGAGCCTAGCAGACACA 7

RESULT 16
LOCUS   CQ003048/c           50 bp      DNA          linear    PAT 16-JAN-2004
DEFINITION   Sequence 1688 from Patent WO0147944.
ACCESSION   CQ003048
VERSION     CQ003048.1 GI:41009680
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL    Patent: WO 0147944-A 1688 05-JUL-2001;

```

```

FEATURES
  source
    Curagen Corporation (US)
    Location/Qualifiers
      1..50
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      25..26
        /note="Nucleotide deleted between bases 25 and 26"
      Accession number CG44019290"

misc_feature
  1 GCTGAGCCTAGCAGATTCATGG 22
  26 GCTGGGCTAGCAGCGACATGG 5

ORIGIN
  Query Match 56.0%; Score 14; DB 6; Length 50;
  Best Local Similarity 77.3%; Pred. No. 4e+04;
  Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGG 22
  ||||| ||||| ||||| |||||
Db 26 GCTGGGCTAGCAGCGACATGG 5

RESULT 17
BD134567
LOCUS BD134567 21 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for assaying an enzyme participating in conjugation with
sulfuric acid in human beings, and probe and kit therefor.
ACCESSION BD134567
VERSION BD134567.1 GI:23229512
KEYWORDS JP 2002085067-A/17.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
TITLE Method for assaying an enzyme participating in conjugation with
sulfuric acid in human beings, and probe and kit therefor
JOURNAL Patent: JP 2002085067-A 17 26-MAR-2002;
OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT OS Human CHST4 gene
PN JP 2002085067-A/17
PD 26-MAR-2002
PF 07-SEP-2000 JP 2000272229
PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA
PC C12N15/09,C12Q1/25,C12Q1/68,G01N21/78,G01N33/53,PC
G01N33/566,
PC C12N15/00
CC Method for assaying an enzyme participating in conjugation CC
with sulfuric
CC acid in human beings, and probe and kit therefor FH Key
Location/Qualifiers
FT source 1..21
FT Location/Qualifiers
  /organism="Human CHST4 gene".

FEATURES
  source
    Location/Qualifiers
      1..21
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

ORIGIN
  Query Match 55.2%; Score 13.8; DB 6; Length 21;
  Best Local Similarity 88.2%; Pred. No. 4.7e+04;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATG 21
  ||||| ||||| ||||| |||||
Db 5 AGCCAGCAAAATTCATG 21

RESULT 18
AX787200/c
LOCUS AX787200 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 7 from Patent WO03031469.
ACCESSION AX787200
VERSION AX787200.1 GI:32954380
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Dna-expression construct for treatment of infections with

```

```

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
TITLE Lopez,S.M. and Jimenez,M.T.
JOURNAL Means for improving immune response
Patent: WO 03031469-A 7 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
FEATURES
  source
    Location/Qualifiers
      1..33
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="1. PCR: Primer left"

ORIGIN
  Query Match 55.2%; Score 13.8; DB 6; Length 33;
  Best Local Similarity 72.0%; Pred. No. 4.9e+04;
  Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
  ||||| ||||| ||||| |||||
Db 32 GGTGACCCCTCGATGTTTCATGGTAC 8

RESULT 19
AX787202/c
LOCUS AX787202 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 9 from Patent WO03031469.
ACCESSION AX787202
VERSION AX787202.1 GI:32954382
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
TITLE Lopez,S.M. and Jimenez,M.T.
JOURNAL Means for improving immune response
Patent: WO 03031469-A 9 17-APR-2003;
Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ; Lopez,
Sonia Moreno (ES) ; Jimenez, Marcos Timon (ES)
FEATURES
  source
    Location/Qualifiers
      1..33
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="2. PCR: Primer left"

ORIGIN
  Query Match 55.2%; Score 13.8; DB 6; Length 33;
  Best Local Similarity 72.0%; Pred. No. 4.9e+04;
  Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
  ||||| ||||| ||||| |||||
Db 32 GGTGACCCCTCGATGTTTCATGGTAC 8

RESULT 20
AX787209/c
LOCUS AX787209 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 6 from Patent WO03031470.
ACCESSION AX787209
VERSION AX787209.1 GI:32954387
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1
TITLE Fuertes,L.L. and Jimenez,M.T.
Dna-expression construct for treatment of infections with

```

—

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGG 22
Db 29 GACTAGCAGATTCACGG 45

RESULT 25
AX294559/c
LOCUS AX294559 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 6321 from Patent WO0179548.
ACCESSION AX294559
VERSION AX294559.1 GI:17056242
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 6321 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 20 GTCCCGCAGATTCAGGCAC 1

RESULT 26
AR148747/c
LOCUS AR148747 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 104 from patent US 6225451.
ACCESSION AR148747
VERSION AR148747.1 GI:15112837
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Ballinger,D.G., Ding,W., Wagner,S. and Hess,M.A.
TITLE Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL CHD1
Patent: US 6225451-A 104 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAAGAGTGATGGCAC 2

RESULT 27
AX289926/c
LOCUS AX289926 24 bp DNA linear PAT 21-NOV-2001

DEFINITION Sequence 1688 from Patent WO0179548.
ACCESSION AX289926
VERSION AX289926.1 GI:17051609
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 1688 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 24 GTCCCGCAGATTCAGGCAC 5

RESULT 28
CQ620789/c
LOCUS CQ620789 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5529 from Patent WO0192524.
ACCESSION CQ620789
VERSION CQ620789.1 GI:41671007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5529 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 25 GCCCAGCATCTCCATGGCAC 6

RESULT 29
CQ620790/c
LOCUS CQ620790 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5530 from Patent WO0192524.
ACCESSION CQ620790
VERSION CQ620790.1 GI:41671008
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5530 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 24 GCCCAGCATCTCCATGGCAC 5
RESULT 30
CO620791/c
LOCUS CO620791 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5531 from Patent WO0192524.
ACCESSION CO620791
VERSION CO620791.1 GI:41671009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5531 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 23 GCCCAGCATCTCCATGGCAC 4
RESULT 31
CO620792/c
LOCUS CO620792 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5532 from Patent WO0192524.
ACCESSION CO620792
VERSION CO620792.1 GI:41671010
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5532 06-DEC-2001;
Acemica, Inc. (US)

FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 22 GCCCAGCATCTCCATGGCAC 3
RESULT 32
CO620793/c
LOCUS CO620793 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5533 from Patent WO0192524.
ACCESSION CO620793
VERSION CO620793.1 GI:41671011
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5533 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCCCAGCATCTCCATGGCAC 2
RESULT 33
CO620794/c
LOCUS CO620794 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 5534 from Patent WO0192524.
ACCESSION CO620794
VERSION CO620794.1 GI:41671012
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 5534 06-DEC-2001;
Acemica, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

```
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      20 GCCCAGCATCTCCATGGCAC 1

RESULT 34
AR461852/c
LOCUS      AR461852      25 bp      DNA
DEFINITION Sequence 5529 from patent US 6686188.
ACCESSION AR461852
VERSION    AR461852.1 GI:42696909
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL    Patent: US 6686188-A 5529 03-FEB-2004;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      23 GCCCAGCATCTCCATGGCAC 4

RESULT 37
AR461855/c
LOCUS      AR461855      25 bp      DNA
DEFINITION Sequence 5532 from patent US 6686188.
ACCESSION AR461855
VERSION    AR461855.1 GI:42696912
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL    Patent: US 6686188-A 5532 03-FEB-2004;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      22 GCCCAGCATCTCCATGGCAC 3

RESULT 38
AR461856/c
LOCUS      AR461856      25 bp      DNA
DEFINITION Sequence 5533 from patent US 6686188.
ACCESSION AR461856
VERSION    AR461856.1 GI:42696913
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
```

```
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      20 GCCCAGCATCTCCATGGCAC 1

RESULT 34
AR461852/c
LOCUS      AR461852      25 bp      DNA
DEFINITION Sequence 5529 from patent US 6686188.
ACCESSION AR461852
VERSION    AR461852.1 GI:42696909
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL    Patent: US 6686188-A 5529 03-FEB-2004;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      25 GCCCAGCATCTCCATGGCAC 6

RESULT 35
AR461853/c
LOCUS      AR461853      25 bp      DNA
DEFINITION Sequence 5530 from patent US 6686188.
ACCESSION AR461853
VERSION    AR461853.1 GI:42696910
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 25)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE      Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
JOURNAL    Patent: US 6686188-A 5530 03-FEB-2004;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      54.4%; Score 13.6; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
Db      24 GCCCAGCATCTCCATGGCAC 5

RESULT 36
AR461854/c
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 05:29:23 ; Search time 172,148 Seconds
(without alignments)
859,686 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	2	AAQ911130
2	25	100.0	25	2	ACA63120
3	25	100.0	25	13	ADRO5306
4	15	60.0	50	6	AB201194
C 5	14.8	59.2	37	12	ADOS9185
C 6	14.6	58.4	25	12	ADK70978
7	14.6	58.4	29	10	ABX95944
8	14.6	58.4	29	12	ADQ67857
9	14.4	57.6	29	6	ABQ76852
C 10	14.4	57.6	33	6	AD311605
C 11	14.2	56.8	22	6	AB559198
12	14.2	56.8	25	2	AAV65080
C 13	14.2	56.8	28	10	ADB67035
C 14	14.2	56.8	29	4	AAH47313
15	14.2	56.8	38	2	AAQ94493
16	14.2	56.8	38	2	AAI38608
17	14.2	56.8	39	2	AAQ12689
18	14.2	56.8	39	2	AAV39382
19	14.2	56.8	39	2	AAx59432
20	14.2	56.8	41	2	AAQ24659

21	14.2	56.8	41	2	AAQ35184
C 22	14.2	56.8	50	4	AAI34502
23	14	56.0	41	12	ADH05434
24	14	56.0	41	12	ADH91221
25	14	56.0	47	2	AAx52556
26	14	56.0	47	3	AAZ68752
C 27	14	56.0	50	4	AAI28480
28	14	56.0	50	6	ABZ05333
29	13.8	55.2	21	6	ABK70835
30	13.8	55.2	25	9	ACK02180
C 31	13.8	55.2	33	10	ADC21315
C 32	13.8	55.2	33	10	ADC21313
C 33	13.8	55.2	33	10	ADC21307
C 34	13.8	55.2	33	10	ADC21305
35	13.8	55.2	49	13	ADQ31581
36	13.8	55.2	50	4	AAI28734
37	13.8	55.2	50	13	ADQ31582
C 38	13.6	54.4	20	6	ABI94601
C 39	13.6	54.4	21	2	AAZ26929
C 40	13.6	54.4	21	4	AAF95928
C 41	13.6	54.4	24	6	ABI85772
42	13.6	54.4	24	6	ABI85773
C 43	13.6	54.4	25	6	ABN05537
C 44	13.6	54.4	25	6	ABN05540
C 45	13.6	54.4	25	6	ABN05539

ALIGNMENTS

RESULT 1

AAQ911130

ID AAQ911130 standard; cDNA; 25 BP.

XX AC AAQ911130;

XX DT 19-FEB-1996 (first entry)

XX DE Beta-cardiac myosin heavy chain PCR primer B9.1R.

XX KW Myosin; heavy chain; non-invasive; hypertrophic cardiomyopathy;

XX OS Synthetic.

XX PF US429923-A.

XX PD 04-JUL-1995.

XX PF 11-DEC-1992; 92US-00989160.

XX PR 11-DEC-1992; 92US-00989160.

XX (HARD) HARVARD COLLEGE.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX (GEOH-) GEN HOSPITAL SHENYANG MILITARY AREA.

XX Seidman J, Seidman C, Watkins H, Rosenzweig A;

XX WPI; 1995-245715/32.

XX Non-invasive method for diagnosis of hypertrophic cardio-myopathy -

XX useful for testing asymptomatic individual(s).

XX Example 1; Col 10; 22pp; English.

AAQ911121-091130 are nested PCR primers used for the amplification and identification of beta-cardiac myosin heavy-chain RNA. They are used in a new non-invasive method for diagnosing hypertrophic cardiomyopathy (HC), the method involves detecting the presence or absence of specific HC-associated mutations in the beta-cardiac myosin heavy-chain obtained from a blood sample. The method may be used to diagnose familial or sporadic HC and the non-invasive method is particularly important when testing

CC asymptomatic individuals suspected of having the disease. The method has
CC a broad applicability and may be used to detect mutations responsible for
CC other genetically inheritable diseases e.g. cystic fibrosis, Gaucher's
CC disease, haemophilia A and B, Duchenne's muscular dystrophy, sickle cell
CC anaemia, Tay-Sachs disease and phenylketonuria

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 2

ACA63120
ID ACA63120 standard; DNA; 25 BP.

AC ACA63120;

DT 28-AUG-2003 (first entry)

DE Human beta cardiac myosin heavy chain PCR primer B9.1R.

XX Human; ss; PCR; primer; beta cardiac myosin heavy chain; FHC;
XX familial hypertrophic cardiomyopathy; SHC; Gaucher's disease;
KW sporadic hypertrophic cardiomyopathy; life expectancy; haemophilia;
KW Duchenne's muscular dystrophy; sickle cell anaemia; Tay-Sachs disease;
KW phenylketonuria; cystic fibrosis.

XX Homo sapiens.

OS US2003054343-A1.

PN 20-MAR-2003.

PD 06-JUN-1995; 95US-00469172.

PF 11-DEC-1992; 92US-00989160.

PR (SEID/) SEIDMAN C.

PA (SEID/) SEIDMAN J.

PA (WATK/) WATKINS H.

PA (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2003-512374/48.

XX Detecting a presence or absence of a mutation associated with
XX hypertrophic cardiomyopathy, useful for diagnosing cystic fibrosis or
XX hemophilia, by detecting a mutation in an amplified product of a beta
XX cardiac myosin heavy-chain DNA.

PS Example 1; Page 5; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy (sporadic or familial, SHC
XX and FHC) comprises detecting a mutation associated with hypertrophic
XX cardiomyopathy in an amplified product of a beta cardiac myosin heavy
XX chain DNA. The mutations associated with SHC/FHC are detected in the
XX myosin gene isolated from blood, by detecting mis-matched areas in RNA-
XX DNA hybrid double strands (RNA from the normal gene, DNA from the suspect
XX sample). FHC associated point mutation can be classified and used to
XX determine life expectancy in affected individuals e.g. using a Kaplan-
XX Meier curve for the classified type of FHC causing point mutation. Also
XX included are an RNA probe comprising ribonucleotides arranged in a
XX sequence which is complementary to at least a portion of beta-cardiac
XX myosin heavy-chain DNA and a set of DNA oligonucleotide primers for
XX amplifying beta-cardiac myosin heavy-chain DNA comprising at least two

CC oligonucleotides capable of amplifying beta-cardiac myosin heavy-chain
CC DNA. The method is useful for detecting the presence or absence of a
CC mutation associated with hypertrophic cardiomyopathy. This method is
CC especially useful for diagnosing SHC and FHC, as well as for determining
CC the estimated life expectancy of a person with familial hypertrophic
CC cardiomyopathy. In particular, the method is useful for determining an
CC individual's genetic information, and diagnosing e.g. Gaucher's disease,
CC haemophilia, Duchenne's muscular dystrophy, sickle cell anaemia, Tay-
CC Sachs disease, phenylketonuria or cystic fibrosis. The present sequence
CC is a PCR primer used to amplify a region of the beta cardiac myosin heavy
CC chain gene containing an FHC-associated mutation

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 3

ADR05306
ID ADR05306 standard; DNA; 25 BP.

XX ADR05306;

XX 21-OCT-2004 (first entry)

DT Human beta cardiac myosin heavy chain mutation detection primer B9.1R.

XX Human; beta cardiac myosin; heavy chain; PCR; primer; ss; FHC; SHC;

XX familial hypertrophic cardiomyopathy;

XX sporadic hypertrophic cardiomyopathy.

XX Homo sapiens.

XX US2004152121-A1.

XX 05-AUG-2004.

XX 27-FEB-2004; 2004US-00788779.

XX 11-DEC-1992; 92US-00989160.

XX 06-JUN-1995; 95US-00469172.

XX (SEID/) SEIDMAN C.

XX (SEID/) SEIDMAN J.

XX (WATK/) WATKINS H.

XX (ROSE/) ROSENZWEIG A.

XX Seidman C, Seidman J, Watkins H, Rosenzweig A;

XX WPI; 2004-592586/57.

XX Detecting mutations associated with hypertrophic cardiomyopathy to

XX diagnose hypertrophic cardiomyopathy, comprises amplifying beta-cardiac

XX myosin heavy-chain DNA and detecting the mutation in the amplified

XX product.

XX Claim 18; SEQ ID NO 10; 22pp; English.

XX The invention relates to detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy (familial or sporadic, FHC,
XX SHC) for facilitating the diagnosis of hypertrophic cardiomyopathy,
XX comprising amplifying beta-cardiac myosin heavy-chain DNA forming an
XX amplified product, and detecting the presence or absence of a mutation
XX associated with hypertrophic cardiomyopathy in the amplified product,
XX thus, facilitating the diagnosis of hypertrophic cardiomyopathy. Also
XX included are a set of DNA oligonucleotide primers for amplifying beta-
XX cardiac myosin heavy-chain DNA comprising at least two oligonucleotides

CC which amplify beta-cardiac myosin heavy-chain DNA (the set of
CC oligonucleotide primers being useful for facilitating the diagnosis of
CC hypertrophic cardiomyopathy by being capable of detecting a hypertrophic
CC cardiomyopathy-associated mutation) and a kit for facilitating the
CC diagnosis of hypertrophic cardiomyopathy (comprising a first container
CC holding an RNA probe completely hybridisable to the beta-cardiac myosin
CC heavy chain DNA, where the RNA probe is capable of detecting a
CC hypertrophic cardiomyopathy-associated mutation, a second container
CC holding primers for amplifying beta-cardiac myosin heavy-chain DNA and
CC instructions for using the components of the kit to detect the presence
CC or absence of a hypertrophic cardiomyopathy-associated mutation in
CC amplified beta-cardiac myosin heavy-chain DNA). The method is used for
CC detecting the presence or absence of a mutation associated with
CC hypertrophic cardiomyopathy for facilitating the diagnosis of
CC hypertrophic cardiomyopathy. Presently, the diagnosis of individuals
CC having hypertrophic cardiomyopathy relies on the presence of typical
CC clinical symptoms and the demonstration of unexplained ventricular
CC hypertrophy. The present invention is non-invasive and based, at least in
CC part, on the discovery that hypertrophic cardiomyopathy is caused by
CC point mutations in the beta cardiac myosin heavy-chain gene. Prior art
CC reveals that there are no extensive studies involving a large number of
CC families which established that this particular disease or disorder was
CC caused by point mutations in the beta cardiac myosin heavy-chain gene.
CC The present sequence is a PCR primer used to amplify a region of the beta
CC cardiac myosin heavy chain having a disease-related point mutation.

XX Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCTTAGCAGATTCATGGCAC 25
|||||
Db 1 GCTGAGCTTAGCAGATTCATGGCAC 25

RESULT 4

ABZ01194
ID ABZ01194 standard; DNA; 50 BP.

XX AC ABZ01194;

XX 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 1185.

XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

XX 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX Ly N, Woodward R, Quettermous T, Johnson F;

XX WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 362; Opp; English.

XX The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX Sequence 50 BP; 21 A; 9 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 15; DB 6; Length 50;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGAGCTTAGCAGATTCATGGCAC 25
|||||
Db 14 TGAGCTTAGCAGATTCATGGCAC 36

RESULT 5

ADO59185/c

ID ADO59185 standard; DNA; 37 BP.

XX AC ADO59185;

XX 26-AUG-2004 (first entry)

XX PCR primer used to amplify human SLC-1 DNA SeqID 7.

XX human; SLC-1; primer; ss; melanin-concentrating hormone receptor;
KW antagonist; heterocyclic ring; anorectic; obesity; PCR.

XX Homo sapiens.

XX WO2004046110-A1.

XX 03-JUN-2004.

XX 14-NOV-2003; 2003WO-JP014534.

XX 15-NOV-2002; 2002JP-00332950.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Kaku H, Kondoh Y, Hayashibe S, Kamikubo T, Iwasaki F;

XX Matsumoto S, Kimura Y, Kurama T;

XX WPI; 2004-440938/41.

XX Melanin concentrating hormone receptor antagonist useful in
PT pharmaceuticals for preventing obesity, contains heterocyclic ring
PT derivative or its salt as active ingredient.

XX Example 359; SEQ ID NO 7; 155pp; Japanese.

XX This invention relates to a novel melanin-concentrating hormone receptor
CC protein antagonist, a heterocyclic ring derivative or a salt thereof.
CC Specifically, it refers to the development of a drug that contains this
CC nitrogen-containing heterocyclic ring as the main skeleton of the
CC antagonist compound, that works as the active ingredient. The present
CC invention describes this antagonist as a melanin-concentrating hormone
CC receptor inhibitor that exhibits anorectic activities and as such can be
CC used to treat and/or prevent obesity. This oligonucleotide sequence is a
CC PCR primer used in an exemplification of the invention.

```

SQ Sequence 37 BP; 7 A; 10 C; 11 G; 8 T; 0 U; 1 Other;

Query Match      59.2%; Score 14.8; DB 12; Length 37;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
      ||||| ||||| ||||| |||||
Db      32 GAGGCTTGCARATCCATGGC 13

RESULT 6
ID ADK70978/c
XX ADK70978 standard; DNA; 25 BP.
AC ADK70978;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Corn root preferential GL5 promoter amplifying primer GWK30.
XX
XX GL4; GL5; corn; root preferential promoter; pest resistance;
KW pathogen resistance; plant; ISPA1; ISPA2; PCR; primer; ss.
XX
OS Zea mays.
OS Synthetic.
XX
XX WO2004013169-A1.
XX
XX
XX 12-FEB-2004.
XX
XX
XX 28-JUL-2003; 2003WO-EP008367.
XX
XX 31-JUL-2002; 2002US-0399383P.
XX
XX (FARB ) BAYER BIOSCIENCE NV.
XX
XX Vanderkimpfen G, Van Eldik G, Meulewaeter F;
XX
XX WPI; 2004-157099/15.
XX
XX New corn root preferential promoters useful for the preferential and/or
XX selective expression of a biologically active RNA in roots of a plant,
XX preferably a corn plant.
XX
XX Claim 1; SEQ ID NO 10; 76pp; English.
XX
XX The invention relates to a corn root preferential promoter fragment. The
XX corn root preferential promoter is useful for the preferential expression
XX of a biologically active RNA in roots of a plant, wherein the plant is a
XX corn plant. The biologically active RNA encodes a protein of interest,
XX which when expressed in the cells of a plant confers pest or pathogen
XX resistance to the plant, wherein the protein is ISPA1 or ISPA2 from
XX Brevibacillus laterosporus. An isolated DNA molecule encoding a GL4 or
XX GL5 protein is useful for the isolation of a corn root preferential
XX promoter or promoter region. SequencesADK70978-ADK70978 represent PCR
XX primers for isolating corn root preferential GL5 promoter fragment.
XX
SQ Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match      58.4%; Score 14.6; DB 12; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGCA 24
      ||||| ||||| ||||| |||||
Db      23 GAGCATAGTCGATTCATGGCA 3

RESULT 7
ABX95944
ID ABX95944 standard; cDNA; 29 BP.
XX
SQ Sequence 37 BP; 7 A; 10 C; 11 G; 8 T; 0 U; 1 Other;

Query Match      59.2%; Score 14.8; DB 12; Length 37;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
      ||||| ||||| ||||| |||||
Db      32 GAGGCTTGCARATCCATGGC 13

RESULT 6
ID ADK70978/c
XX ADK70978 standard; DNA; 25 BP.
AC ADK70978;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Corn root preferential GL5 promoter amplifying primer GWK30.
XX
XX GL4; GL5; corn; root preferential promoter; pest resistance;
KW pathogen resistance; plant; ISPA1; ISPA2; PCR; primer; ss.
XX
OS Zea mays.
OS Synthetic.
XX
XX WO2004013169-A1.
XX
XX
XX 12-FEB-2004.
XX
XX
XX 28-JUL-2003; 2003WO-EP008367.
XX
XX 31-JUL-2002; 2002US-0399383P.
XX
XX (FARB ) BAYER BIOSCIENCE NV.
XX
XX Vanderkimpfen G, Van Eldik G, Meulewaeter F;
XX
XX WPI; 2004-157099/15.
XX
XX New corn root preferential promoters useful for the preferential and/or
XX selective expression of a biologically active RNA in roots of a plant,
XX preferably a corn plant.
XX
XX Claim 1; SEQ ID NO 10; 76pp; English.
XX
XX The invention relates to a corn root preferential promoter fragment. The
XX corn root preferential promoter is useful for the preferential expression
XX of a biologically active RNA in roots of a plant, wherein the plant is a
XX corn plant. The biologically active RNA encodes a protein of interest,
XX which when expressed in the cells of a plant confers pest or pathogen
XX resistance to the plant, wherein the protein is ISPA1 or ISPA2 from
XX Brevibacillus laterosporus. An isolated DNA molecule encoding a GL4 or
XX GL5 protein is useful for the isolation of a corn root preferential
XX promoter or promoter region. SequencesADK70978-ADK70978 represent PCR
XX primers for isolating corn root preferential GL5 promoter fragment.
XX
SQ Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match      58.4%; Score 14.6; DB 12; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGCA 24
      ||||| ||||| ||||| |||||
Db      23 GAGCATAGTCGATTCATGGCA 3

RESULT 7
ABX95944
ID ABX95944 standard; cDNA; 29 BP.
XX
SQ Sequence 37 BP; 7 A; 10 C; 11 G; 8 T; 0 U; 1 Other;

Query Match      59.2%; Score 14.8; DB 12; Length 37;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
      ||||| ||||| ||||| |||||
Db      32 GAGGCTTGCARATCCATGGC 13

RESULT 6
ID ADK70978/c
XX ADK70978 standard; DNA; 25 BP.
AC ADK70978;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Corn root preferential GL5 promoter amplifying primer GWK30.
XX
XX GL4; GL5; corn; root preferential promoter; pest resistance;
KW pathogen resistance; plant; ISPA1; ISPA2; PCR; primer; ss.
XX
OS Zea mays.
OS Synthetic.
XX
XX WO2004013169-A1.
XX
XX
XX 12-FEB-2004.
XX
XX
XX 28-JUL-2003; 2003WO-EP008367.
XX
XX 31-JUL-2002; 2002US-0399383P.
XX
XX (FARB ) BAYER BIOSCIENCE NV.
XX
XX Vanderkimpfen G, Van Eldik G, Meulewaeter F;
XX
XX WPI; 2004-157099/15.
XX
XX New corn root preferential promoters useful for the preferential and/or
XX selective expression of a biologically active RNA in roots of a plant,
XX preferably a corn plant.
XX
XX Claim 1; SEQ ID NO 10; 76pp; English.
XX
XX The invention relates to a corn root preferential promoter fragment. The
XX corn root preferential promoter is useful for the preferential expression
XX of a biologically active RNA in roots of a plant, wherein the plant is a
XX corn plant. The biologically active RNA encodes a protein of interest,
XX which when expressed in the cells of a plant confers pest or pathogen
XX resistance to the plant, wherein the protein is ISPA1 or ISPA2 from
XX Brevibacillus laterosporus. An isolated DNA molecule encoding a GL4 or
XX GL5 protein is useful for the isolation of a corn root preferential
XX promoter or promoter region. SequencesADK70978-ADK70978 represent PCR
XX primers for isolating corn root preferential GL5 promoter fragment.
XX
SQ Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

Query Match      58.4%; Score 14.6; DB 10; Length 29;
Best Local Similarity 81.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 AGCCTAGCAGATTCATGGCAC 25
      ||||| ||||| ||||| |||||
Db      8 AGCAGAGCAGAGTGTATGGCAC 28

RESULT 8
ADQ67857
ID ADQ67857 standard; DNA; 29 BP.
XX
XX ADQ67857;
XX
DT 07-OCT-2004 (first entry)
XX

```

DE Human CRAM RT-PCR primer for exon 3.
 XX Human; ss; PCR; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
 XX chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
 KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
 KW development; inflammatory condition; asthma; RT-PCR;
 KW reverse transcriptase PCR; primer; CRAM.
 XX Mus sp.
 OS
 XX
 PN US2004137578-A1.
 XX
 XX 15-JUL-2004.
 PD
 XX
 XX 09-JAN-2004; 2004US-00754071.
 PF
 XX 05-JUL-1996; 96US-0021664P.
 PR 11-OCT-1996; 96US-0028329P.
 PR 04-JUN-1997; 97US-0048593P.
 PR 03-JUL-1997; 97US-0088797P.
 PR 03-JAN-2002; 2002US-00039659.
 XX
 XX (WANG/) WANG W.
 PA (GISH/) GISH K C.
 PA (SCHA/) SCHALL T J.
 PA (VICA/) VICARI A.
 PA (ZLOT/) ZLOTNIK A.
 XX
 PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
 XX WPI; 2004-533376/51.
 DR
 XX
 XX New substantially pure or isolated Thymus Expressed Chemokine (TECK),
 PT useful for treating conditions associated with abnormal physiology or
 PT development, including inflammatory conditions, e.g. asthma.
 XX
 XX Example 6; SEQ ID NO 24; 54pp; English.
 PS
 XX The invention relates to a substantially pure or isolated polypeptide
 CC comprises the mature protein of human TECK (thymus expressed chemokine)
 CC whose full length sequence appears as ADQ67837. Also included are an
 CC isolated or recombinant nucleic acid encoding mature TECK, an expression
 CC vector comprising the nucleic acid, a host cell comprising the expression
 CC vector and a method for producing the polypeptide. Also disclosed are the
 CC mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta
 CC (and their encoding cDNAs), and the cDNAs and encoded proteins
 CC corresponding to human chemokine receptors DCCR (dendritic cell receptor
 CC for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for
 CC chemokine). The polypeptide is useful for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions, e.g. asthma. An experiment was performed analysing the
 CC expression of human CRAM (not defined, unclear what its relation to TECK
 CC is). The present sequence is a reverse transcriptase (RT)-PCR primer used
 CC in the above analysis.
 XX
 XX Sequence 29 BP; 11 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 58.4%; Score 14.6; DB 12; Length 29;
 Best Local Similarity 81.0%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 AGCCTAGCAGATTCATGGCAC 25
 ||| ||||| ||||| |||||
 DB 8 AGCAGAGCAGAGTGATGGCAC 28
 ||| ||||| ||||| |||||
 RESULT 9
 ABQ76852
 ID ABQ76852 standard; DNA; 29 BP.
 XX
 XX AC ABQ76852;
 XX
 DT 25-MAR-2003 (first entry)

XX DC3 promoter associated oligonucleotide DC3a #4.
 XX Promoter; expression cassette; structural gene; plant; transgenic;
 KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 KW heart disease; seed-specific; PCR; primer; ss.
 XX
 XX Synthetic.
 OS
 XX
 PN DE10102338-A1.
 XX
 XX 25-JUL-2002.
 PD
 XX
 XX 19-JAN-2001; 2001DE-01002338.
 PF
 XX 19-JAN-2001; 2001DE-01002338.
 PR
 XX (BADI) BASF PLANT SCI GMBH.
 PA
 XX Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J;
 PI WPI; 2002-675961/73.
 XX
 DR New expression cassette for plant genes, useful for preparing transgenic
 XX plants that have increased production of polyunsaturated fatty acids.
 PT
 XX Example 13; Page 40; 188pp; German.
 PS
 XX This invention describes novel expression cassette (EC) containing at
 CC least one each of plant promoter (P) and structural gene (SG) expressed
 CC in plants, flanked by specific restriction enzyme (RE) recognition sites.
 CC The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker
 CC (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
 CC sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
 CC sequences and n = 1-3. The invention discloses a vector containing this
 CC EC, an organism containing the EC or the vector and a transgenic plant
 CC containing a (non-)functional nucleic acid in the vector. Transgenic
 CC plants e.g. linseed can be prepared with improved production of fatty acid
 CC esters with an increased content of polyunsaturated fatty acids (PUFA),
 CC useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
 CC PUFA are known to reduce levels of cholesterol in the blood and to
 CC protect against heart disease. The expression cassettes of the invention
 CC provide increased and more efficient production of fine chemicals
 CC (especially PUFA), including seed-specific production. This sequence
 CC represents a PCR primer used to illustrate the method of the invention
 XX
 XX Sequence 29 BP; 4 A; 7 C; 8 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 57.6%; Score 14.4; DB 6; Length 29;
 Best Local Similarity 75.0%; Pred. No. 4.2e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GCTGAGCCTAGCAGATTCATGGCA 24
 ||| ||||| ||||| |||||
 DB 2 GCGGATCCTAGCTTTTCTTGGCA 25
 ||| ||||| ||||| |||||
 RESULT 10
 AAD31605/c
 ID AAD31605 standard; DNA; 33 BP.
 XX
 XX AC AAD31605;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX Human reaper (hRpr) ORF amplifying primer, Fwd13.
 DE
 XX Human; reaper protein; Rpr; detection; purification; screening; therapy;
 KW tumour; cytostatic; open reading frame; ORF; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX

```

PN WO200212540-A2.
XX
PD 14-FEB-2002.
XX
XX
PF 08-AUG-2001; 2001WO-US024765.
XX
XX
PR 08-AUG-2000; 2000US-0223699P.
XX
XX
PA (UYDU-) UNIV DUKE.
XX
XX
PI Kornbluth SA, Holley C;
XX
XX
PI WPI; 2002-241769/29.
XX
XX
PT New human homologue of Drosophila melanogaster reaper protein (hrpr),
PT useful for generating antibodies and for screening compounds, which can
PT inhibit or enhance hrpr activity.
XX
XX
PS Example 1; Page 24; 45pp; English.
XX
XX
CC The invention relates to human homologue of Drosophila melanogaster
CC Reaper protein (hrpr) and its corresponding nucleic acid. The hrpr
CC polypeptides are useful for generating antibodies, which can be used in
CC detection or purification protocols designed to detect or purify the
CC polypeptide to which the antibody is directed. These sequences are also
CC used for screening compounds, which can enhance or inhibit hrpr and for
CC treating tumours. The hrpr polynucleotides are useful as a probe or
CC primer. The present sequence is a PCR primer used to amplify human hrpr
CC open reading frame (ORF)
XX
XX
SQ Sequence 33 BP; 4 A; 12 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 57.6%; Score 14.4; DB 6; Length 33;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCTAGCAGATTCATGGCA 24
    ||||| ||| |||| |||||
Db 32 GCTGGGCCAGCAGCACCATGGCA 9

RESULT 11
ABS55198/c
ID ABS55198 standard; DNA; 22 BP.
XX
XX
AC ABS55198;
XX
XX
DT 05-NOV-2002 (first entry)
XX
XX
DE Human G-protein coupled receptor, forward primer #116.
XX
XX
KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW primer; PCR; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200259313-A2.
XX
XX
PD 01-AUG-2002.
XX
XX
PF 18-DEC-2001; 2001WO-US049394.
XX
XX
PR 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
XX

```

```

PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone DJ, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX
XX
DR WPI; 2002-599789/64.
XX
XX
PT New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
XX
PS Claim 1; Page 617; 685pp; English.
XX
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albright hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABS58747-ABS59231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX
SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 56.8%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTCATG 21
    ||||| ||||| |||||
Db 21 TGGTCTCTACCAGATTCATG 3

RESULT 12
AAV65080
ID AAV65080 standard; DNA; 25 BP.
XX
XX
AC AAV65080;
XX
XX
DT 05-FEB-1999 (first entry)
XX
XX
DE Human ZPA PCR primer huZPA5 #2.
XX
XX
KW ZPA; human; vector; expression; secretion; fertility control antigen;
KW attenuated Salmonella; Gram-negative; oral vaccine; haemolysin operon;
KW hly specific promoter; hlyR enhancer-like regulator; contraception;
KW PCR primer; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.

```

```

XX DE19720761-A1.
XX 12-NOV-1998.
XX
XX 07-MAY-1997; 97DE-01020761.
XX
XX 07-MAY-1997; 97DE-01020761.
XX (SCHD ) SCHERING AG.
XX
XX Donner P, Goebel W, Demuth A, Gentschev I, Hess J, Kaufmann S;
XX WPI; 1998-596140/51.
XX
XX Oral contraceptive vaccine containing recombinant salmonella -
XX transformed with vector containing gene for fertility control antigen.
XX
XX Disclosure; Page 6; 17pp; German.
XX
XX AAV65071-V65104 are PCR primers used in the construction of a novel
XX vector for expression and secretion of a fertility control antigen in
XX attenuated salmonella or other attenuated Gram-negative vaccine strains
XX to produce an oral vaccine. The vector comprises a gene encoding the
XX fertility control antigen under the control of a complete haemolysin
XX operon, including the hly specific promoter and the hlyR enhancer-like
XX regulator but excluding most of the hlyA gene. The vector is used for
XX immunological contraception by oral administration
XX
XX Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 2; Length 25;
XX Best Local Similarity 84.2%; Pred. No. 5, 1e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 6 GCCTAGCAGATTCATGGCA 24
XX ||||| ||| |||||
XX 1 GCCTAGAGGATGCATGGCA 19
XX
XX RESULT 13
XX ADB67035/c
XX ID ADB67035 standard; DNA; 28 BP.
XX
XX AC ADB67035;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Mouse Galanin-like Peptide, GALP, primer mG-300R, SEQ ID 3.
XX
XX KW Cytostatic; Anorectic; Antidiabetic; Nootropic; Neuroprotective;
XX Gynaecological; mouse; Galanin-like Peptide; GALP; prostate cancer;
XX ovarian cancer; gynaecological disorder; diabetes; dementia;
XX eating disorder; primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO2003070950-A1.
XX
XX PD 28-AUG-2003.
XX
XX PF 20-FEB-2003; 2003WO-JP001856.
XX
XX PR 22-FEB-2002; 2002JP-00047006.
XX
XX PR 24-APR-2002; 2002JP-00123170.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kumano S, Kobayashi H, Ohtaki T;
XX WPI; 2003-671814/63.
XX
XX Novel DNA for constructing knockout animals applicable in clarifying

```

```

PT physiological function of the galactose membrane transporter and in
PT screening preventives or remedies for diseases, e.g. cancer.
XX
XX Example 1; Page 36; 118pp; Japanese.
XX
XX The present invention relates to mouse Galanin-like Peptide (GALP)
XX sequences (ADB67033-ADB67032). The sequences are useful for constructing
XX knockout animals which are useful in clarifying the physiological
XX function of GALP and in screening preventives or remedies for diseases
XX due to hypo- or hypersecretion of LH, e.g. prostate cancer, ovarian
XX cancer, gynaecological disorders, diabetes, dementia and eating
XX disorders, e.g. obesity and other disorders. The present sequence is a
XX primer for mouse GALP, which was used in an example from the invention.
XX
XX Sequence 28 BP; 5 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 10; Length 28;
XX Best Local Similarity 84.2%; Pred. No. 5, 2e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 GCTGAGCCTGACGATTCA 19
XX ||||| ||| ||||| ||
XX Db 22 GCTGAGCCTGGCAGAAACA 4
XX
XX RESULT 14
XX AAH47313/c
XX ID AAH47313 standard; DNA; 29 BP.
XX
XX AC AAH47313;
XX
XX DT 30-NOV-2001 (first entry)
XX
XX DE Mouse MCHIR cDNA amplifying primer MCHIR (Eco RI).
XX
XX KW Melanin concentrating hormone receptor; MCHR; MCH; chimeric; fusion;
XX fluorescent polypeptide; orexigenic; anabolic; food intake; MCHIR;
XX green fluorescent protein; GFP; PCR primer; ss.
XX
XX OS Mus sp.
XX
XX PN WO200168706-A1.
XX
XX PD 20-SEP-2001.
XX
XX PF 14-MAR-2001; 2001WO-US008071.
XX
XX PR 15-MAR-2000; 2000US-0189698P.
XX (MERI ) MERCK & CO INC.
XX
XX PA Marsh DJ;
XX
XX PI WPI; 2001-565791/63.
XX
XX DR Fusion proteins comprising melanin concentrating hormone receptor
XX peptides and fluorescent proteins, useful for identifying appetite
XX stimulants.
XX
XX Example 2; Page 33; 71pp; English.
XX
XX The invention provides melanin concentrating hormone (MCH) receptor
XX (MCHR) chimeric and fusion proteins. The MCHR chimeric proteins comprise
XX MCHR polypeptide regions from different species. The MCHR fusion protein
XX comprise MCHR polypeptide region and a fluorescent polypeptide region
XX joined directly, or via a linker, to the carboxy side of the MCHR
XX polypeptide region. The MCHR fusion proteins can be expressed by standard
XX recombinant methodology. MCH action promotes feeding (orexigenic) and up
XX regulation of MCH activity stimulates food intake. Sequences AAH7313-14
XX represent PCR primers for amplifying mouse MCHIR cDNA, used in the
XX construction of mouse MCHIR-linker-green fluorescent protein (GFP)
XX variant fusion constructs
XX

```

```

SQ Sequence 29 BP; 7 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
  Query Match          56.8%; Score 14.2; DB 4; Length 29;
  Best Local Similarity 84.2%; Pred. No. 5.2e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGG 22
   ||| ||| ||| ||| ||| |||
Db 28 GAGGCTTGCCAGATTCATGG 10

RESULT 15
AAQ94493
ID AAQ94493 standard; DNA; 38 BP.
XX
AC AAQ94493;
XX
DT 16-JAN-1996 (first entry)
XX
DE Human antibody ONS-M21 CDR PCR primer C.
XX
KW Human; ONS-M21 antibody; chimeric protein; CDR; medulloblastoma;
KW brain tumour; treatment; diagnosis; PCR primer C;
KW complementarity determining region; ss.
XX
OS Synthetic.
XX
PN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PF 19-OCT-1994; 94WO-JP001763.
XX
PR 19-NOV-1993; 93JP-00291078.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
XX
WPI; 1995-200347/26.
XX
Reconstituted antibody against human medullo:blastoma cells - contains
high proportion of human antibody origin and has low antigenicity.
XX
Example 5; Page 62; 120pp; Japanese.
XX
AAQ94492-Q94497 are human antibody ONS-M21 CDR PCR primers. The cDNA
encoding the CDRA was used in the construction of an expression vector,
contg. cDNA encoding a human/murine chimeric antibody, reactive with
human medulloblastoma (a brain tumour) cells. The chimeric antibody can
be used in the diagnosis and treatment of this disease
XX
SQ Sequence 38 BP; 8 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
  Query Match          56.8%; Score 14.2; DB 2; Length 38;
  Best Local Similarity 84.2%; Pred. No. 5.5e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
   ||| ||| ||| ||| ||| |||
Db 16 GGTGTGCCAAGCAGATTCA 34

RESULT 16
AAT38608
ID AAT38608 standard; DNA; 38 BP.
XX
AC AAT38608;
XX
DT 09-DEC-1996 (first entry)
XX
DE Chimaeric human/murine MAB ONS-M21 PCR primer D.
XX

```

```

KW Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera;
KW single stranded Fv region; PCR; low human antigenicity; diagnosis;
KW treatment; cerebral tumour; reshaped; primer; polymerase chain reaction;
KW ss.
XX Synthetic.
XX
PN JP08169900-A.
XX
PD 02-JUL-1996.
XX
PF 18-NOV-1994; 94JP-00285057.
XX
PR 19-NOV-1993; 93JP-00291078.
XX
PR 18-OCT-1994; 94JP-00252166.
XX
PA (CHUS ) CHUGAI PHARM CO LTD.
XX
DR WPI; 1996-358509/36.
XX
PT Reshaped anti-human myeloblastoma cell human antibody - has low human
PT antigenicity, and is therefore useful for diagnosis and treatment of
PT cerebral tumours, e.g. myeloblastoma.
XX
PS Example 5; Page 23; 45pp; Japanese.
XX
CC The present sequence is a primer for the chimaeric human/murine
CC monoclonal antibody (MAB) ONS-M21. The MAB was prepd. by combining light
CC and heavy variable region DNA, from a murine anti-human myeloblastoma
CC cell MAB, with human light and heavy constant region sequences,
CC respectively to produce chimaeric human/murine light and heavy chain DNA
CC mols. A recombinant vector for the expression of the heavy and light
CC chain DNA mols. was prepd., and used to transform a host cell. The host
CC cell was then cultured, and the expression prods. of the heavy and light
CC chain DNA mols. sepd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent for the
CC diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
XX
SQ Sequence 38 BP; 8 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
  Query Match          56.8%; Score 14.2; DB 2; Length 38;
  Best Local Similarity 84.2%; Pred. No. 5.5e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
   ||| ||| ||| ||| ||| |||
Db 16 GGTGTGCCAAGCAGATTCA 34

RESULT 17
AAQ12689
ID AAQ12689 standard; DNA; 39 BP.
XX
AC AAQ12689;
XX
DT 01-OCT-1991 (first entry)
XX
DE Rei light chain variable region primer #R4.
XX
DE Monoclonal antibody; complementarity determining region; CDR; integrin;
XX hybridoma 1B4; protein REI; Ig; ss.
XX
OS Synthetic.
XX
PN EP438310-A.
XX
PD 24-JUL-1991.
XX
PF 17-JAN-1991; 91EP-00300362.
XX
PR 19-JAN-1990; 90US-00467700.
XX
PR 20-DEC-1990; 90US-00627423.

```


XX (MERI) MERCK & CO INC.
 XX Law MF, Mark GE, Williamson AR;
 XX WPI; 1991-216983/30.
 XX Prodn. of humanised recombinant immunoglobulin - including polymerase
 PT chain reaction amplification of murine antibody light and heavy chain
 PT variable portions.
 XX Disclosure; Fig 4; 78pp; English.
 XX The sequences in AAQ12685-Q12692 are primers for PCR mutagenesis and
 CC amplification of the Rei light chain variable region template so as to
 CC graft the CDRs of murine 1B4 into the Rei light chain variable region.
 CC See also EP-438312
 XX Sequence 39 BP; 11 A; 11 C; 9 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 |||||
 DB 19 GGTGTGCCAAGCAGATTCA 37

RESULT 18
 AAV39382
 ID AAV39382 standard; DNA; 39 BP.
 XX AC
 AC AAV39382;
 XX DT 21-SEP-1998 (first entry)
 XX DE Humanised anti-HM1.24 antibody PCR primer SEQ ID NO:50.
 XX KW Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;
 KW framework region; complementarity determining region; antigenicity;
 KW PCR primer; ss.
 XX OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX WO9814580-A1.
 XX PD 09-APR-1998.
 XX PF 03-OCT-1997; 97WO-JP003553.
 XX PR 04-OCT-1996; 96JP-00264756.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Ono K, Ontomo T, Tsuchiya M, Yoshimura Y, Koishihara Y, Kosaka M;
 XX WPI; 1998-286421/25.
 XX Humanised anti-HM1.24 antibody - for treatment of myeloma.
 XX Example 9; Page 134; 210pp; Japanese.
 XX A humanised anti-HM1.24 antibody has been developed which comprises human
 CC L and H chain C regions, and L and/or H chain V regions containing
 CC material originating in mouse anti-HM1.24 antibody. The V regions contain
 CC framework (FR) regions of human origin and complementarity determining
 CC regions (CDR) of mouse origin, leading to a reshaped humanised antibody.
 CC The C regions are human Ck (L-chain) and human C gamma (especially C
 CC gamma 1) (H-chain). The FR regions of the L chain V region are derived
 CC from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions

CC of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3
 CC from human antibody HG3 and FR4 from human antibody JH6). The present
 CC sequence represents a PCR primer used in an example from the present
 CC invention. The antibodies are used for the treatment of myeloma,
 CC especially by injection, intravenously, intramuscularly or
 CC subcutaneously. The antibodies are used at 0.01-1000 (especially 5-100)
 CC mg/kg body weight. The humanised antibody has low antigenicity and is
 CC therefore effective therapeutically in humans
 XX

SQ Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
 Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 |||||
 DB 19 GGTGTGCCAAGCAGATTCA 37

RESULT 19
 AAX59432
 ID AAX59432 standard; DNA; 39 BP.
 XX AC
 AC AAX59432;
 XX DT 16-JUL-1999 (first entry)
 XX DE Primer used in construction of humanised anti-HM1.24 antibody.
 XX KW Reconstituted human antibody; peptide antigen HM1.24; framework region;
 KW complementary determining region; CDR; anti-HM1.24 antibody; myeloma;
 KW humanised antibody; primer; ss.
 XX OS Synthetic.
 XX WO9918212-A1.
 XX PD 15-APR-1999.
 XX PF 02-OCT-1998; 98WO-JP004469.
 XX PR 03-OCT-1997; 97JP-00271726.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Tsuchiya M;
 XX WPI; 1999-277273/23.
 XX Reconstituted human antibody useful in the treatment of myeloma.
 XX Disclosure; Page 114; 256pp; Japanese.
 XX The specification describes a reconstituted human antibody recognizing
 CC the peptide antigen HM1.24. This human antibody contains natural human
 CC framework regions modified by amino acid substitutions to provide
 CC homogeneity with a previously designed framework region (which may arise
 CC from a human or non-human source); and complementary determining regions
 CC (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted
 CC antibody is useful in the treatment of diseases in which the surface
 CC antigen HM1.24 is implicated such as myeloma. The present sequence is
 CC used in the creation of the antibodies of the invention
 XX

SQ Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
 Query Match 56.8%; Score 14.2; DB 2; Length 39;
 Best Local Similarity 84.2%; Pred. No. 5.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCA 19
 |||||
 DB 19 GGTGTGCCAAGCAGATTCA 37

```

DE XX Light chain primer EL.
KW KW Probe; myeloma; Y3-Ag 1.2.3; primer; rat; monoclonal; antibody; COS;
KW YFC51.1.1; CD18; humanised; antigen; leukocyte; lung; sepsis; asthma;
KW endotoxin shock; adult respiratory distress syndrome; inflammation;
KW immunotoxin; transient expression; PCR; polymerase chain reaction; ss.
XX OS Synthetic.
XX XX
XX PN WO9302191-A1.
XX XX
XX PD 04-FEB-1993.
XX XX
XX PF 15-JUL-1992; 92WO-GB001289.
XX PR 16-JUL-1991; 91GB-00015364.
XX XX
XX PA (WELL ) WELLCOME FOUND LTD.
XX XX
XX PI Waldmann H, Sims M, Crowe S;
XX DR WPI; 1993-058788/07.
XX XX
XX PT New humanised antibody specific for human CD-18 antigen - inhibits influx
XX of leukocytes into the lungs, useful for treating endotoxic shock, adult
XX respiratory distress syndrome, asthma, etc.
XX PS Disclosure; Page 47; 59pp; English.
XX XX
XX CC The sequences given in AAQ35180-87 are primers which were used to amplify
XX and humanise the light chain isolated from the rat antibody YFC51.1.1.
XX CC The light chain of YFC51.1.1 was isolated using a non-radioactively
XX CC labelled clone of the light chain from rat myeloma Y3-Ag 1.2.3. The
XX CC isolated sequences were amplified, humanised and constructed into the
XX CC light chain genes using these primers. The gene construction, and a
XX CC corresponding one for the heavy chain (see also AAQ35188-95) were
XX CC transformed into COS cells which transiently expressed the humanised
XX CC YFC51.1.1. YFC51.1.1 is a CD18 antibody which was used as a basis for the
XX CC production of a humanised antibody with specificity for CD18 antigen. The
XX CC antibody may be useful in treating leukocyte-mediated conditions, such as
XX CC inhibiting influx of leukocytes into the lung and other organs during
XX CC sepsis, endotoxin shock or adult respiratory distress syndrome. The
XX CC antibodies may also be used to treat asthma and inflammation and may form
XX CC part of an immunotoxin. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 2; Length 41;
XX Best Local Similarity 84.2%; Pred. No. 5.6e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1 GCTGAGCCTAGCAGATTCA 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 22
AAQ34502/c
ID AAL34502 standard; DNA; 50 BP.
XX XX
XX AC AAL34502;
XX XX
XX DT 24-JAN-2002 (first entry)
XX XX
XX DE Human SNP oligonucleotide #7710.
XX XX
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; cholesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX KW

```

```

RESULT 20
AAQ24659
ID AAQ24659 standard; DNA; 41 BP.
XX XX
XX AC AAQ24659;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-NOV-1992 (first entry)
XX XX
XX DE PCR primer EL for CAMPATH-1H light chain.
XX XX
XX KW Polymerase chain reaction; humanised antibody; CAMPATH-1H;
KW rat anti-human CD18 light chain; YFC51.1.1; human IgG1 heavy chain;
KW PCR grafting; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9207075-A1.
XX XX
XX PD 30-APR-1992.
XX XX
XX PF 08-OCT-1991; 91WO-GB001744.
XX PR 10-OCT-1990; 90GB-00022011.
XX XX
XX PA (WELL ) WELLCOME FOUND LTD.
XX XX
XX PI Crowe JS, Lewis AP;
XX XX
XX DR WPI; 1992-167155/20.
XX XX
XX PT Prepn. of chimeric humanised antibodies - using a new polymerase chain
XX reaction technique.
XX XX
XX PS Example 2; Page 45; 67pp; English.
XX XX
XX CC The YFC51.1.1 rat anti-human -CD18 light chain was humanised as follows:
XX CC Primer EL (AAQ24659) was used with primer FL (AAQ24660) in a PCR reaction
XX CC using as template CAMPATH-1H light chain (i.e. humanised CAMPATH-1 on REI
XX CC framework; Biotechnology 9:64-68 (1991)) to produce fragment EFL. Three
XX CC other PCR reactions were performed on the same template, generating
XX CC fragments ABL, CDL and GHL. Fragments EFL and GHL were combined and used
XX CC as the template for a PCR reaction with primers EL and HL (AAQ24662) to
XX CC produce fragment EHL. Similarly, fragment ADL was produced from ABL and
XX CC CDL using the primers AL and DL (AAQ24655 and AAQ24658, respectively).
XX CC The products ADL and EHL were purified and combined in a recombinant PCR
XX CC reaction using primers AL and HL. The final humanised light chain
XX CC product, AHL, was cloned into the HindIII site of pUC18 (primers AL and
XX CC HL both contain HindIII sites). (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 41 BP; 9 A; 8 C; 12 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 56.8%; Score 14.2; DB 2; Length 41;
XX Best Local Similarity 84.2%; Pred. No. 5.6e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1 GCTGAGCCTAGCAGATTCA 19
   ||| ||| ||| ||| ||| ||| |||
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 21
AAQ35184
ID AAQ35184 standard; cDNA; 41 BP.
XX XX
XX AC AAQ35184;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1993 (first entry)
XX XX

```

KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Claim 1; Page 3617; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 5 A; 8 C; 15 G; 22 T; 0 U; 0 Other;
Query Match 56.8%; Score 14.2; DB 4; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCTGAGCCTAGCAGATTCA 19
DB 25 GCAGAGCCTAGCAGACACA 7
RESULT 23
ADH05434
ID ADH05434 standard; DNA; 41 BP.
XX
AC ADH05434;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gene polymorphism detection method-related primer/probe #400.
XX
KW gene polymorphism detection; primer; probe; SNP analysis;
KW single nucleotide polymorphism analysis; drug selection; ss.
XX
OS Unidentified.
XX
XX WO2003097877-A1.
PN
XX 27-NOV-2003.
PD
XX 16-MAY-2003; 2003WO-JP006141.
PF

XX 17-MAY-2002; 2002JP-00143185.
PR 17-OCT-2002; 2002JP-00303528.
XX
PA (RIKE) RIKEN KK.
PA (NAKA/) NAKAMURA Y.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
PI WPI; 2004-012542/01.
XX
DR Detecting gene polymorphism for single nucleotide polymorphism analysis
PT and drug selection.
XX
XX Claim 2; SEQ ID NO 400; 166pp; Japanese.
XX
CC The invention comprises a method for detecting gene polymorphisms, the
CC method involves constructing an oligonucleotide primer and/or probe
CC containing the polymorphism site in a receptor gene or its complementary
CC sequence, amplifying that part and detecting it with the probe and/or
CC primer. The method of the invention is useful for the analysis of SNPs
CC and in drug selection. The present DNA sequence represents a primer/probe
CC of the invention.
XX
SQ Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;
Query Match 56.0%; Score 14; DB 12; Length 41;
Best Local Similarity 87.5%; Pred. No. 7e+03;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 GAGCCTAGCAGATTCA 19
DB 20 GRGCCTAGCAGAGTCA 35
RESULT 24
ADH91221
ID ADH91221 standard; DNA; 41 BP.
XX
AC ADH91221;
XX
DT 06-MAY-2004 (first entry)
XX
DE 1-beta-methylcarbapenem compound-related human DNA sequence #400.
XX
KW 1-beta-methylcarbapenem compound; antimicrobial; bacterial infection;
KW respiratory infection; human; ds.
XX
OS Homo sapiens.
XX
XX WO2003095454-A1.
PN
XX 20-NOV-2003.
PD
XX 14-MAY-2003; 2003WO-JP006028.
XX
XX 14-MAY-2002; 2002JP-00138448.
PR
XX (SANY) SANKYO CO LTD.
PA
XX Kobayashi Y, Ashida Y, Uchida T, Kojima K;
XX WPI; 2004-081882/08.
DR
XX New carbapenem compounds resistant to beta-lactamase (except metallo-beta
XX -lactamase), useful for treating microbial infections especially
XX respiratory infections.
XX
XX Disclosure; SEQ ID NO 400; 726pp; Japanese.
XX

CC The invention comprises 1-beta-methylcarbapenem compounds which are
CC useful as antimicrobials to treat bacterial infections, especially
CC respiratory infections in warm-blooded animals (e.g. humans). The present
CC human DNA sequence is included in the sequence listing of this patent.

SQ Sequence 41 BP; 14 A; 11 C; 8 G; 7 T; 0 U; 1 Other;

Query Match 56.0%; Score 14; DB 12; Length 41;

Best Local Similarity 87.5%; Pred. No. 7e+03;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCA 19

DB 20 GRGCTAGCAGAGTCA 35

RESULT 25

AAZ52556

ID AAZ52556 standard; DNA; 47 BP.

XX AC AAZ52556;

DT 30-JUN-1999 (first entry)

DE Human genome biallelic marker 24.

XX Biallelic marker; human; high density disequilibrium map; disease; trait;
KW identification; Alzheimer's disease; drug response; drug efficacy;
KW drug toxicity; ss.

XX Homo sapiens.

XX WO9904038-A2.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-IB001193.

XX 18-JUL-1997; 97EP-00401740.

XX 21-APR-1998; 98US-0082614P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Tchoumakov I;

XX WPI; 1999-132278/11.

XX Production of biallelic markers - by obtaining a genomic DNA library,
PT determining the order and sequence of DNA fragments and identifying
PT nucleotides which vary between individuals.

XX Example 6; Page 134; 288pp; English.

XX This invention describes a novel method for obtaining a set of biallelic
CC markers represented in AAX52533-X52632 and AAX52833-X52843 for use in
CC constructing a high density equilibrium map of the human genome. The
CC method involves (a) obtaining a nucleic acid library comprising genomic
CC DNA fragments comprising the full genome or a portion (b) determining the
CC order of genomic DNA fragments in the genome, (c) determining the
CC sequence of selected regions of the genomic DNA fragments and (d)
CC identifying nucleotides in the genomic DNA fragments which vary between
CC individuals, thereby defining a set of biallelic markers. The methods can
CC be used for identifying traits such as disease (e.g. Alzheimer's
CC disease), drug response, drug efficacy and drug toxicity. They can be
CC used for selecting an individual for inclusion in a clinical trial. The
CC method is used to map the position of genes in a genome (preferably the
CC human genome). The sequences described in AAX52633-X52832 and AAX52844-
CC X52868 represent primers used in the method of the invention

SQ Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 2; Length 47;

Best Local Similarity 77.3%; Pred. No. 7.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTTCATGGCAC 25

DB 3 GAGCCTGGAGCTTTCATGCAC 24

RESULT 26

AAZ68752

ID AAZ68752 standard; DNA; 47 BP.

XX AC AAZ68752;

DT 10-SEP-2001 (first entry)

DE Human map-related biallelic marker SEQ ID NO:3104.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation; diagnosis;
KW single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT variation replace(24,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX Claim 3; Page 892; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses; they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

SQ Sequence 47 BP; 13 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 3; Length 47;

Best Local Similarity 77.3%; Pred. No. 7.2e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTTCATGGCAC 25

```
Db 3 GAGCCTTGGAAGTTCATGACAC 24

RESULT 27
RAL28480/C
ID AAL28480 standard; DNA; 50 BP.
XX
AC AAL28480;
XX
XX
DT 24-JAN-2002 (first entry)
XX
XX
DE Human SNP oligonucleotide #1688.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 1863; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
XX Sequence 50 BP; 13 A; 22 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 4; Length 50;
Best Local Similarity 77.3%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GCTGAGCCTAGCAGATTCATGG 22
|||||
Db 26 GCTGGGCTAGCAGGACATGG 5

us-10-788-779-10.rng

RESULT 28
ABZ05333
ID ABZ05333 standard; DNA; 50 BP.
XX
AC ABZ05333;
XX
XX
DT 09-JAN-2003 (first entry)
XX
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 5324.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
XX Homo sapiens.
OS
XX WO200257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quertemous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 500; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 14 A; 14 C; 10 G; 12 T; 0 U; 0 Other;

Query Match 56.0%; Score 14; DB 6; Length 50;
Best Local Similarity 77.3%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 TGAGCCTAGCAGATTCATGGCA 24
|||||
Db 3 TGAGCCAGGGGGTTTCATGACA 24

RESULT 29
ABK70835
ID ABK70835 standard; DNA; 21 BP.
XX
AC ABK70835;
XX
XX
DT 15-JUL-2002 (first entry)
XX
XX PCR primer for human gene CHST4 #2.
XX
```

KW Human; sulphuric acid conjugation; ss; PCR; CHST1; CHST3; primer; CHST4;
KW CHST5; CST; HNK-1ST; SULTAL; SULTB1; SULTX3; STE; TPST2.
XX
OS Homo sapiens.
XX
FN JP2002085067-A.
XX
XX 26-MAR-2002.
PD
XX 07-SEP-2000; 2000JP-00272229.
XX
XX 07-SEP-2000; 2000JP-00272229.
XX
XX (SAKA) OTSUKA SEIYAKU KOGYO KK.
PA
XX WPI; 2002-378272/41.
DR
XX Determination of enzymes participating in sulfuric acid conjugation in
PT humans, useful for confirmation of safety of investigational drugs,
PT comprises using oligonucleotide probes.
XX
XX Claim 8; Page 11; 13pp; Japanese.
XX
XX The invention relates to classification and quantitative determination of
CC enzymes participating in sulphuric acid conjugation comprising using
CC oligonucleotide probes hybridising to the following regions: (a) 885-911
CC region of CHST1 gene; (b) 174-197 region of CHST3 gene; (c) 1003-1032
CC region of CHST4 gene; (d) 322-346 region of CHST5 gene; (e) 737-765
CC region of CST gene; (f) 703-732 region of HNK-1ST gene; (g) 299-325
CC region of SULT2A1 gene; (h) 358-382 region of SULT2B1 gene; (i) 554-582
CC region of SULTX3 gene; (j) 451-478 region of STE gene; and (k) 652-677
CC region of TPST2 gene. Also included are PCR primers for the above genes,
CC kits and methods for determination. The probes, primers and the method
CC are used in the determination of sulphuric acid conjugation for
CC confirmation of the safety of investigational drugs. The present sequence
CC is a PCR primer for one of the above listed genes
XX
XX
SQ Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 6; Length 21;
Best Local Similarity 88.2%; Pred. No. 7.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATG 21
|||||
Db 5 AGCCGAGCAATTCATG 21

RESULT 30
ACK02180
ID ACK02180 standard; DNA; 25 BP.
XX
XX ACK02180;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 102161.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
KW
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA

XX Mittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 102161; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TAGCAGATTCATGGCAC 25
|||||
Db 2 TAGCGATTAAATGGCAC 18

RESULT 31
ADC21315/c
ID ADC21315 standard; DNA; 33 BP.
XX
XX ADC21315;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Plasmid pMOKp36 PCR primer #3.
DE
XX
XX expression construct; vaccine; intradermal injection;
KW type 1 cell-mediated immune response; antiviral; hepatotropic;
KW antiinflammatory; protozoacide; MIDGE;
KW minimalistic immunologically defined gene expression vector;
KW hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;
KW PCR.
XX
XX Synthetic.
OS
XX
XX WO2003031469-A2.
XX
XX 17-APR-2003.
PD
XX
XX 02-OCT-2002; 2002WO-DE003798.
PF
XX
XX 02-OCT-2001; 2001DE-01048697.
XX
XX 12-NOV-2001; 2001DE-01056678.
PR

```

XX PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
XX PA (LOPEZ/) LOPEZ S M.
XX PA (JIME/) JIMENEZ M T.
XX PI Lopez SM, Jimenez MT;
XX DR WPI; 2003-372085/35.
XX PT Use of a DNA expression construct encoding one or more antigens and
XX PT covalently linked to oligopeptides for preparing intradermal vaccine,
XX PT useful for treating e.g. hepatitis and leishmaniasis.
XX PS Example 4; SEQ ID NO 9; 32pp; German.
XX CC This invention describes a novel DNA expression construct, functional in
XX CC eukaryotic cells, to prepare a vaccine, for intradermal injection, to
XX CC generate a type 1 cell-mediated immune response. The construct encodes
XX CC one or more antigens (Ag) under control of a promoter and, to improve
XX CC transfection efficiency, is covalently linked to one or more
XX CC oligopeptides. The products of the invention have antiviral,
XX CC hepatotropic, antiinflammatory and protozoacide activity. Mice were
XX CC immunized intradermally (twice at an interval of 11 weeks) with a MIDGE
XX CC (minimalistic immunologically defined gene expression vector) that
XX CC encoded hepatitis B surface antigen. The resulting antibody titer
XX CC (expressed as optical density in enzyme linked immunosorbent assay) was
XX CC about 0.45, about the same as when using a plasmid for expression. When
XX CC the MIDGE used was modified by binding the Tat protein-derived peptide
XX CC Tyx-Gly-Arg-(lys)_2-(Arg)_2-Gln-(Arg)_3 the optical density was over 0.9.
XX CC The constructs are used, particularly in human medicine, to generate a
XX CC type 1 cell-mediated immune response, specifically against hepatitis B
XX CC virus surface antigen, but also against the p36 antigen of Leishmania
XX CC major. Attachment of the oligopeptides increases transport of the
XX CC construct to the nucleus, resulting in a stronger immune response. This
XX CC sequence represents a PCR primer used in the construction of construct
XX CC pMOKp36 used to make the vaccines described in the disclosure of the
XX CC invention.
XX SQ Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 10; Length 33;
Best Local Similarity 72.0%; Pred. No. 8.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25
Db 32 GGTGACCTCGTATGTTTCATGTAC 8

RESULT 32
ADC21313/c
ID ADC21313 standard; DNA; 33 BP.
XX AC ADC21313;
XX DT 18-DEC-2003 (first entry)
XX DE Plasmid pMOKp36 PCR primer #1.
XX KW expression construct; vaccine; intradermal injection;
XX KW type 1 cell-mediated immune response; antiviral; hepatotropic;
XX KW antiinflammatory; protozoacide; MIDGE;
XX KW minimalistic immunologically defined gene expression vector;
XX KW hepatitis B surface antigen; p36 antigen; Leishmania major; ss; primer;
XX KW PCR.
XX OS Synthetic.
XX OS WO2003031469-A2.
XX PN 17-APR-2003.
XX PD 02-OCT-2002; 2002WO-DE003798.
XX PF

XX PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
XX PA (LOPEZ/) LOPEZ S M.
XX PA (JIME/) JIMENEZ M T.
XX PI Lopez SM, Jimenez MT;
XX DR WPI; 2003-372085/35.
XX PT Use of a DNA expression construct encoding one or more antigens and
XX PT covalently linked to oligopeptides for preparing intradermal vaccine,
XX PT useful for treating e.g. hepatitis and leishmaniasis.
XX PS Example 4; SEQ ID NO 7; 32pp; German.
XX CC This invention describes a novel DNA expression construct, functional in
XX CC eukaryotic cells, to prepare a vaccine, for intradermal injection, to
XX CC generate a type 1 cell-mediated immune response. The construct encodes
XX CC one or more antigens (Ag) under control of a promoter and, to improve
XX CC transfection efficiency, is covalently linked to one or more
XX CC oligopeptides. The products of the invention have antiviral,
XX CC hepatotropic, antiinflammatory and protozoacide activity. Mice were
XX CC immunized intradermally (twice at an interval of 11 weeks) with a MIDGE
XX CC (minimalistic immunologically defined gene expression vector) that
XX CC encoded hepatitis B surface antigen. The resulting antibody titer
XX CC (expressed as optical density in enzyme linked immunosorbent assay) was
XX CC about 0.45, about the same as when using a plasmid for expression. When
XX CC the MIDGE used was modified by binding the Tat protein-derived peptide
XX CC Tyx-Gly-Arg-(lys)_2-(Arg)_2-Gln-(Arg)_3 the optical density was over 0.9.
XX CC The constructs are used, particularly in human medicine, to generate a
XX CC type 1 cell-mediated immune response, specifically against hepatitis B
XX CC virus surface antigen, but also against the p36 antigen of Leishmania
XX CC major. Attachment of the oligopeptides increases transport of the
XX CC construct to the nucleus, resulting in a stronger immune response. This
XX CC sequence represents a PCR primer used in the construction of construct
XX CC pMOKp36 used to make the vaccines described in the disclosure of the
XX CC invention.
XX SQ Sequence 33 BP; 10 A; 7 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 10; Length 33;
Best Local Similarity 72.0%; Pred. No. 8.4e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25
Db 32 GGTGACCTCGTATGTTTCATGTAC 8

RESULT 33
ADC21307/c
ID ADC21307 standard; DNA; 33 BP.
XX AC ADC21307;
XX DT 18-DEC-2003 (first entry)
XX DE Plasmid pMOKp36 PCR primer #3.
XX KW immunization; leishmaniasis; vaccine; protozoacide; p36 antigen;
XX KW TAT peptide; ss; primer; PCR.
XX OS Synthetic.
XX OS WO2003031470-A2.
XX PN 17-APR-2003.
XX PD 02-OCT-2002; 2002WO-DE003799.
XX PF

```


DR WPI; 2004-552653/53.

XX Analyzing multiple targets in polynucleotide, by providing multiple

XX primers with target nucleic acids, digesting nucleic acid products with

PT cognate restriction enzymes, amplifying digested products, and detecting

XX amplified products.

PS Example 1; SEQ ID NO 39; 65pp; English.

XX

XX The invention relates analysing multiple targets in polynucleotide.

CC involves providing a set or sets of multiple primers with target nucleic

CC acids in separate reactions of primer extension or amplification, where

CC the reactions produce nucleic acid products in that each nucleic acid

CC fragments comprise at least one restriction site, digesting nucleic acid

CC products of the separate reactions on the restriction sites with cognate

CC restriction enzymes, joining digested products derived from the separate

CC reactions together, where randomly joining nucleic acid fragments from

CC the separated reactions are created, amplifying the joined products, and

CC detecting the amplified products. Also included are an oligonucleotide

CC primer for detecting target nucleic acid sequence (comprising a 3'

CC complementary portion and 5' non-complementary portion, where the 5' non-

CC complementary portion comprises a restriction enzyme site, where the

CC restriction site acts as detection marker in the process of detecting

CC target nucleic acid sequence, where the detection signal generated from

CC enzymatic manipulation on restriction site of reaction product is

CC indicative of the presence of target nucleic acid sequence) and a kit for

CC use in analysis and detection of multiple targets in a polynucleotide

CC (comprising a set or sets of multiple primers, universal primers,

CC restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all

CC enzymes, and dNTPs). The method is useful for analysing multiple targets

CC in a polynucleotide and for genotyping mutations, preferably single

CC nucleotide polymorphisms (SNPs), and for analysing differential gene

CC expression profiles, genomic methylation patterns and any specific

CC nucleic acids from any source. The method enables analysis of multiple

CC targets quantitatively. An experiment was performed, using the method of

CC the invention, where 8 SNPs were detected in human genomic DNA,

CC simultaneously. The present sequence is a primer used in the above

XX experiment.

SQ Sequence 49 BP; 15 A; 11 C; 13 G; 10 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 13; Length 49;

Best Local Similarity 88.2%; Pred. No. 9.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGG 22

Db 28 GACTAGCAGATTCACGG 44

RESULT 36

AAL28734

ID AAL28734 standard; DNA; 50 BP.

XX AC

XX AAL28734;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human SNP oligonucleotide #1942.

XX

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;

KW amyloid protein; angiotensin; apoptosis related protein; cadherin;

KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KW complement related protein; cytochrome; kinesin; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;

KW multifactorial disease; autoimmune disease; infection;

KW nervous system disease; ss.

XX

OS Homo sapiens.

XX

XX WO200147944-A2.

XX

PD 05-JUL-2001.

XX

XX 28-DEC-2000; 2000WO-US035498.

XX

XX 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX

XX (CURA-) CURAGEN CORP.

PA

XX Shimkets RA, Leach M;

PI

XX WPI; 2001-465210/50.

DR

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,

PT autoimmune diseases and infections.

XX

PS Claim 1; Page 1936; 4143pp; English.

XX

XX The present invention relates to oligonucleotides encoding polymorphic

CC variants of proteins related to amylases, amyloid proteins, angiotensin,

CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC histones, kinases, colony stimulating factors, complement related

CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-

CC protein coupled receptors and thioesterases. The present sequence is one

CC such oligonucleotide. The oligonucleotides and the peptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of the proteins listed above.

CC Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythematosus and Grave's disease), inflammation, cancer

CC (e.g. cancers of the bladder, brain, breast, colon and kidney,

CC leukaemia), diseases of the nervous system and an infection of pathogenic

CC organisms

XX

SQ Sequence 50 BP; 6 A; 15 C; 19 G; 10 T; 0 U; 0 Other;

Query Match 55.2%; Score 13.8; DB 4; Length 50;

Best Local Similarity 72.0%; Pred. No. 9.1e+03;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

Db 17 GCTTGGCCAGCAGCTCCAGGGCCC 41

RESULT 37

ADQ31582

ID ADQ31582 standard; DNA; 50 BP.

XX

XX ADQ31582;

XX

DT 21-OCT-2004 (first entry)

XX

DE Multiplex detection of human SNPs, primer F10G.

XX

KW Human; Multiplex nucleic acid detection; ss; PCR; primer; SNP;

KW single nucleotide polymorphism.

XX

XX Homo sapiens.

OS

XX US2004146866-A1.

PN

XX 29-JUL-2004.

PD

XX 24-JAN-2003; 2003US-00349780.

PF

XX 24-JAN-2003; 2003US-00349780.

PR

XX (FUGG/) FU G.

XX

PI Fu G;

```

XX WPI; 2004-552653/53.
XX
XX Analyzing multiple targets in polynucleotide, by providing multiple
PT primers with target nucleic acids, digesting nucleic acid products with
PT cognate restriction enzymes, amplifying digested products, and detecting
PT amplified products.
XX
XX Example 1; SEQ ID NO 40; 65pp; English.
XX
XX The invention relates analysing multiple targets in polynucleotide,
XX involves providing a set or sets of multiple primers with target nucleic
XX acids in separate reactions of primer extension or amplification, where
XX the reactions produce nucleic acid products in that each nucleic acid
XX fragments comprise at least one restriction site, digesting nucleic acid
XX products of the separate reactions on the restriction sites with cognate
XX restriction enzymes, joining digested products derived from the separate
XX reactions together, where randomly joining nucleic acid fragments from
XX the separated reactions are created, amplifying the joined products, and
XX detecting the amplified products. Also included are an oligonucleotide
XX primer for detecting target nucleic acid sequence (comprising a 3'
XX complementary portion and 5' non-complementary portion, where the 5' non-
XX complementary portion comprises a restriction enzyme site, where the
XX restriction site acts as detection marker in the process of detecting
XX target nucleic acid sequence, where the detection signal generated from
XX enzymatic manipulation on restriction site of reaction product is
XX indicative of the presence of target nucleic acid sequence) and a kit for
XX use in analysis and detection of multiple targets in a polynucleotide
XX (comprising a set or sets of multiple primers, universal primers,
XX restriction enzymes, DNA ligase, DNA polymerase, ddNTP, buffers for all
XX enzymes, and dNTPs). The method is useful for analysing multiple targets
XX in a polynucleotide and for genotyping mutations, preferably single
XX nucleotide polymorphisms (SNPs), and for analysing differential gene
XX expression profiles, genomic methylation patterns and any specific
XX nucleic acids from any source. The method enables analysis of multiple
XX targets quantitatively. An experiment was performed, using the method of
XX the invention, where 8 SNPs were detected in human genomic DNA.
XX simultaneously. The present sequence is a primer used in the above
XX experiment.
XX
XX Sequence 50 BP; 16 A; 10 C; 15 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 55.2%; Score 13.8; DB 13; Length 50;
XX Best Local Similarity 88.2%; Pred. No. 9.1e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 6 GCCTAGCAGATTCATGG 22
XX | | | | | | | | | |
XX Db 29 GACTAGCAGATTCACGG 45
XX
XX RESULT 38
XX ABI94601/C
XX ID ABI94601 standard; DNA; 20 BP.
XX
XX AC ABI94601;
XX
XX AC ABI94601;
XX
XX DT 16-FEB-2002 (first entry)
XX
XX DE Capture oligonucleotide Zip ID#1688 oligo #9.
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
XX
XX OS WO200179548-A2.
XX
XX FN 25-OCT-2001.
XX
XX PD
XX

```

```

PP 04-APR-2001; 2001WO-US010958.
XX
XX PR 14-APR-2000; 2000US-0197271P.
XX
XX PA (CORR ) CORNELL RES FOUND INC.
XX
XX XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
XX DR WPI; 2002-034366/04.
XX
XX PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
XX PS Example 5; Fig 29; 30pp; English.
XX
XX CC The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridize with little mismatch, where
XX (1) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX
XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. ABI82074 to
XX ABI97546 represent oligonucleotide sequences used in the exemplification
XX of the present invention
XX
XX Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 54.4%; Score 13.6; DB 6; Length 20;
XX Best Local Similarity 80.0%; Pred. No. 9.7e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX Qy 6 GCCTAGCAGATTCATGGCAC 25
XX | | | | | | | | | |
XX Db 20 GTCCCGCAGATTCAGGCAC 1
XX
XX RESULT 39
XX AA226929/C
XX ID AA226929 standard; DNA; 21 BP.
XX
XX AC AA226929;
XX
XX AC AA226929;
XX
XX DT 18-NOV-1999 (first entry)
XX
XX DE Human chromosome 11 linked CHD1 gene mutation screening PCR primer #67.
XX
XX KW Human; coronary heart disease susceptibility gene; CHD1; mutation;
XX chromosome 11; diagnosis; screening; PCR primer; metabolic disorder;
XX detection; hypophosphatemia; familial combined hyperlipidaemia;
XX insulin resistant syndrome X; multiple metabolic disorder; obesity;
XX diabetes; dyslipidaemic hypertension; ss.
XX
XX Synthetic.
XX
XX OS Homo sapiens.
XX
XX FN WO9945112-A2.
XX
XX PD 10-SEP-1999.
XX

```

```

XX PF 04-MAR-1999; 98WO-US004682.
XX PF 04-MAR-1998; 98US-00034941.
XX PR 06-APR-1998; 98US-0080934P.
XX XX (MYRI-) MYRIAD GENETICS INC.
XX PA Ballinger DG, Ding W, Wagner S, Hess MA;
XX PI WPI; 1999-540844/45.
XX DR
XX PT New isolated coronary heart disease susceptibility gene, used to develop
XX PT products for diagnosis and treatment of coronary heart disease and
XX PT metabolic disorders.
XX PS Example 6; Page 98; 297pp; English.
XX CC The present invention describes the human chromosome 11-linked coronary
XX CC heart disease susceptibility gene (CHD1). Mutations in the CHD1 locus in
XX CC the germline are indicative of a predisposition to coronary heart disease
XX CC or to metabolic disorders related to lipid metabolism. Products from the
XX CC present invention can be used in the diagnosis of predisposition to
XX CC coronary heart disease and to metabolic disorders, including
XX CC hypolipoproteinemia, familial combined hyperlipidaemia, insulin
XX CC resistant syndrome X or multiple metabolic disorder, obesity, diabetes
XX CC and dyslipidaemic hypertension. CHD1 proteins can be used for treating
XX CC coronary heart disease and metabolic disorders. The products can also be
XX CC used for detection and drug screening. AA226832 to AA226841 and AA227027
XX CC to AA227029 represent human CHD1 nucleotide sequences. AA229917 to
XX CC AA229926 represent human CHD1 proteins and protein sequences used in the
XX CC exemplification of the present invention. AA226842 to AA226862 represent
XX CC primers used in the identification of human CHD1; AA226863 to AA227014
XX CC represent PCR primers used in the screening of mutations in human CHD1;
XX CC AA227015 to AA227026 represent oligonucleotides used in the
XX CC exemplification of the present invention
XX SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 54.4%; Score 13.6; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAGAGCTGATGGCAC 2

RESULT 40
AAF95928/c
ID AAF95928 standard; DNA; 21 BP.
XX AC AAF95928;
XX DT 18-NOV-2004 (revised)
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #689.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT variation 11
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.

```

```

XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX DR WPI; 2001-226749/23.
XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.
XX PS Example; Page 95; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX CC Revised record issued on 18-NOV-2004 : The variantion feature was
XX CC incorrectly given a captial V
XX SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 54.4%; Score 13.6; DB 4; Length 21;
Best Local Similarity 80.0%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
Db 21 AGCCTAGCAGATAGATGCA 2

Search completed: November 18, 2005, 11:52:38
Job time : 175.148 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 11:22:09 ; Search time 1195.82 Seconds
(without alignments)
795.779 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	49	1	AI789860 ue65d12.r
2	14.2	56.8	44	1	AI256664 ui29h04.y
3	13.8	55.2	50	1	AU102770 AU102770
4	13.8	55.2	50	1	AU102772 AU102772
5	13.4	53.6	23	1	AL932459 AL932459
6	13.2	52.8	34	8	AZ829250 2M0106X17
7	13.2	52.8	47	7	D12221 HUM000S362
8	13	52.0	30	8	AZ782156 2M0022X09
9	13	52.0	35	9	AL757317 Arabidops
10	13	52.0	50	1	AU103585 AU103585
11	13	52.0	50	4	BI824288 603040689
12	12.8	51.2	30	8	BH790466 SALK 0571
13	12.8	51.2	33	9	TA317P10Q
14	12.8	51.2	39	2	BE732614
15	12.8	51.2	46	1	AA715909 nv76904.r
16	12.8	51.2	50	1	AU105049 AU105049
17	12.8	51.2	50	1	AU105060 AU105060
18	12.8	51.2	50	1	AU105083 AU105083
19	12.8	51.2	50	1	AU105084 AU105084
20	12.8	51.2	50	1	AU105091 AU105091
21	12.6	50.4	28	8	AZ480878
22	12.6	50.4	45	9	TA372A04P
23	12.4	49.6	36	7	T65804 ycl1h12.s1
24	12.4	49.6	38	8	AZ824424 2M0099D06

25	12.4	49.6	39	9	AL938370 Arabidops
26	12.4	49.6	42	7	H97155 yv91f07.e1
27	12.4	49.6	44	8	AZ491459 1M0325R05
28	12.4	49.6	50	4	BG405996 sac40901.
29	12.2	48.8	43	1	AI182198 uc64f11.r
30	12.2	48.8	50	1	AU102762 AU102762
31	12.2	48.8	50	1	AU102764 AU102764
32	12.2	48.8	50	1	AU102765 AU102765
33	12.2	48.8	50	1	AU102768 AU102768
34	12.2	48.8	50	1	AU102771 AU102771
35	12.2	48.8	50	1	AU102773 AU102773
36	12.2	48.8	50	1	AU102775 AU102775
37	12.2	48.8	50	1	AU102777 AU102777
38	12.2	48.8	50	1	AU102778 AU102778
39	12.2	48.8	50	1	AU102782 AU102782
40	12.2	48.8	50	1	AU102784 AU102784
41	12.2	48.8	50	1	AU102785 AU102785
42	12.2	48.8	50	1	AU102786 AU102786
43	12.2	48.8	50	1	AU102787 AU102787
44	12.2	48.8	50	1	AU102788 AU102788
45	12.2	48.8	50	1	AU102789 AU102789

ALIGNMENTS

RESULT 1
AI789860
LOCUS
DEFINITION
ue65d12.r1 Soares mammary_gland NMLMG Mus musculus cDNA clone
IMAGE:1495991 5', similar to SW:KClA_CHICK P70065 CASEIN KINASE I,
ALPHA ISOFORM ;, mRNA sequence.
ACCESSION
AI789860
VERSION
AI789860.1 GI:5337576
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.;
REFERENCE
1 (bases 1 to 49)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapps-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:933595

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .49
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1495991"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NMLMG"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaudo."

ORIGIN

Query Match 60.0%; Score 15; DB 1; Length 49;
 Best Local Similarity 78.3%; Pred. No. 3e+04; 5; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GCTGAGCCTACGAGATTCATGGC 23
 ||||| ||||| ||||| ||||| |||||
 Db 3 GCTGGGCCAGGAGATCCATGCAC 25

RESULT 2

AI256664
 LOCUS u129h04.y1 Soares mouse urogenital ridge NMUR Mus musculus cDNA
 DEFINITION clone IMAGE:1852759 5' similar to gb:M39438 TRANSDUCIN-LIKE
 ENHANCER PROTEIN 3 (HUMAN);, mRNA sequence.

ACCESSION AI256664.1 GI:3864189

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 44)
 Mailla, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:968187

Trace considered overall poor quality

Seq primer: -40RP from Gibco

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..44

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1852759"

/sex="equal ratio of male:female"

/tissue_type="urogenital ridge (embryonic)"

/dev_stage="fetal, mixture of 11.5 and 12.5 dpc"

/lab_host="DH10B"

/clone_lib="Soares mouse urogenital ridge NMUR"

/note="Organ: gonad; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAACTGAAGGCGCGCCGATTCCTTTTCTTTTCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library went through two rounds of normalization, and was

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 56.8%; Score 14.2; DB 1; Length 44;
 Best Local Similarity 84.2%; Pred. No. 7.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCA 24

||||| ||||| ||||| ||||| |||||

Db 9 GCCTTGGGATACATGGCA 27

RESULT 3

LOCUS AU102770/c

DEFINITION

AU102770 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

CAS02715, mRNA sequence.

ACCESSION AU102770

KEYWORDS EST.

SOURCE AU102770.1 GI:13552291

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CAS02715"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 55.2%; Score 13.8; DB 1; Length 50;

Best Local Similarity 72.0%; Pred. No. 1.1e+05;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25

||||| ||||| ||||| ||||| |||||

Db 28 GCGGAGACTCGCGGATACAGAGCAC 4

RESULT 4

LOCUS AU102772/c

DEFINITION

AU102772 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

CAS03205, mRNA sequence.

ACCESSION AU102772

KEYWORDS EST.

SOURCE AU102772.1 GI:13552293

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS03205"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match : 55.2%; Score 13.8; DB 1; Length 50;
 Best Local Similarity 72.0%; Pred. No. 1.1e+05;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 |||||
 Db 29 GCGGAGACTGGCGGATACAAAGCAC 5

RESULT 5

AL932459 23 bp mRNA linear EST 14-NOV-2002
 LOCUS AL932459 NAP1 Anopheles gambiae cDNA clone NAPI-P95-D-09-5, mRNA
 DEFINITION sequence.

ACCESSION

AL932459

VERSION

AL932459.1 GI:24974439

KEYWORDS

EST.

SOURCE

Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota, Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Anopheles.

REFERENCE

1 (bases 1 to 23)
 Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.
 and Kafatos,P.C.
 Anopheles gambiae EST, European Molecular Biology Laboratory
 Unpublished (2002)
 Contact: Christophides GK
 Fotis C. Kafatos laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany
 Tel: +49 6221 387-440
 Fax: +49 6221 387-306
 Email: christop@embl-heidelberg.de
 Plate: P95 row: D column: 09.

FEATURES

Location/Qualifiers
 1..23
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:7165"
 /clone="NAPI-P95-D-09-5"
 /lab_host="E. coli DH10B"
 /clone_lib="NAPI"

/note="Vector: pRTT3D-Pac (Pharmacia); Site_1: NotI;
 Site_2: EcoRI; ESTs sequenced from the T7 priming site
 that reads from the 5' end of cDNA. The NAP1 is a
 directionally cloned and normalized, oligo-T primed cDNA
 library constructed from a mixture of Anopheles gambiae
 developmental stages according to: Bonaldo, Lennon &
 Soares (1996): Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery, Genome Research
 6, 791-806."

ORIGIN

Query Match 53.6%; Score 13.4; DB 1; Length 23;
 Best Local Similarity 77.8%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

1 GCTGAGCCTAGCAGATTC 18

Db

2 GNNNATCCTAGCAGATTC 19

RESULT 6

AZ829250/c

LOCUS AZ829250

DEFINITION

2M0106K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0106K17 R, genomic survey sequence.

ACCESSION AZ829250

VERSION AZ829250.1 GI:12999158

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 34)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0106 row: K column: 17

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 34.

Location/Qualifiers

1..34

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0106K17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 52.8%; Score 13.2; DB 8; Length 34;
 Best Local Similarity 83.3%; Pred. No. 2.1e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy      2 CTGAGCCTAGCAGATTCA 19
      ||||| ||||| ||||| |||||
Db      21 CAGAGCATAGCAGATGCA 4

RESULT 7
D12221/c
LOCUS      D12221
DEFINITION HUM000S362 Liver HepG2 cell line. Homo sapiens cDNA clone #362,
mRNA sequence.
ACCESSION D12221
VERSION   D12221.1 GI:2148401
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
and Matsubara,K.
TITLE     Large scale cDNA sequencing for analysis of quantitative and
qualitative aspects of gene expression
JOURNAL   Nat. Genet. 2, 173-179 (1992)
MEDLINE   94258199
PUBMED    1345164
COMMENT   Contact: Kousaku Okubo, Nachiro Hori, Ryo Matoba, Toshiyuki
Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
Osaka University
1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES             source
    Location/Qualifiers
        1..47
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:D05772E"
            /db_xref="taxon:9606"
            /clone="s362"
            /lab_host="E.coli"
            /clone_lib="Liver HepG2 cell line."
            /note="3'-directed regional cDNA library. Cleaved by MboI
and transformed into E.coli."

ORIGIN

Query Match      52.8%; Score 13.2; DB 7; Length 47;
Best Local Similarity 83.3%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CTAGCAGATTTCATGGCAC 25
      ||||| ||||| ||||| |||||
Db      41 CTAGACCTTTCATGGAC 24

RESULT 8
AZ782156/c
LOCUS      AZ782156
DEFINITION 2M0022K09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0022K09 F, genomic survey sequence.
ACCESSION AZ782156
VERSION   AZ782156.1 GI:12915573
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss

Qy      5 AGCCTAGCAGATTTCATGGCAC 25
      | ||||| ||||| ||||| |||||
Db      27 ACCTAGCCGACTCAGCAGAC 7

RESULT 9
AL757317/c
LOCUS      AL757317
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-120G10-012516,
genomic survey sequence.
ACCESSION AL757317
VERSION   AL757317.1 GI:21495665
KEYWORDS  GSS.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
TITLE     GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE   22755829
PUBMED    12874060

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0022 row: K column: 09
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
    1..30
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUC2M0022K09"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```



```

ORIGIN
Query Match          52.0%; Score 13; DB 4; Length 50;
Best Local Similarity 76.2%; Pred. No. 2.7e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
    ||||| ||||| ||||| |||||
Db 4 GCGGCGCCCGCAGAGTCAGG 24

RESULT 12
BH790466          30 bp DNA linear GSS 02-APR-2002
LOCUS             SALK_057108.32.55.x Arabidopsis thaliana TDNA insertion lines
DEFINITION        Arabidopsis thaliana genomic clone SALK_057108.32.55.x, genomic
                  survey sequence.
ACCESSION         BH790466
VERSION           BH790466.1 GI:19883564
KEYWORDS          GSS.
SOURCE            Arabidopsis thaliana (thale cress)
ORGANISM          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE         1 (bases 1 to 30)
AUTHORS           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
                  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
                  Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE             A Sequence-Indexed Library of Insertion Mutations in the
                  Arabidopsis Genome
JOURNAL           Unpublished (2001)
COMMENT           Contact: Joseph R. Ecker
                  Salk Institute Genomic Analysis Laboratory (SIGnAL)
                  The Salk Institute for Biological Studies
                  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                  Tel: 858 453 4100 x1752
                  Fax: 858 558 6379
                  Email: ecker@salk.edu
                  This is single pass sequence recovered from the left border of
                  TDNA. This sequence lies within an annotated exon of Atg14330.
                  Class: TDNA tagged.
FEATURES          Location/Qualifiers
                  1..30
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="SALK_057108.32.55.x"
                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                    each of which contains one or more TDNA insertion
                    elements. The resultant fragment for each line was
                    directly sequenced to determine the genomic sequence at
                    the site of insertion. Details of the protocols used can
                    be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          51.2%; Score 12.8; DB 8; Length 30;
Best Local Similarity 70.8%; Pred. No. 3.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGCA 24
    ||||| ||||| ||||| |||||
Db 2 GCTGAGCCCAACACACATCGGA 25

RESULT 13
TA317F10Q        33 bp DNA linear GSS 13-DEC-2000
LOCUS             T. brucei sheared genomic DNA clone 317F10, reverse sequence,
DEFINITION        T. brucei sheared genomic DNA clone 317F10, reverse sequence,

```

```

genomic survey sequence.
AL491482          GI:11867130
VERSION           AL491482.1
KEYWORDS          GSS.
SOURCE            Trypanosoma brucei
ORGANISM          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                  Trypanosoma.
REFERENCE         1 (bases 1 to 33)
AUTHORS           Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                  Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                  Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE             Direct Submission
JOURNAL           Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                  nh@sanger.ac.uk
COMMENT           Constructed at the Institute for Genomic Research (TIGR),
                  Rockville, MD. Genomic DNA isolated from a cloned population of
                  Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                  to give a tight size distribution (
                  4 kb). The v + i method used for the library construction is
                  described in detail in Smith, H. and Venter, J.C. (Making small
                  insert libraries for whole genome shotgun sequencing projects. In
                  Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                  Barrell, Oxford University Press, 1999).
                  Email: nelsayed@tigr.org
                  Details of T. brucei sequencing at the Sanger Centre are available
                  at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES          Location/Qualifiers
                  1..33
                    /organism="Trypanosoma brucei"
                    /mol_type="genomic DNA"
                    /strain="TREU927"
                    /db_xref="taxon:5691"
                    /clone="317f10"

ORIGIN
Query Match          51.2%; Score 12.8; DB 9; Length 33;
Best Local Similarity 70.8%; Pred. No. 3.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGCA 24
    ||||| ||||| ||||| |||||
Db 5 GCTGATCATTCGCAATTCCTTGCCA 28

RESULT 14
BE732614/c        39 bp mRNA linear EST 15-SEP-2000
LOCUS             BE732614
DEFINITION        601571185F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3925725 5',
                  mRNA sequence.
ACCESSION         BE732614
VERSION           BE732614.1 GI:10146606
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 39)
AUTHORS           NIH-MGC http://mgs.nci.nih.gov/.
TITLE             National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL           Unpublished (1999)
COMMENT           Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
                  Tissue Procurement: ATCC
                  cDNA Library Preparation: Ling Hong/Rubin Laboratory
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                  Plate: L1CM752 row: i column: 22.
FEATURES          Location/Qualifiers

```

```

source
1. 39
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3925725"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 51.2%; Score 12.8; DB 2; Length 39;
Best Local Similarity 70.8%; Pred. No. 3.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTCTTGGCAC 25
Db 34 CCGTACCTGCCCGATTCTTGGCAC 11

RESULT 15
LOCUS AA715909 46 bp mRNA linear EST 22-JAN-1998
DEFINITION nv76904.r1 NCI CGAP Br4 Homo sapiens cDNA clone IMAGE:1235766
similar to SW:NUAM GORGO P03907 NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 4 ; mRNA sequence.

ACCESSION AA715909
VERSION AA715909.1 GI:2728183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 562 Std Error: 0.00
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1235766"
/sex="female"
/tissue_type="normal ductal tissue"
/lab_host="DH10B"
/clone_lib="NCI CGAP Br4"
/note="Organ: breast; Vector: pAMP10; mRNA made from
normal breast ductal tissue, cDNA made by oligo-dT

priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 46;
Best Local Similarity 87.5%; Pred. No. 3.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAGCCTAGCAGATTCTCA 19
Db 10 GTGCCTAGCAGATTCTCA 25

RESULT 16
LOCUS AU105049 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU105049 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00293, mRNA sequence.

ACCESSION AU105049
VERSION AU105049.1 GI:13554570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
REFERENCE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT00293"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 CTGAGCCTAGCAGATTCTTGGCAC 25
Db 25 CTGAGCGTGTCTCATTTTCATAGCAC 2

RESULT 17
LOCUS AU105060 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU105060 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT04574, mRNA sequence.

ACCESSION AU105060
VERSION AU105060.1 GI:13554581
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT04574"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTCCACCTTCATGGCAC 2

RESULT 18
AUI05083/c
LOCUS
DEFINITION AUI05083 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT10532, mRNA sequence.
ACCESSION AUI05083
VERSION AUI05083.1 GI:13554604
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10532"

```

```

/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTCCACATTTCATAGCAC 2

RESULT 19
AUI05084/c
LOCUS
DEFINITION AUI05084 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT10642, mRNA sequence.
ACCESSION AUI05084
VERSION AUI05084.1 GI:13554605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT10642"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 51.2%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 3.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTCATGGCAC 25
Db 25 CTCACGCTGTCCACATTTCATAGCAC 2

RESULT 20
AUI05091/c
LOCUS
DEFINITION AUI05091 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSE01778, mRNA sequence.
ACCESSION AUI05091
VERSION AUI05091.1 GI:13554612
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)

```

```

/db_xref="taxon:10090"
/clone="UUGC1M0302122"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match          50.4%;   Score 12.6;   DB 8;   Length 28;
Best Local Similarity 78.9%;   Pred. No. 3.9e+05;
Matches 15;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      2   CTCGAGCTAGCAGATTTCAT 20
        ||||| | |||||
Db       6   CTTAGCTTTGGAGATTTCAT 24

RESULT 22
TA372A04P/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT
Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrel, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. . 45
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
source
FEATURES

```


Best Local Similarity 72.7%; Pred. No. 5.1e+05; Mismatches 6; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 1 GCTGAGCCTAGCAGATTCATGG 22
||||| ||||| ||||| |||||
Db 10 GCTGAGAAATCCAGATGCATGG 31

RESULT 25
AL938370
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-234D12-014337,
genomic survey sequence.

AL938370

AL938370.1 GI:24370164

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1

Li.Y., Rosso.M.G., Strizhov.N., Viehoveer,P. and Weishaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

22755829

12874060

2

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weishaar,B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

2317147

14756321

3

Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weishaar,B.

High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)

14682050

4 (bases 1 to 39)

Rosso,M.G., Li,Y., Strizhov,N. and Weishaar,B.

Direct Submission

Submitted (31-MAR-2004)

Weishaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At3g56610.

Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..39

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-234D12-014337"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 49.6%; Score 12.4; DB 9; Length 39;
Best Local Similarity 72.7%; Pred. No. 5.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTCATGG 22

||||| ||||| ||||| |||||

Db 8 GATGAGACTAAACACTCATGG 29

RESULT 26

H97155/c

LOCUS

DEFINITION

H97155 42 bp mRNA linear EST 11-DEC-1995
YV91f07.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:250117 3' similar to gb:XS4156_rnal CELLULAR TUMOR ANTIGEN
P53 (HUMAN);, mRNA sequence.

H97155

VERSION

KEYWORDS

SOURCE

ORGANISM

H97155.1 GI:1114198
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 42)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfsing,T., Soares,M., Tan,F.,
Trevasakis,B., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1247 Std Error: 0.00

Seq primer: Promega -21ml3

High quality sequence stop: 1.

Location/Qualifiers

1..42

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3867823"

/db_xref="taxon:9606"

/clone="IMAGE:250117"

/sex="Male"

/tissue type="melanocyte"

/lab host="DH10B (ampicillin resistant)"

/clone_lib="Soares melanocyte 2NbHM"

/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 49.6%; Score 12.4; DB 7; Length 42;
Best Local Similarity 72.7%; Pred. No. 5.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy      3  TGAGCCTAGCAGATTTCATGGCA 24
      |||||
Db      30  TGAGCCAGGAGTTTGAGGCCA 9

RESULT 27
LOCUS   AZ491459/c
DEFINITION  AZ491459F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
      clone UUGC1M0325H05 F, genomic survey sequence.
ACCESSION  AZ491459
VERSION    AZ491459.1 GI:10663188
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0325 row: H column: 05
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
1..44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0325H05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G1/473114|G5|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES             source
1..50
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Raiden"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl062-2594"
/tissue_type="stem tissue of greenhouse grown plants"
/dev_stage="1 month old"
/lab_host="DH10B"
/clone_lib="Gm-cl062"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match      49.6%; Score 12.4; DB 8; Length 44;
Best Local Similarity 92.9%; Pred. No. 5.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4  GAGCCTAGCAGATTTCATGGCAC 25
      |||||
Db      25  GAGATGAGGAGATCATGGCTC 46

RESULT 28
LOCUS   BG405996
DEFINITION  BG405996 50 bp mRNA linear EST 22-JUL-2004
      ssc4901.y1 Gm-cl062 Glycine max cDNA clone GENOME SYSTEMS CLONE
      ID: Gm-cl062-2594 5', mRNA sequence.
ACCESSION  BG405996
VERSION    BG405996.1 GI:13312345
KEYWORDS   EST.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 50)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,S., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email:
info@biogeneticservices.com).
Location/Qualifiers
1..50
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Raiden"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl062-2594"
/tissue_type="stem tissue of greenhouse grown plants"
/dev_stage="1 month old"
/lab_host="DH10B"
/clone_lib="Gm-cl062"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match      49.6%; Score 12.4; DB 4; Length 50;
Best Local Similarity 72.7%; Pred. No. 5.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4  GAGCCTAGCAGATTTCATGGCAC 25
      |||||
Db      25  GAGATGAGGAGATCATGGCTC 46

```


RESULT 29
 A1182198/c
 LOCUS A1182198 43 bp mRNA linear EST 08-OCT-1998
 DEFINITION uc54f11.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
 IMAGE:1430445 5' similar to TR:Q90574 Q90574 FILAMIN. i, mRNA
 sequence.
 ACCESSION A1182198
 VERSION A1182198.1 GI:3732836
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:914513

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.

FEATURES
 source
 1. 43
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1430445"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stages="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares mammary_gland NbMMG"
 /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5', TGTTACCAATCTGAAGTGGGCGCCGCGAATGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
 ORIGIN
 Query Match 48.8%; Score 12.2; DB 1; Length 43;
 Best Local Similarity 82.4%; Pred. No. 6.4e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CCTAGCAGATTCATGGC 23
 |||||
 Db 31 CTTACCAGATTCCTGGC 15
 |||||

RESULT 30
 A102762/c

LOCUS A102762 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION A102762 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 CAS00532, mRNA sequence.
 ACCESSION A102762
 VERSION A102762.1 GI:13552283
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yezuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1. 50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAS00532"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
 Best Local Similarity 68.0%; Pred. No. 6.5e+05;
 Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
 |||||
 Db 30 GCGGAGACTGGAGGATACAGAGCAC 6
 |||||

RESULT 31
 A102764/c
 LOCUS A102764 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION A102764 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 CAS01012, mRNA sequence.
 ACCESSION A102764
 VERSION A102764.1 GI:13552285
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yezuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. 50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01012"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Db 28 GCGGAGACTGGAGGTACAGAGCAC 4

RESULT 32

AU102765/c

LOCUS

DEFINITION AU102765 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01084, mRNA sequence.

ACCESSION

VERSION AU102765

KEYWORDS AU102765.1 GI:13552286

SOURCE EST.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. 50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01084"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Db 31 GCGGAGACTGGAGGTACAGAGCAC 7

RESULT 33

AU102768/c

LOCUS

DEFINITION AU102768 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01084, mRNA sequence.

CAS01704, mRNA sequence.

ACCESSION AU102768

VERSION AU102768.1

KEYWORDS GI:13552289

SOURCE EST.

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. 50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS01704"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Db 29 GCGGAGACTGGAGGTACAGAGCAC 5

RESULT 34

AU102771/c

LOCUS

DEFINITION AU102771 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS03060, mRNA sequence.

ACCESSION

VERSION AU102771

KEYWORDS AU102771.1 GI:13552292

SOURCE EST.

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

```

149-156 (1997).
FEATURES             source
  SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CAS03060"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 37
AUI02777/c
LOCUS
AUI02777 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS05434, mRNA sequence.
DEFINITION
AUI02777
VERSION
AUI02777.1 GI:13552298
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04123, mRNA sequence.
DEFINITION
AUI02775
VERSION
AUI02775.1 GI:13552294
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04123, mRNA sequence.
DEFINITION
AUI02775
VERSION
AUI02775.1 GI:13552294
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04123, mRNA sequence.
DEFINITION
AUI02775
VERSION
AUI02775.1 GI:13552294
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04123, mRNA sequence.
DEFINITION
AUI02775
VERSION
AUI02775.1 GI:13552294
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAGCAC 5

RESULT 36
AUI02775/c
LOCUS
AUI02775 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04123, mRNA sequence.
DEFINITION
AUI02775
VERSION
AUI02775.1 GI:13552294
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
  Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             Location/Qualifiers
  source
  1..50
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="CAS03358"
    /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match
Best Local Similarity
Matches
17; Conservative
0; Mismatches
8; Indels
0; Gaps
0;

Qy
1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||
29 GCGGAGACTGCGGATACAGAG
```

```

source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CAS05434"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCTACGACATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 28 GCGGAGACTGGAGGATACAGGCAC 4

RESULT 38
AU102778/c
LOCUS AU102778 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS06130, mRNA sequence.
ACCESSION AU102778
VERSION AU102778.1 GI:13552299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CAS06130"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCTACGACATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 28 GCGGAGACTGGAGGATACAGGCAC 4

RESULT 39
AU102782/c
LOCUS AU102782 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS07667, mRNA sequence.
ACCESSION AU102782
VERSION AU102782.1 GI:13552303
KEYWORDS EST.

```

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CAS07667"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCTGAGCTACGACATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db 29 GCGGAGACTGCCGATACAAAGCAC 5

RESULT 40
AU102784/c
LOCUS AU102784 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS08174, mRNA sequence.
ACCESSION AU102784
VERSION AU102784.1 GI:13552305
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CA508174"
/clone_lib="Sugano Homo sapiens cDNA library"

```

ORIGIN

```

Query Match      48.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 68.0%; Pred. No. 6.5e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      1  GCTGAGCCTAGCAGATTTCATGGCAC 25
          |||||  |||||  |||||  |||||
Db      28  GCGGAGACTGGAGGATACAGAGCAC 4

```

Search completed: November 18, 2005, 21:12:58
Job time : 1196.82 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 00:26:13 ; Search time 48.5741 Seconds
(without alignments)
842.154 Million cell updates/sec

Title: US-10-788-779-10
Perfect score: 25
Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	1	US-07-989-160-10
2	14.6	58.4	29	4	US-10-039-659A-24
3	14.2	56.8	38	3	US-08-646-265A-37
4	14.2	56.8	39	4	US-09-269-921-50
5	14.2	56.8	41	2	US-08-039-198B-17
6	14.2	56.8	41	2	US-08-182-067-22
7	14.2	56.8	41	2	US-08-465-313-22
8	14.2	56.8	41	4	US-09-378-967-22
9	14.2	56.8	49	4	US-08-407-620A-41
10	14	56.0	25	4	US-09-396-196G-24574
11	13.8	55.2	25	4	US-09-396-196G-43320
12	13.8	55.2	25	4	US-09-396-196G-43321
13	13.8	55.2	25	4	US-09-396-196G-43332
14	13.8	55.2	25	4	US-09-396-196G-61733
15	13.8	55.2	25	4	US-09-396-196G-110219
16	13.6	54.4	21	3	US-09-262-773-104
17	13.6	54.4	25	4	US-09-866-108A-5529
18	13.6	54.4	25	4	US-09-866-108A-5530
19	13.6	54.4	25	4	US-09-866-108A-5531
20	13.6	54.4	25	4	US-09-866-108A-5532
21	13.6	54.4	25	4	US-09-866-108A-5533
22	13.6	54.4	25	4	US-09-866-108A-5534
23	13.6	54.4	25	4	US-09-396-196G-24817
24	13.6	54.4	25	4	US-09-396-196G-65707
25	13.6	54.4	25	4	US-09-396-196G-104940
26	13.6	54.4	47	4	US-09-422-978-3104
27	13.4	53.6	25	4	US-09-396-196G-22130

C 28	13.4	53.6	25	4	US-09-396-196G-22131	Sequence 22131, A
C 29	13.4	53.6	25	4	US-09-396-196G-54320	Sequence 54320, A
C 30	13.4	53.6	33	4	US-09-826-509-105	Sequence 105, App
C 31	13.4	53.6	49	3	US-08-916-576B-33	Sequence 33, Appl
C 32	13.4	53.6	49	4	US-10-078-337-33	Sequence 33, Appl
C 33	13.2	52.8	21	4	US-09-657-472-693	Sequence 693, App
C 34	13.2	52.8	25	4	US-09-647-563-17	Sequence 17, Appl
C 35	13.2	52.8	25	4	US-09-396-196G-104928	Sequence 104928, A
C 36	13.2	52.8	25	4	US-09-396-196G-104929	Sequence 104929, A
C 37	13.2	52.8	33	3	US-09-136-605-26	Sequence 26, Appl
C 38	13.2	52.8	36	2	US-08-484-993B-56	Sequence 56, Appl
C 39	13.2	52.8	36	2	US-08-484-158B-56	Sequence 56, Appl
C 40	13.2	52.8	36	2	US-08-484-596A-56	Sequence 56, Appl
C 41	13.2	52.8	36	2	US-08-480-150A-56	Sequence 56, Appl
C 42	13.2	52.8	36	3	US-08-458-731-56	Sequence 56, Appl
C 43	13.2	52.8	36	3	US-08-149-223A-56	Sequence 56, Appl
C 44	13	52.0	18	4	US-09-422-978-4829	Sequence 4829, Ap
C 45	13	52.0	25	4	US-09-396-196G-21353	Sequence 21353, A

ALIGNMENTS

RESULT 1
US-07-989-160-10
; Sequence 10, Application US/07989160
; Patent No. 5429923
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-07-989-160-10

Query Match 100.0%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTTCATGGCAC 25
|||||

```
Db      1 GCTGAGCCTAGCAGATTGATGGCAC 25

RESULT 2
US-10-039-659A-24
; Sequence 24, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589KIB US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exon 3-specific CRAM primer
US-10-039-659A-24

Query Match      58.4%; Score 14.6; DB 4; Length 29;
Best Local Similarity 81.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 AGCCTAGCAGATTGATGGCAC 25
      ||| ||||| |||||
Db      8 AGCAGAGCAGAGTGATGGCAC 28

RESULT 3
US-08-646-265A-37
; Sequence 37, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763

; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-646-265A-37

Query Match      56.8%; Score 14.2; DB 3; Length 38;
Best Local Similarity 84.2%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
      ||| ||||| |||||
Db      16 GGTGTGCCAAGCAGATTCA 34

RESULT 4
US-09-269-921-50
; Sequence 50, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-269-921-50

Query Match      56.8%; Score 14.2; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCA 19
      ||| ||||| |||||
Db      19 GGTGTGCCAAGCAGATTCA 37

RESULT 5
US-08-039-198B-17
; Sequence 17, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
```


;; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
;; TITLE OF INVENTION: RECOMBINANT PCR STRATEGY
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHYE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/039,198B
;; FILING DATE: 29-JUL-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB91/01744
;; FILING DATE: 08-OCT-91
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WILSON, MARY J.
;; REGISTRATION NUMBER: 32,955
;; REFERENCE/DOCKET NUMBER: 1430-86
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: ssDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-039-198B-17

Query Match 56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GCTGAGCCTAGCAGATTCA 19
| | | | | | | | | | | | | | | | | |
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 6
US-08-182-067-22
; Sequence 22, Application US/08182067
; Patent No. 5985279
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN
; APPLICANT: CROWE, SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,067

;; FILING DATE: 23-MAR-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB92/01289
;; FILING DATE: 15-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9115364.3
;; FILING DATE: 16-JUL-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ERNST, BARBARA G.
;; REGISTRATION NUMBER: 30,377
;; REFERENCE/DOCKET NUMBER: 1786-118A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 783-6040
;; TELEFAX: (202) 783-6031
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 41 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-182-067-22

Query Match 56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GCTGAGCCTAGCAGATTCA 19
| | | | | | | | | | | | | | | | | |
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 7
US-08-465-313-22
; Sequence 22, Application US/08465313
; Patent No. 5997867
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROWE, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,313
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOK, DAVID B.
; REGISTRATION NUMBER: 22,592

```
; REFERENCE/DOCKET NUMBER: LYNX91-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-465-313-22

Query Match          56.8%; Score 14.2; DB 2; Length 41;
Best Local Similarity 84.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 8
US-09-378-967-22
; Sequence 22, Application US/09378967
; Patent No. 6689869
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROWE, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILLITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,967
; FILING DATE: 23-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,313
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WENDLER, HELEN E.
; REFERENCE/DOCKET NUMBER: 37,964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-378-967-22

Query Match          56.8%; Score 14.2; DB 4; Length 41;
Best Local Similarity 84.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 22 GGTGTGCCAAGCAGATTCA 40

RESULT 9
US-08-407-620A-41
; Sequence 41, Application US/08407620A
; Patent No. 6569430
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: CLARK, MICHAEL R.
; APPLICANT: WINTER, GREGORY P.
; APPLICANT: RIECHMANN, LUTZ
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,620A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,705
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,480
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,601
; FILING DATE: 03-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/424,233
; FILING DATE: 12-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 88036228
; FILING DATE: 12-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8804464
; FILING DATE: 25-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-325
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEFAX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
```

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-407-620A-41

Query Match 56.8%; Score 14.2; DB 4; Length 49;
Best Local Similarity 84.2%; Pred. No. 1.e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 19
Db 12 GGTGTCCACAGCAGATTCA 30

RESULT 10
US-09-396-196G-24574/c
; Sequence 24574, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24574
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24574

Query Match 56.0%; Score 14; DB 4; Length 25;
Best Local Similarity 77.3%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCA 22
Db 25 GCAGACAAGCAGACCCATGG 4

RESULT 11
US-09-396-196G-43320
; Sequence 43320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43320

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTC 18
Db 5 CTGAGCCAGCAGCTTC 21

RESULT 12
US-09-396-196G-43321
; Sequence 43321, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43321

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTC 18
Db 3 CTGAGCCAGCAGCTTC 19

RESULT 13
US-09-396-196G-43332
; Sequence 43332, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-43332

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTTC 18
Db 1 CTGAGCCAGCAGCTTC 17

RESULT 14
US-09-396-196G-61733/c
; Sequence 61733, Application US/09396196G
; Patent No. 6821724

; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-61733

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATCA 19
Db 21 TGAGCCTAGAGATCCA 5

RESULT 15
US-09-396-196G-110219/c
; Sequence 110219, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110219
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-110219

Query Match 55.2%; Score 13.8; DB 4; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CCTAGCAGATTCATGGC 23
Db 25 CCTCCAGATTCATGGC 9

RESULT 16
US-09-262-773-104/c
; Sequence 104, Application US/09262773
; Patent No. 6225451
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ding, Wei
; APPLICANT: Wagner, Susanne
; APPLICANT: Hesse, Mark A.
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
; FILE REFERENCE: Myriad 3
; CURRENT APPLICATION NUMBER: US/09/262,773

; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 21
; TYPE: DNA
; ORGANISM: primer
US-09-262-773-104

Query Match 54.4%; Score 13.6; DB 3; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCTTAGCAGATTCATGGCAC 25
Db 21 GCTTAGAAGAGTGTATGGCAC 2

RESULT 17
US-09-866-108A-5529/c
; Sequence 5529, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5529

Query Match 54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCTTAGCAGATTCATGGCAC 25
Db 25 GCCCAGCATCTCCATGGCAC 6

```

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236.359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; REMAINING PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORIGIN: 866-108A-5531
;
Query Match          54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      6 GCCTAGCAGATTCATGGCAC 25
      ||||| ||||| |||||
Db      23 GCCAGCATCTCATGGCAC 4

RESULT 20
US-09-866-108A-5532/c
; Sequence 5532, Application US/098666108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN. Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5532

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5532

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 22 GCCCAGCATCTCCATGGCAC 3

RESULT 21

US-09-866-108A-5533/c

; Sequence 5533, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5533

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5533

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 21 GCCCAGCATCTCCATGGCAC 2

RESULT 22

US-09-866-108A-5534/c

; Sequence 5534, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 5534

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-5534

Query Match 54.4%; Score 13.6; DB 4; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGCAC 25

Db 20 GCCCAGCATCTCCATGGCAC 1

RESULT 23

US-09-396-196G-24817

; Sequence 24817, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 24817
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24817

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAGCCTAGCAGATTTCATGG 22
Db 1 TTAGCCTGCCAGATTTCATGG 20

RESULT 24
US-09-396-196G-65707/c
; Sequence 65707, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65707
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65707

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTTCATGGCA 24
Db 24 AGTCTAGCTCATTTCAGGCA 5

RESULT 25
US-09-396-196G-104940/c
; Sequence 104940, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104940

Query Match      54.4%; Score 13.6; DB 4; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTTCATGGC 23
Db 24 GCGACCAGCAGCTTCATGGC 5

RESULT 26
US-09-422-978-3104
; Sequence 3104, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3104
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2342-217 : polymorphic base C or T
US-09-422-978-3104

Query Match      54.4%; Score 13.6; DB 4; Length 47;
Best Local Similarity 72.7%; Pred. No. 2.1e+03;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTTCATGGC 25
Db 3 GAGCCTTGGAGCTTTCATGACAY 24

RESULT 27
US-09-396-196G-22130/c
; Sequence 22130, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22130

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AGCAGATTTCATGGCA 24
Db 10 AGCAGATTTCATGGCA 24
```

```
Db      22 AGCAGATTCATGGAA 8

RESULT 28
US-09-396-196G-22131/c
; Sequence 22131, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-22131

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 AGCAGATTCATGGCA 24
        |||||
Db      16 AGCAGATTCATGGAA 2

RESULT 29
US-09-396-196G-54320/c
; Sequence 54320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54320

Query Match      53.6%; Score 13.4; DB 4; Length 25;
Best Local Similarity 73.9%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 CTGAGCCTAGCAGATTCATGGCA 24
        |||||
Db      24 CTGAGCAGAGCTGATGACGGAA 2

RESULT 30
US-09-826-509-105
; Sequence 105, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 105
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-105

Query Match      53.6%; Score 13.4; DB 4; Length 33;
Best Local Similarity 73.9%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GCTGAGCCTAGCAGATTCATGGC 23
        |||||
Db      6 GCTTGCCCAAGAGTGTCTATGGC 28

RESULT 31
US-08-916-576B-33/c
; Sequence 33, Application US/08916576B
; Patent No. 6171816
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: EBER, REINHARD
; APPLICANT: ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,576B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/024,347
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-916-576B-33
```


Query Match 53.6%; Score 13.4; DB 3; Length 49;
Best Local Similarity 73.9%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
||||| ||||| |||||
Db 33 GCTGAGTGTAGCATCATGATGGC 11

RESULT 32

US-10-078-337-33/c
; Sequence 33, Application US/10078337
; Patent No. 6818412
; GENERAL INFORMATION:
; APPLICANT: YU, GUO-LIANG
; DILLON, PATRICK J.
; EBER, REINHARD
; ENDRESS, GREGORY A.
; TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/078,337
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,576
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0500001
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2640
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-10-078-337-33

Query Match 53.6%; Score 13.4; DB 4; Length 49;
Best Local Similarity 73.9%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
||||| ||||| |||||
Db 33 GCTGAGTGTAGCATCATGATGGC 11

RESULT 33

US-09-657-472-693/c
; Sequence 693, Application US/09657472
; Patent No. 672063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-693

Query Match 52.8%; Score 13.2; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCA 24
||||| ||||| |||||
Db 21 AGCCTAGCACRTAGATGTCA 2

RESULT 34

US-09-647-563-17/c
; Sequence 17, Application US/09647563
; Patent No. 6706475
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America
; TITLE OF INVENTION: Oligonucleotide Probes for Detecting Enterobacteriaceae and Quinolones
; FILE REFERENCE: 6395-57017
; CURRENT APPLICATION NUMBER: US/09/647,563
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-647-563-17

Query Match 52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GCCTAGCAGATTCATGGC 23
||||| ||||| |||||
Db 25 GCCTAGTACGTTTCATGGC 8

RESULT 35

US-09-396-196G-104928/c
; Sequence 104928, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

```

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104928

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 GCCTAGCAGATTCATGGC 23
Db      25 GACCAGCAGCTTCATGGC 8

RESULT 36
US-09-396-196G-104929/c
; Sequence 104929, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-104929

Query Match      52.8%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 GCCTAGCAGATTCATGGC 23
Db      24 GACCAGCAGCTTCATGGC 7

RESULT 37
US-09-136-605-26
; Sequence 26, Application US/09136605A
; Patent No. 6140052
; GENERAL INFORMATION:
; APPLICANT: He, Tong-Chuan
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to
; FILE REFERENCE: 1107.75741
; CURRENT APPLICATION NUMBER: US/09/136,605A
; CURRENT FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 08/821,355
; EARLIER FILING DATE: 1997-03-20
; EARLIER APPLICATION NUMBER: 09/003,687
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Homo sapiens

```

GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Pharmaceutical Compositions for
TITLE OF INVENTION: Immunococontraception
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,158B
FILING DATE: 07-JUNE-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-92
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 32794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-484-158B-56

Query Match 52.8%; Score 13.2; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CTAGCAGATTCATGGCAC 25
|||||||
Db 5 CTAGCAGATCTATGGCGC 22

RESULT 40

US-08-484-596A-56
Sequence 56, Application US/08484596A
Patent No. 5981228
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunococontraception
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,596A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-484-596A-56
Query Match 52.8%; Score 13.2; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 8 CTAGCAGATTCATGGCAC 25
|||||||
Db 5 CTAGCAGATCTATGGCGC 22
Search completed: November 18, 2005, 11:22:03
Job time : 48.5741 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 18, 2005, 06:36:48 ; Search time 336.027 Seconds
(without alignments)
615.265 Million cell updates/sec

Title: US-10-788-779-10

Perfect score: 25

Sequence: 1 GCTGAGCCTAGCAGATTTCATGGCAC 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11093112

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

1: /cgn2_6/ptodata/1/pubpna/pct_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	US-08-469-172-10
2	25	100.0	25	20	US-10-788-779-10
c 3	16.8	67.2	25	26	US-11-036-317-506713
4	16.6	66.4	25	26	US-11-060-756-179689
5	16.2	64.8	25	24	US-10-719-956-625525

6	16.2	64.8	25	26	US-11-060-756-203326	Sequence 203326,
7	16.2	64.8	25	26	US-11-060-756-203327	Sequence 203327,
c 8	15.8	63.2	25	24	US-10-719-956-696370	Sequence 696370,
c 9	15.6	62.4	25	26	US-11-036-317-644145	Sequence 644145,
10	15.6	62.4	25	26	US-11-036-317-738392	Sequence 738392,
c 11	15.2	60.8	25	22	US-10-719-900-30711	Sequence 30711, A
c 12	15.2	60.8	25	22	US-10-719-900-841582	Sequence 841582,
c 13	15.2	60.8	25	22	US-10-956-157-161796	Sequence 161796,
c 14	15.2	60.8	25	24	US-10-719-956-320514	Sequence 320514,
c 15	15.2	60.8	25	24	US-10-719-956-460571	Sequence 460571,
c 16	15.2	60.8	25	24	US-10-719-956-625734	Sequence 625734,
c 17	15.2	60.8	25	26	US-11-036-317-506712	Sequence 506712,
c 18	15.2	60.8	25	26	US-11-036-317-743982	Sequence 743982,
c 19	15.2	60.8	25	26	US-11-060-756-185070	Sequence 185070,
c 20	15	60.0	25	22	US-10-719-900-81247	Sequence 81247, A
c 21	15	60.0	25	22	US-10-719-900-384887	Sequence 384887,
c 22	15	60.0	25	22	US-10-719-900-616192	Sequence 616192,
c 23	15	60.0	25	24	US-10-719-956-40306	Sequence 40306, A
c 24	15	60.0	25	24	US-10-719-956-513171	Sequence 513171,
c 25	15	60.0	25	26	US-11-036-317-567135	Sequence 567135,
c 26	15	60.0	50	18	US-10-131-827-1185	Sequence 1185, Ap
c 27	14.8	59.2	25	22	US-10-719-900-21139	Sequence 21139, A
c 28	14.8	59.2	25	22	US-10-719-900-853965	Sequence 853965,
c 29	14.8	59.2	25	24	US-10-719-956-369596	Sequence 369596,
c 30	14.6	58.4	25	20	US-10-623-500-10	Sequence 10, Appl
c 31	14.6	58.4	25	22	US-10-719-900-697665	Sequence 697665,
c 32	14.6	58.4	25	22	US-10-956-157-16200	Sequence 16200, A
c 33	14.6	58.4	25	22	US-10-956-157-16201	Sequence 16201, A
c 34	14.6	58.4	25	22	US-10-956-157-16202	Sequence 16202, A
c 35	14.6	58.4	25	22	US-10-956-157-16203	Sequence 16203, A
c 36	14.6	58.4	25	22	US-10-956-157-16206	Sequence 16206, A
c 37	14.6	58.4	25	24	US-10-719-956-625526	Sequence 625526, A
c 38	14.6	58.4	25	26	US-11-036-317-30872	Sequence 30872, A
c 39	14.6	58.4	25	26	US-11-036-317-435368	Sequence 435368,
c 40	14.6	58.4	29	26	US-11-036-317-482048	Sequence 482048,
c 41	14.6	58.4	29	22	US-10-754-071-24	Sequence 24, Appl
c 42	14.6	58.4	29	22	US-10-759-860-24	Sequence 394784,
c 43	14.4	57.6	25	22	US-10-719-900-906265	Sequence 906265,
c 44	14.4	57.6	25	24	US-10-719-956-643918	Sequence 643918,
c 45	14.4	57.6	25	24	US-10-719-956-643918	Sequence 643918,

ALIGNMENTS

RESULT 1
US-08-469-172-10
; Sequence 10, Application US/08469172
; Publication No. US200300543A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; APPLICANT: SEIDMAN, JOHN
; APPLICANT: WATKINS, HUGH
; APPLICANT: ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; TITLE OF INVENTION: DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE:
; CLASSIFICATION:

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-172-10

Query Match 100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 2
US-10-788-779-10
; Sequence 10, Application US/10788779
; Publication No. US2004015212A1
; GENERAL INFORMATION:
; APPLICANT: SEIDMAN, CHRISTINE
; SEIDMAN, JOHN
; WATKINS, HUGH
; ROSENZWEIG, ANTHONY
; TITLE OF INVENTION: A METHOD FOR DETECTING
; DISEASE-ASSOCIATED MUTATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, Suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/788,779
; FILING DATE: 27-Feb-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,172
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,160
; FILING DATE: 11-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HANLEY, ELIZABETH A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: GWL-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-788-779-10

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGCAC 25
Db 1 GCTGAGCCTAGCAGATTCATGGCAC 25

RESULT 3
US-11-036-317-506713/c
; Sequence 506713, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 506713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-506713

Query Match 67.2%; Score 16.8; DB 26; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGCCTAGCAGATTCATGGC 23
Db 22 GAGCCTAGTAGATTGATGGC 3

RESULT 4
US-11-060-756-179689
; Sequence 179689, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TARGET GENES
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-179689

Query Match 66.4%; Score 16.6; DB 26; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGGC 23
Db 3 GCGGAGCCTAGCAGACTCAGGCC 25
```

```
RESULT 5
US-10-719-956-625525
; Sequence 625525, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625525

Query Match      64.8%; Score 16.2; DB 24; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 2 GCTGAGCCAGCTGATGATG 22

RESULT 6
US-11-060-756-203326
; Sequence 203326, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203326
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203326

Query Match      64.8%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 4 GCGGAGCCTAGCAGACTCAGG 24

RESULT 7
US-11-060-756-203327
; Sequence 203327, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203327
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-203327

Query Match      64.8%; Score 16.2; DB 26; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| |||||
Db 4 GCGGAGCCTAGCAGACTCAGG 24

RESULT 8
US-10-719-956-696370/c
; Sequence 696370, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 696370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-696370

Query Match      63.2%; Score 15.8; DB 24; Length 25;
Best Local Similarity 89.5%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGAGCCTAGCAGATTCAT 20
   ||||| ||||| ||||| |||||
Db 23 CTGAGCCAGCAGATCAT 5

RESULT 9
US-11-036-317-644145/c
; Sequence 644145, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 644145
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-644145

Query Match      62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCTGAGCCTAGCAGATTCATGG 22
   ||||| ||||| ||||| |||||
Db 24 GCTGTGCCGCGCAGATCATGG 3
```

```
RESULT 10
US-11-036-317-738392
; Sequence 738392, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 738392
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-738392
Query Match 62.4%; Score 15.6; DB 26; Length 25;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GCTGAGCCTAGCAGATTCATGG 22
| | | | | | | | | | | | | | | | | | | | |
Db 4 GCTGTGACTAGAAGATCCATGG 25
| | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-719-900-30711/c
; Sequence 30711, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30711
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-30711
Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CTGAGCCTAGCAGATTCATG 21
| | | | | | | | | | | | | | | | |
Db 22 CTAAGGCTAGCAGAATCATG 3
| | | | | | | | | | | | | | | | |

RESULT 12
US-10-719-900-841582/c
; Sequence 841582, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 841582
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841582
Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CTGAGCCTAGCAGATTCATG 21
| | | | | | | | | | | | | | | | |
Db 25 CTAAGGCTAGCAGAATCATG 6
| | | | | | | | | | | | | | | | |

RESULT 13
US-10-956-157-161796
; Sequence 161796, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-161796
Query Match 60.8%; Score 15.2; DB 22; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 AGCCTAGCAGATTCATGGCA 24
| | | | | | | | | | | | | | | | |
Db 2 AGCCTGGCAGATGCTGGCA 21
| | | | | | | | | | | | | | | | |

RESULT 14
US-10-719-956-320514
; Sequence 320514, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320514
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-320514
Query Match 60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 6 GCCTAGCAGATTCATGGCAC 25
| | | | | | | | | | | | | | | | |
Db 1 GACCAGCAGATTCCTGGCAC 20
| | | | | | | | | | | | | | | | |
```



```
RESULT 15
US-10-719-956-460571/c
; Sequence 460571, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 460571
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-460571

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCCTAGCAGATTCATGGCAC 25
      |||||
Db      22 GCCTAGCAGAGCCTTGGCAC 3

RESULT 16
US-10-719-956-625734/c
; Sequence 625734, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625734
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625734

Query Match      60.8%; Score 15.2; DB 24; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 AGCCTAGCAGATTCATGGCA 24
      |||||
Db      23 AGCTTCTCAGATTCATGGCA 4

RESULT 17
US-10-719-956-506712/c
; Sequence 506712, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 506712
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-506712

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
      |||||
Db      22 GAGCCTAGTTGATTGATGGC 3

RESULT 18
US-11-036-317-743982
; Sequence 743982, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 743982
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-743982

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 TGAGCCTAGCAGATTCATGG 22
      |||||
Db      6 TTAGCCTAGCAGATGTATGG 25

RESULT 19
US-11-060-756-185070
; Sequence 185070, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 185070
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-185070

Query Match      60.8%; Score 15.2; DB 26; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GAGCCTAGCAGATTCATGGC 23
      |||||
Db      2 GAGCAGAGGAGATTCATGGC 21
```

```
RESULT 20
US-10-719-900-81247/c
; Sequence 81247, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81247
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-81247

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 CTGAGCCTAGCAGATTTCATGGCA 24
    ||||| ||||| ||||| |||||
Db  25 CTCAGCTTGGGAGATTCTTGCCA 3

RESULT 21
US-10-719-900-384887
; Sequence 384887, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 384887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-384887

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6 GCCTAGCAGATTTCAT 20
    ||||| ||||| |||||
Db  7 GCCTAGCAGATTTCAT 21

RESULT 22
US-10-719-900-616192
; Sequence 616192, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 616192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616192

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TGAGCCTAGCAGATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db  23 TGTGCTTGGCAGATTTCATCCAC 1
```

```
; SEQ ID NO 616192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-616192

Query Match          60.0%; Score 15; DB 22; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCTGAGCCTAGCAGATTTCATGGC 23
    ||||| ||||| ||||| |||||
Db  2 GCCGAGCATAGCAGTTTCTTGGC 24

RESULT 23
US-10-719-956-40306/c
; Sequence 40306, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 40306
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-40306

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCTGAGCCTAGCAGATTTCATGGC 23
    ||||| ||||| ||||| |||||
Db  25 GCTGAGCGCAGCCACATTTCATGGC 3

RESULT 24
US-10-719-956-513171/c
; Sequence 513171, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 513171
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-513171

Query Match          60.0%; Score 15; DB 24; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 TGAGCCTAGCAGATTTCATGGCAC 25
    ||||| ||||| ||||| |||||
Db  23 TGTGCTTGGCAGATTTCATCCAC 1
```

```
RESULT 25
US-11-036-317-567135/c
; Sequence 567135, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 567135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-567135

Query Match          60.0%; Score 15; DB 26; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTTCATGCG 23
   ||||| ||||| ||||| ||||| |||||
Db 25 GCTGAGCCTCGTAGATGCACTGC 3

RESULT 26
US-10-131-827-1185
; Sequence 1185, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1185
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1185

Query Match          60.0%; Score 15; DB 18; Length 50;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGAGCCTAGCAGATTTCATGCGCAC 25
   ||||| ||||| ||||| ||||| |||||
Db 14 TGAGCCGAGCAGTTTCAAGACAC 36

RESULT 27
US-10-719-900-21199/c
; Sequence 21199, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21199
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-21199

Query Match          59.2%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTTCATGG 22
   ||||| ||||| ||||| |||||
Db 24 AGCCTACCACATTCATGG 7

RESULT 28
US-10-719-900-853965
; Sequence 853965, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 853965
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-853965

Query Match          59.2%; Score 14.8; DB 22; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGAGCCTAGCAGATTTC 18
   ||||| ||||| ||||| |||||
Db 4 GCTGGCCTAGTAGATTTC 21

RESULT 29
US-10-719-956-369596/c
; Sequence 369596, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 369596
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-369596

Query Match          59.2%; Score 14.8; DB 24; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 7 CCTAGCAGATTCATGGCA 24
 Db 20 CCTAGGAGATTCATGACA 3

RESULT 30

US-10-623-500-10/c
 ; Sequence 10, Application US/10623500
 ; Publication No. US20040133945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer BioScience N.V.
 ; APPLICANT: Greet, Vanderkimpfen
 ; APPLICANT: Gerben, Van Eldik
 ; APPLICANT: Frank, Meulwaeter
 ; TITLE OF INVENTION: Corn root preferential promoters and uses thereof
 ; FILE REFERENCE: 021565-119
 ; CURRENT APPLICATION NUMBER: US/10/623,500
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 60/399383
 ; PRIOR FILING DATE: 2002-07-31
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide primer GVK30
 US-10-623-500-10

Query Match 58.4%; Score 14.6; DB 20; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAGCTAGCAGATTCATGGCA 24
 Db 23 GAGCATAGTCGATCATGGCA 3

RESULT 31

US-10-719-900-697665
 ; Sequence 697665, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 697665
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-697665

Query Match 58.4%; Score 14.6; DB 22; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGACCTGATCAGATTCATGGC 23
 Db 2 TGACCTGATCAGATTCATGGC 22

RESULT 32

US-10-956-157-16200/c
 ; Sequence 16200, Application US/10956157
 ; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 16200
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 US-10-956-157-16200

Query Match 58.4%; Score 14.6; DB 22; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
 Db 23 AGCCTCTCAGATTCATTGAAC 3

RESULT 33

US-10-956-157-16201/c
 ; Sequence 16201, Application US/10956157
 ; Publication No. US20050118625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 16201
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 US-10-956-157-16201

Query Match 58.4%; Score 14.6; DB 22; Length 25;
 Best Local Similarity 81.0%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AGCCTAGCAGATTCATGGCAC 25
 Db 24 AGCCTCTCAGATTCATTGAAC 4

RESULT 34

US-10-956-157-16202/c
 ; Sequence 16202, Application US/10956157
 ; Publication No. US20050118625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 16202
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 US-10-956-157-16202

```
Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 21 AGCCTCTCAGATTCATTGAAC 1

RESULT 35
US-10-956-157-16203/c
; Sequence 16203, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; CURRENT APPLICATION NUMBER: 031896-043000 (AM 101081)
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16203

Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 22 AGCCTCTCAGATTCATTGAAC 2

RESULT 36
US-10-956-157-16206/c
; Sequence 16206, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; CURRENT APPLICATION NUMBER: 031896-043000 (AM 101081)
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16206
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-16206

Query Match      58.4%; Score 14.6; DB 22; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
   ||||| ||||| ||||| ||||| |||||
DB 25 AGCCTCTCAGATTCATTGAAC 5

RESULT 37
US-10-719-956-625526
; Sequence 625526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-625526
```

```
Query Match      58.4%; Score 14.6; DB 24; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| ||||| |||||
DB 2 GCTGAGCCCGAGTGATGATG 22
   ||||| ||||| ||||| ||||| |||||
```

```
RESULT 38
US-11-036-317-30872
; Sequence 30872, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-30872
```

```
Query Match      58.4%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GCTGAGCCTAGCAGATTCATG 21
   ||||| ||||| ||||| ||||| |||||
DB 4 GCTGAGCCTGGAGTTTCCTG 24
   ||||| ||||| ||||| ||||| |||||
```

```
RESULT 39
US-11-036-317-435368
; Sequence 435368, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 435368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
```

US-11-036-317-435368

Query Match 58.4%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCTGAGCTAGCAGATTCATG 21
|||||
Db 4 GCTGAGCTGGGAGTTTCCTG 24

RESULT 40

US-11-036-317-482048/c
; Sequence 482048, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 482048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-482048

Query Match 58.4%; Score 14.6; DB 26; Length 25;
Best Local Similarity 81.0%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AGCCTAGCAGATTCATGGCAC 25
|||||
Db 24 AGCCTAGCCCGTTCATGTCAC 4

Search completed: November 18, 2005, 15:41:10
Job time : 336.027 secs